A COMPREHENSIVE ASSOCIATION STUDY OF APOLIPOPROTEIN *E-C1-C4-C2* GENE CLUSTER VARIATION WITH PLASMA LIPOPROTEIN TRAITS

by

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ABSTRACT

Apolipoproteins are major determinants of plasma lipoprotein-lipid distribution. Dyslipidemia with elevated level of low-density lipoprotein cholesterol (LDL-C) and decreased level of high-density lipoprotein cholesterol (HDL-C) is associated with increased risk of cardiovascular disease (CVD), which is a major public health problem worldwide. Therefore, unraveling the genetic basis of plasma lipoprotein-lipid traits would provide insight into risk prediction and contribute to the developing of new therapeutic and intervention measures to reduce the CVD burden, which has a public health importance. The objective of this study was to characterize genetic variation in the *APOE-C1-C4-C2* gene cluster on chromosome 19q13.32 by resequencing selected individuals from non-Hispanic White (NHW) and African Black populations with extreme lipid profile and then genotyping the identified sequence variants (common tagSNPs and rare variants) along with the HapMap tagSNPs covering the intergenic regions in the entire datasets (623 NHWs, and 788 Blacks) to evaluate their association with major lipid traits. Sequencing of the four apolipoprotein genes along with their hepatic control regions in subjects falling in the upper (47 NHWs, 48 Blacks), and lower (48 NHWs, 47 Blacks) 10^{th} percentile distribution of HDL-C/triglycerides (TG) revealed 230 variants (215 substitution, 15 indels), of which 63 were shared in both populations, 52 were NHW-specific and 115 were Black-specific. A total of 70 variants (65 sequencing-identified, 5 HapMap tagSNPs) in NHWs and 108 variants (103 sequencing-identified, 5 HapMap tagSNPs) in Blacks were successfully genotyped in the

entire datasets and were considered for the association analyses. Twenty variants in NHWs and twenty-four variants in Blacks (MAF>1%) showed nominally significant association (P<0.05) with at least one lipid trait. Although the major contribution of the *APOE-C1-C4-C2* gene cluster was on LDL-C and apolipoprotein (apo) B, we observed multiple associations with other lipid traits, including TG, HDL-C, and apoA1. In addition to the significant contribution of common variants, rare/less common variants showed significant association with lipid traits. Our findings confirm the significant contribution of *APOE-C1-C4-C2* genetic variation in affecting plasma lipid profile in the general population and consequently the CVD risk.

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PREFACE

I would like to express my deepest appreciation to my committee chair, Dr. Kamboh for giving me the opportunity to participate in this exciting project and for his endless effort in patient guidance, valuable suggestions, enthusiastic encouragements, useful critiques of this research work throughout my graduate studies. Also, I would like to extend my deepest appreciation to my Co-Advisor: Dr. Demirci. I could not find words to thank Dr, Demirci for her professional guidance, valuable support, informative advice and tremendous assistance in keeping my progress on schedule. Without their guidance, persistent help, technical and editorial advice, this dissertation would not have been possibly completed. I am also indebted to Dr. Barmada for his valuable and constructive suggestions during the planning and development of this research work. I would like to express my sincere gratitude to the other committee members; Dr. Barmada, and Dr.Bunker for the time they spend on reading previous drafts of this dissertation and providing many valuable comments and suggestions.

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1.0 IMPORTANCE AND SIGNIFICANCE

Cardiovascular disease (CVD) continues to be a leading cause of death worldwide (Ordovas and Shen, 2008), which makes CVD a public health burden, and determining individuals with high risk of developing CVD is a public health initiative. CVD is a complex disease in which multiple genetic and environmental factors modulate its risk (Ordovas and Shen, 2008). Hyperlipidemia with increased low-density lipoprotein cholesterol (LDL-C), and decreased high-density lipoprotein cholesterol (HDL-C) amplifies the risk of CVD (Kones, 2011). Although lipoprotein-lipids are complex quantitative traits in which multiple genetic and environmental factors influence their distribution pattern in the circulation, about 40-80% of their inter-individual variation is under genetic control (Beekman et al., 2003; Lusis et al., 2004).

Genome-wide association studies (GWAS), which are based on "Common Disease Common Variants" (CDCV) hypothesis, had accelerated success in identifying about 100 loci for plasma lipid traits (Teslovich et al., 2010). However, the identified variants from GWAS explain a small portion of lipid trait heritability (Weisglass-Volkov and Pajukanta, 2010). This indicates that CDCV hypothesis is not sufficient to explain the entire genetic basis of complex traits and emphasizes on the role of multiple rare variants with moderate to large effect sizes that may explain the remaining variance of lipid traits (Manolio, 2009; Schork et al., 2009; Johansen et al., 2010; Johansen and Hegele, 2012; Cohen et al., 2004; Cohen et al., 2005; Kotowski et al., 2006; Romeo et al., 2007; Pollin et al., 2008). Since the existing data support both CDCV and

"Common Disease-Rare Variants" (CDRV) hypotheses (Anderson et al., 2011), in this study we have integrated both hypotheses to investigate the potential effect of both rare and common genetic variation in biological candidate genes on plasma lipoprotein-lipid traits.

1.1 CARDIOVASCULAR DISEASE

Cardiovascular disease, the leading cause of morbidity and mortality worldwide, is a complex disease in which multiple genetic and environmental factors modulate its risk (Ordovas and Shen, 2008). Several CVD risk factors have been defined, including non-modifiable factors such as age, sex, and genetic background, and modifiable factors such as dyslipidemia, obesity, hypertension, and insulin resistance. Most of the CVD risk factors have genetic determinants and there is strong evidence that genes affect lipoproteins levels, blood pressure, diabetes, obesity, coagulation, immune system, and the vessel walls integrity and reactivity, all influence the CVD risk (Breslow, 2000).

Cardiovascular disease is a common disease and it is estimated that 1 in 3 subjects are affected with this CVD. Moreover, CVD is the leading cause of death in United States and it accounts for 36% of the total deaths (Rosamond et al., 2008; CDC, 2010). The annual direct and indirect health care cost of CVD is approximately $444 billion (CDC, 2010). Therefore, CVD is a major public health problem and lowering the prevalence of CVD is a public health challenge. CVD risk could be manageable in individuals with a high genetic risk through modulating their life style. Because of the inverse correlation between HDL-C and CVD risk (Kones, 2011), increasing HDL-C is the primary therapeutic target. Life style modification including, regular exercise, weight control, increased monosaturated fat intake, and smoking cessation, has been

recommended to be the primary intervention measures to treat patients with low HDL-C level (Gotto, 2001).

Atherosclerosis is the primary manifestation of CVD as a result of cholesterol accumulation on the arterial walls resulting in narrowing down the vascular vessels diameter and blockage the blood flow. Atherosclerosis is a complicated mechanism that involves multiple cellular types and biological processes. Under normal condition, cholesterol-containing lipoproteins such as, chylomicron remnants (CM), very low-density lipoprotein (VLDL), and LDL do not accumulate in the vascular endothelium cells. On the other hand, under abnormal condition of the lipid metabolism, cholesterol gets accumulated in the peripheral tissues and penetrated to the vascular endothelium cells. Once the cholesterol gets retained in the vascular sub endothelium cells, it gets oxidatively modified followed by triggering of the immune response and initiating of the atherosclerosis process (Williams and Tabas, 1995; 1998; von Eckardstein et al., 2001). Atherosclerosis process is depicted in **Figure 1**. Elevated level of the circulatory cholesterol promotes atherosclerosis development, which explains the positive established association between cholesterol and atherosclerosis (Tabas, 2002). The modified lipoproteins are responsible for foam cells formation and act as extracellular signals triggering immune system, and initiating the inflammatory process (Tabas, 2002). More strikingly, high-density lipoprotein (HDL) poses specialized functions including, reverse cholesterol transport (RCT) mechanism, antioxidant, anti-inflammatory, and anticoagulant factors making HDL an antiatherogenic agent.

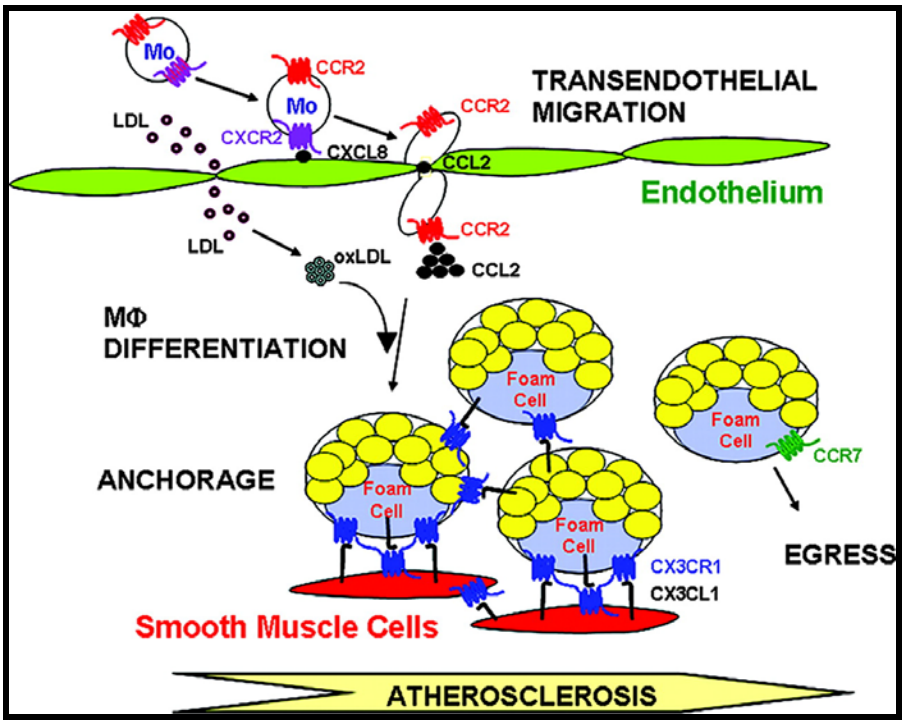

Figure 1. Atherosclerosis initiation process (adapted from Barlic and Murphy, 2007)

1.2 LIPID AND CARDIOVASCULAR DISEASE

Variation in plasma lipoprotein-lipid levels and their particle size are good indicators of CVD risk (Tian and Fu, 2010). It has been known for a while that LDL-C and HDL-C have opposite effects on CVD risk, whereas LDL-C has a positive effect and HDL-C has a negative influence on the CVD risk (Kones, 2011). It is estimated that 40% of patients with CVD have low HDL-C (Genest et al., 1992; Genest et al., 1993), and most of the CVD patients have multiple risk factor such as, high triglycerides (TG), obesity, diabetes militius (DM), hypertension along with low HDL-C (Dastani et al., 2006; Weber et al., 1997), implying that HDL-C may not be an independent risk factor of CVD. However, for each 1mg/dl increase in HDL-C, the CVD risk is

decreased by 2-3% (Chapman et al., 2004), indicating the protective effect of HDL-C on CVD. Additionally, it is found that increasing total cholesterol (TC) from 200 mg/dl to 240 mg/dl in men is associated with a three-fold increase in the mortality rate of CVD (Stamler et al., 2000), and the risk ratio of CVD is increased 1.3 in males and 1.8 in females for each 1 mmol/l increases in TG level (Austin et al, 1998). Thus, dyslipidemic profile with elevated TG, LDL-C, TC, and decreased HDL-C levels increases the risk of CVD (Austin et al., 1998; Castelli et al., 1992; Brunzell et al., 1984; Lusis, 2000).

The percentage of individuals with uncontrolled LDL-C level has been declined 9.3% between 1999 and 2010 in the United States because of the tremendous improvements in understanding the pathology of genetic diseases, access to health care, medical consultation and medications, and implementation of intervention measures (Fryar et al., 2012). More strikingly, the risk of coronary heart disease (CHD) differs among different ethnic groups in which Blacks tend to have more CHD than whites (Schiller et al., 2010), indicating the importance of different genetic architecture and environmental exposure on modulating the CHD risk.

1.3 LIPOPROTEIN AND LIPID METABOLISM

Lipoprotein particles are water-soluble macromolecules that play a key role in lipid transportation and distribution in the circulation (Ordovas, 2009). They are composed mainly of lipid and proteins and synthesized primarily in the liver and intestine (Ordovas, 2009). Lipoprotein particles composed of two layers with different constituents; inner hydrophobic core of cholesterol ester and triglycerides, and outer hydrophilic layer with a phospholipid, free cholesterol and apolipoproteins (Breslow, 2000). There are six classes of lipoprotein particles

with a different lipid and protein composition that influence their size, density, and function, including chylomicrons (CM), chylomicron remnants, very low density lipoprotein (VLDL), low density lipoprotein (LDL), intermediate density lipoprotein (IDL), and high density lipoprotein (HDL). Variation in the lipoprotein composition, size, shape and functions has different contribution to the CVD risk.

Lipid and lipoprotein metabolism (**Figure 2**) is a complex biological mechanism with multiple pathways that involve large number of nuclear factors, binding proteins, apolipoproteins, enzymes, and receptors (Ordovas, 2009). Broadly, three inter-related pathways; endogenous, exogenous and reverse cholesterol transport metabolism pathways are involved in lipid metabolism. The exogenous pathway accounts for dietary lipid metabolism. The dietary lipids are transferred in a TG-form and carried out in CM that is synthesized in the intestine. In the circulation, CM acquires apoE from HDL particle and under the lipoprotein lipase (LPL) action, TG is hydrolyzed into free fatty acids and glycerol. After TG hydrolysis, CM becomes CM remnants, which can be taken up by the liver through the remnants receptor. The free fatty acids transferred to the muscle cells to be used as energy source or to the adipose tissues for storage. Because of the effect of hepatic lipozymes, the CM remnants are hydrolyzed and their cholesterol is either excreted into bile or incorporated into endogenous lipoprotein synthesis (Ahmad et al., 2004).

Endogenous pathway involves lipoprotein synthesis of VLDL, which contains more fatty acids and little cholesterol, with apoB-100, apoCs, and apoE as primary apolipoproteins. In the circulation, VLDL acquires apoCs and apoE from HDL. ApoC-II mediates VLDL lipolysis under LPL action, and transfers VLDL into remnants (IDL). Then, VLDL remnants can be taken up by the liver through apoE-mediated endocytosis. Most VLDL remnants undergo further

lipolysis and forms LDL with apoB-100 as a primary apolipoprotein of LDL particle. Hepatic or extra-hepatic tissues can take up LDL-C through apoB-100 receptors (Ahmad et al., 2004). As a result of exogenous and endogenous lipid metabolism, cholesterol (mainly LDL-C) accumulates in the extra-hepatic tissues in which HDL plays important role in transporting cholesterol back to the liver. This mechanism is known as reverse cholesterol transport (RCT). ApoAs and apoE are the main apolipoprotein constituents of HDL particles (Ahmad et al., 2004).

Since lipid metabolism involves participation of multiple factors, genetic variation in their encoding genes can affect the efficiency of lipid metabolism and consequently the distribution of plasma lipoprotein-lipid levels.

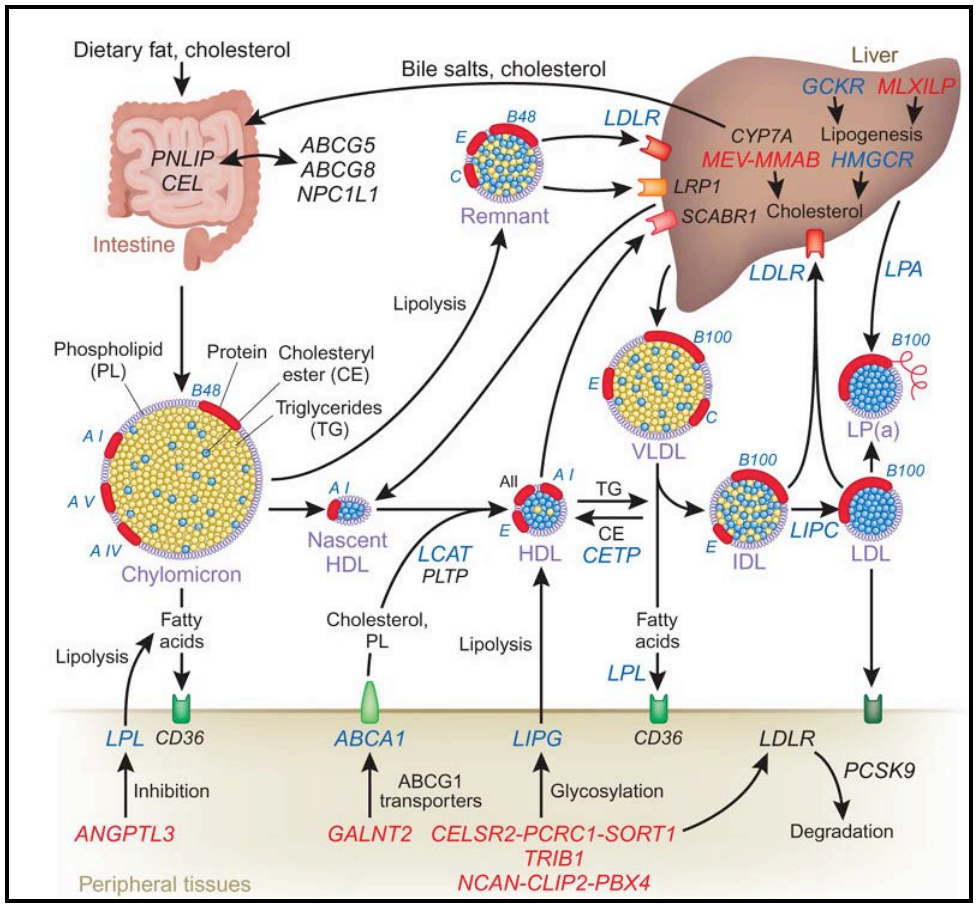

Figure 2. Lipoprotein metabolism
(adopted from: Lusis and Pajukanta, 2008)

1.3.1 High-density lipoprotein

High-density lipoprotein is a heterogeneous molecule with different sub-fractions having distinct composition, density, shape, size, and function (Rye et al., 2009). In general, HDL particles contain a cholesteryl ester and small amount of TG in the hydropobic core surrounded by a layer of phospholipid, free cholesterol and apolipoproteins (Rye et al., 2009; Florentin et al., 2008). ApoA-I and apoA-II are the primary HDL apolipoproteins. HDL molecule contains other minor apolipoproteins such as apoA-IV, apoC-I/C-II/C-III, apoD, apoE, apoJ, apoL, and apoM (Rye et al., 2009; de Silva et al., 1990; Duchateau et al., 1997; Christoffersen et al., 2006). Also, HDL contains enzymes involved in the lipid metabolism, including paraoxonase 1 (PON1), lecithin cholesterol acyltransferase (LCAT), cholesteryl ester transfer protein (CETP), and phospholipid transfer protein (PLTP) (Link et al, 2007).

1.3.1.1 High-density Lipoprotein metabolism

Complex interaction of several enzymes, lipids transfer molecules and apolipoproteins are involved in the cholesterol efflux and HDL maturation process. ATP binding cassette transporter (ABC) A1 [ABCA1] plays important role in cholesterol efflux mechanism, which is the initial step in HDL metabolism. Cholesterol efflux is mediated by interaction of apoA1 with ABCA1 on the cell membrane. ABCA1 transfers free cholesterol and phospholipids from atherogenic tissues to nascent HDL molecules. LCAT is a key component in the HDL maturation process, which esterifies free cholesterol into cholesterol ester that promotes discoidal HDL to be converted into spherical mature-HDL. HDL remodeling occurs in the plasma under influence of several enzymes, including CETP, hepatic lipase (HL), endothelial lipase (EL), and phospholipids transfer protein (PLTP) (Daniels et al., 2009; Fisher et al., 2012).

1.3.1.2 Antiatherogenic role of HDL-C

The HDL-C antiatherogenic properties come from its involvement in RCT (Kontush and Chapman, 2006; Von Eckardstein et al., 2001), and having antioxidant, anti-inflammatory (Kwan et al., 2007), and anti-aggregation (Myers et al., 1996) properties. RCT mechanism is an essential process and transports excess cholesterol from extra-hepatic tissues back to the liver for bile excretion or to steroidgenic tissues for apolipoprotein, vitamin D, and steroid hormone synthesis (Genest et al., 1999; Stein and Stein, 1999; von Eckardstein and Assmann, 2000). RCT mechanism is complex and can be accomplished through three ways; 1) the large HDL particle with multiple copies of apoE can be taken by the liver through LDL receptor (Bruce et al., 1998); 2) the accumulated cholesteryl ester can be taken selectively by the liver through SR-B1 (Acton et al., 1996; Fisher et al., 2012); 3) or the cholesteryl ester can be transferred from HDL to triglyceride-rich lipoproteins (TGRL) through CETP (Bruce et al., 1998; Fisher et al., 2012) to remove the excess cholesterol from peripheral tissues back to the liver.

1.3.2 Apolipoprotein structure and function

Apolipoproteins are major constituents of lipoprotein particles and play important role in lipid metabolism as enzyme cofactors, receptor ligands, and lipid transfer carriers (Cai et al., 2009). Apolipoproteins are composed of two functional domains; lipid-binding domain on the carboxyl terminal (-COOH) and lipoprotein receptor-binding domain on the amino terminal (-NH3). The lipid-binding domain has multiple α-helical structures with amphipathic feature to facilitate binding to lipid molecules (Segrest et al., 1974). There are several major classes of apolipoproteins and many other subclasses including, A (apoA-I, apoA-II, apoA-IV, and apoA-V), B (apoB-48, and apoB-100), C (apoC-I, apoC-II, apoC-III, and apoC-IV), apoD, apoE, apoH,

apoJ, apoL, and apoM (Cai et al., 2009; Rye et al., 2009, de Silva et al., 1990; Duchateau et al., 1997; Christoffersen et al., 2006).

ApoA-I is the primary apolipoprotein constituent of HDL followed by apoA-II and there is inverse correlation between plasma HDL-C and apoA-I concentration and CHD risk (Cai et al., 2009). ApoC2 is the major constituent of CM, VLDL, and HDL particles and has fundamental role in activating LPL enzyme (Cai et al., 2009). ApoB-48 is present on CM, while ApoB-100 is the major constituent of LDL. ApoC-III is present on VLDL that inhibits LPL and HL activity (Cai et al., 2009).

Human apoCs are major constituent of CM, VLDL and HDL and represent 40-80% of the apolipoprotein percentage on these lipoprotein particles (Jong et al., 1999; Tian et al., 2009). A little attention has been paid on the roles of apoCs in lipid metabolism as compared to apoE (Jong et al., 1999). Their encoding genes, *APOC1*, *APOC2*, *APOC4*, are located on chromosome 19 along with the *APOE* gene as a member of 45 kb gene cluster (Li et al., 1988). Apolipoprotein Cs play important role in TG metabolism and their concentrations in plasma are critical for optimal lipid metabolism (Jong et al., 1999).

1.3.3 *APOE-C1-C4-C2* gene cluster

APOE-C1-C4-C2 gene cluster encodes for four distinct amphipathic lipid-binding proteins that have significant involvement in lipid metabolism and share structural and sequencing properties (Allan et al., 1995; Lauer et al., 1988; Li et al., 1988). All genes in this gene cluster contain 4 exons and 3 introns, except *APOC4* contains 3 exons and 2 introns (Paik et al., 1985; Das et al., 1985). The protein products of *APOE-C1-C4-C2* genes are present predominantly on CM, VLDL and HDL (Tian et al., 2009; Jong et al., 1999), and are the major determinants of lipoproteins

fate and role in lipid metabolism. Thus, normal concentration of apolipoproteins in plasma is critical for optimal lipid metabolism (Jong et al., 1999). **Figure 3** represents the structure of *APOE-C1-C4-C2* gene cluster.

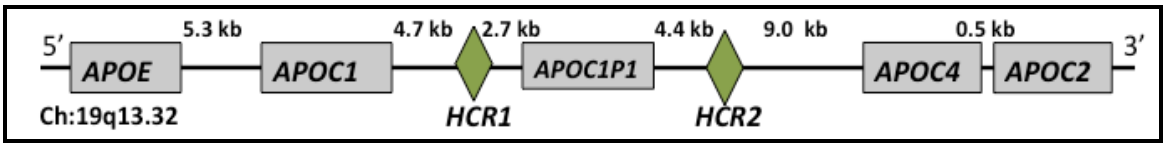

Figure 3. ***APOE-C1-C4-C2*** **gene cluster.**
APOE**: (apolipoprotein E);** ***APOC1*****: (apolipoprotein C-I);** ***HCR1*****: (hepatic control region 1);** ***APOC1P1*****: (apolipoprotein C1 pseudo gene);** ***HCR2*****: (hepatic control region 2);** ***APOC4*****: (apolipoprotein C4);** ***APOC2*****: (apolipoprotein C2).**

1.3.3.1 Apolipoprotein E

ApoE is a glycoprotein present predominantly on TG-rich lipoproteins (CM and VLDL) and HDL-C and has a pivotal role in lipid metabolism (Mahley et al., 1984; Mahley, 1988). The two key roles of apoE in lipid metabolism are participation in TG clearance and in RCT (Miettinen et al., 1992). Moreover, apoE has antioxidant activity and prevents LDL oxidation (Miyata and Smith, 1996). Besides its involvement in lipid metabolism, apoE is involved in multiple functions in the human body, including nerve growth and regeneration (Pitas et al., 1987; Boyles and Zoeliner, 1989; Westlye et al., 2012; Dumanis et al., 2013), cognitive function, immunoregulation, and influencing susceptibility to infectious disease (Mahely and Rall, 2000; Kuhlmann et al., 2010; Nikodemova et al., 2013). Because of the multiple functional roles of apoE in the human body, *APOE* genetic variation is associated with wide-range of diseases.

The *APOE* gene is 3.7 kb in size with 4 exons and 3 introns (Das et al., 1985). *APOE* is expressed in multiple tissues with the liver as a primary site followed by the brain (Pitas et al., 1987). In addition to the promoter region, multiple tissue-specific enhancers and regulatory

elements regulate its expression (Paik et al., 1985). The *APOE* gene is translated into 317 amino acids with the first 18 amino acids as a signal peptide (Tata et al., 1984). ApoE is composed of two main functional domains, an amino terminal domain that includes LDL receptor-binding site (22 kD fragment), and a carboxy terminal domain that has lipid-binding site (10 kD fragment) (Breslow, 1985). The LDL receptor-binding domain mapped to amino acid (1-183) (Wilson, 1990), while the lipid-binding domain mapped to amino acid (216-299) includes multiple amphipathic α-helical structure to facilitate lipid-binding mechanism (Breslow, 1985). Optimal plasma level of apoE is critical for normal physiological function, whereas apoE deficiency diminishes TG-rich lipoprotein clearance; apoE overexpression stimulates TG-rich lipoproteins production and inhibits their lipolysis and both states contribute to hypertriglyceridemia (Mahley et al., 2009).

A common polymorphism due to amino acid substitutions at codons 112 and 158 and resulting into three alleles, *APOE*2, APOE*3*, and *APOE*4*, exists in the *APOE* gene. ApoE3 is the most common form and has cystein at codon 112 and arginine at codon 158, while ApoE2 has cystein and ApoE4 has arginine at both codons. As a consequence of three alleles, six genotypes are present in the general population with three homozygous (E2/E2, E3/E3, E4/E4), and three heterozygous (E2/E3, E2/E4, E4/E3) (Beisiegel et al., 1989).

Cystein-Arginine interchange is associated with different lipid receptor-binding activity, affinity to lipoprotein particles, various serum lipid profile, and CVD risk (Davignon et al., 1988; Mahely and Rall, 2000). In comparison with the reference apoE3, apoE2 has a lower lipid receptor-binding efficiency. While apoE4 has similar receptor–binding efficiency, as does apoE3, apoE4-associated lipoproteins have high turnover. Consequently, apoE2 is associated with high TG and low LDL-C levels, while apoE4 is associated with low TG and high LDL-C

level. Therefore, *APOE*4* allele is a risk factor for CVD, while *APOE*2* is protective in absence of type III hyperlipoproteinemia (Sing and Davignon, 1985: Davignon et al., 1988; Mahely and Rall, 2000; Medina-Urrutia et al., 2004).

1.3.3.2 Apolipoprotein C-I

ApoC-I is constituent of various lipoprotein particles (VLDL, IDL, and HDL) and has multiple roles in lipid metabolism, including maintaining HDL structure regulating LCAT activity (Weisgraber et al., 1990), and displacing apoE from lipoproteins and interfering with their hepatic clearance (Windler et al., 1980; Quarfordt et al., 1982). Although the contribution of apoC-I in TG metabolism is not clear, it is hypothesized that apoC-I displaces apoE on TG-rich lipoproteins (TGRL) and interferes with apoE-mediated binding to LDL receptor (LDL-R) and LDL receptor related protein1 (LRP1) (Weisgraber et al., 1990). *APOC1* transgenic mice developed hyperlipidemia with increased TG and TC levels (Jong et al., 1998; Shachter et al., 1996; Simonet et al., 1991), confirming the apoC-I inhibition role of TGRL clearance (Jong et al., 1999). In addition to the interference with hepatic uptake of TGRL, apoC-I inhibits the lipolytic function of LPL (Conde-Knape et al., 2002). In vitro studies have confirmed the apoC-I involvement in HDL metabolism through activating LCAT (Soutar et al., 1975; Jonas et al., 1984; de Haan et al., 2008), and inhibiting CETP activities (Gautier et al., 2000; de Haan et al., 2008).

APOC1 is a 4.7 kb long gene, with 4 exons, and 3 introns, expressed mainly in the liver and to a lesser extent in other tissues such as lung, testis, skin, and spleen (Lauer et al., 1988). It is located either 4.3 kb (Myklebost and Rogne, 1986) or 5.3 kb (Lauer et al., 1988) downstream from *APOE*. Another copy of *APOC1* is located 7.5 kb downstream of *APOC1* (Lauer et al., 1988) with no protein product and is called as *APOC1* pseudo gene (*APOC1P1*). *APOC1* gene

encodes for 83 amino acids long protein containing 26 residues as a signal peptide (Knott et al., 1984). ApoC-I has three amphipathic helical structures mapped to residue (7-14), (18-29), and (33-53) that facilitate lipid binding process (Segrest et al., 1974) and residues 17-57 contain all the functional domains to activate LCAT enzyme (Soutar et al., 1975).

Several genetic variations in the *APOC1* gene have showed significant association with plasma lipid variation. A 4-base insertion at -317 bp of the transcription initiation site (known as *Hpal* polymorphism) is the most common polymorphism in *APOC1* promoter region (Smit et al., 1988) and it has been shown to be associated with increased *APOC1* gene expression (Xu et al., 1999). Although several single-nucleotide polymorphisms (SNPs) have identified in genome-wide association studies (GWAS) are mapped to *APOC1* gene, their functional roles have yet to be characterized.

1.3.3.3 Apolipoprotein C-IV

The *APOC4* gene spans 3.3 kb, composed of three exons and two introns, and encodes for a 127 amino acid protein with the first 26 residues as a signal peptide (Allan et al., 1995). The first exon encodes most of the signal peptides, while the remaining exons encode the C-terminal region and each has amphipathic helical structure (lipid-binding domain) (Zhang et al., 1996). Exon 1 encodes for amino acid 1-25, exon 2 encodes for amino acid 26-73 and exon 3 encodes for the remaining amino acid (Kotite et al., 2003). *APOC4* is expressed only in the liver with undetectable level in the plasma and its expression level is 100-fold lower than the *APOC2* expression level (Allan et al., 1995). Lacking the typical TATA box in *APOC4* promoter region, having weak Sp1 Motif (Allan et al., 1995) and only one copy of purine-rich region (Kotite et al., 2003), explain the lower expression level of *APOC4* in humans.

In normotriglyceridemic condition, more than 80% of apoC-IV is present on VLDL (representing 0.7% of apo VLDL) and most of the remainder is on HDL, while apoC-I and apoC-II distribute equally to both HDL and VLDL (Kashyap et al., 1977; Schonfeld et al., 1979). Overexpression of *APOC4* in transgenic mice causes hypertrigylceridemia, which suggests a direct association between apoC-IV and TG metabolism (Allan and Taylor, 1996). The similar hypertrigylceridemic phenotype of expression all apoCs suggests that all human apoCs have a common underlying mechanism in TG metabolism (Allan and Taylor, 1996).

There are two assumptions behind accumulation of TG-rich lipoprotein (VLDL) in *APOC4* transgenic mice: 1) impairing hepatic uptake of VLDL through interfering with apoE mediated cellular uptake, and 2) impairing the TG lipolysis mechanism through interfering with LPL or HL activity (Allan and Taylor, 1996). Additional evidence from in vitro study suggests the potential role of apoC-IV in lipid metabolism and atherosclerosis. Expression of *APOE-C1-C4-C2* gene cluster in lipid-loaded macrophages, suggests their potential antiatherogenic role in cholesterol efflux in a similar manner to the RCT mechanism (Mak et al., 2002).

1.3.3.3 Apolipoprotein C-II

ApoC-II is the major constituent of VLDL, and HDL particles and this is a required cofactor for LPL (Cai et al., 2009; Bier and Havel, 1970; LaRosa et al., 1970). ApoC-II is synthesized with 22-residue signal peptide that is cleaved cotranslationally and resulting a 79 amino acid mature protein with a molecular mass of 8.8 kDs (Fojo et al., 1984). Its encoding gene, *APOC2* is a 3.4 kb long and includes 4 exons and 3 introns (Das et al., 1987; Wei et al., 1985; Fojo et al., 1987).

Several mutations have been found in either *APOC2* or *LPL* that cause indistinguishable phenotype of hypertriglycerdemia (Brunzell, 1995). ApoC-II protein is composed of three helical regions spanning amino acid 16-36, 50-56, and 63-77. LPL activating region has been localized

to the C-terminal region (44-79), while the N-terminal region (1-43) is involved in phospholipid binding (Sparrow and Gotto, 1980; Vainio et al., 1983; MacPhee et al., 1999). It is proposed that binding of apoC-II to LPL enzyme causes conformational changes in LPL, which makes LPL more efficient in lipolytic activity (Bengtsson and Olivecrona, 1982).

Previous studies have shown quantitative variation in apoC-II either low (Brechinridge et al., 1978) or high (Shachter et al., 1994) apoC-II level impairs TG lypolysis activity and results in hypertriglycerdemic phenotype. Moreover, quantitative variation of apoC-II affects the distribution of HDL subfractions and overexpression of apoC-II disrupts HDL maturation process and impairs the RCT mechanism (Tian et al., 2009). Mutations in *APOC2* leads to familial I hyperlipoprotienemia, which is characterized with extremely severe hypertriglycerdemia due to accumulation of CM (Brunzell et al., 1989). Several mutations in *APOC2* have been identified in different families causing familial chylomicronemia and hyperlipidemia (Jong et al., 1999). Therefore, *APOC2* genetic variation affects the distribution of all lipoprotein lipid levels and affects the RCT efficiency.

1.3.4 Regulation expression of the *APOE-C1-C4-C2* gene cluster

The expression of all four genes in the *APOE-C1-C4-C2* gene cluster is regulated by the action of two hepatic control regions (*HCR-1* and *HCR-2*). The first control region (*HCR-I*) is 774 bp long and is located 19 kb downstream of the *APOE* transcription initiation site and 9 kb downstream of the *APOC1* promoter region (Simonet et al., 1993). Additional copy of the hepatic control region (*HCR-2*) in the same cluster is located 5.5 kb downstream of the *APOC1P1* pseudo gene and shares an 85% homology with the functional domain (319 bp) of the first hepatic control region (*HCR-I*) (Allan et al., 1995), which has the full activity of regulating

APOE-C1-C4-C2 gene cluster expression (Shachter et al., 1993). The unique functional domain in *HCR-1* is mapped to the sequence 6-325 bp at the 5' end and it is associated with prominent liver specific Dnase 1 hypersenstivity (Dang et a., 1995).

It has been shown that the presence of at least one of the hepatic control regions is sufficient for expression all the four genes within the cluster. If both are present, *HCR-1* regulates the expression of its nearby genes, *APOE* and *APOCI*, while *HCR-2* regulates the expression of the farther genes, *APOC4* and *APOC2* (Allan et al., 1997).

However, regulating the expression of all four genes in the same cluster is complicated, and requires an interaction between tissue specific regulatory elements and enhancer sequences in the promoter region to direct the hepatic expression of *APOE* gene cluster (Dang et al., 1995). Accordingly, the promoters of *APOE*, *APOC1*, *APOC4*, and *APOC2* genes are not sufficient for their full hepatic expression (Allan et al., 1997; Simonet et al., 1993) and additional cis-acting tissue specific elements could regulate their hepatic and extra-hepatic expression. The first hepatic control region has an advantage over the second one of regulating the expression of all the four genes in extra hepatic tissues in addition to the hepatic tissues (Allan et al., 1997). The proximity of *HCR-1* to *APOE* and *APOC1* genes makes their expression level in non-hepatic tissue higher than the expression level of the other two genes, *APOC2* and *APOC4* (Allan et al., 1997).

The high degree of homology between the two hepatic control regions suggests that *HCR-2* has been arisen from a duplication event occurred in primate lineage similar to what happened to *APOC1P1* pseudo gene (Allan et al., 1995). Since no enhancer elements have been found within the upstream 30 kb of *APOE* gene (Simonet et al., 1993), and similarly no enhancer elements have been found within the 3 kb downstream of *APOC2* gene (Allan et al., 1997),

suggesting that *HCR-1* and *HCR-2* are the only regulatory regions in 80 kb genomic cluster regulating the hepatic expression of all four genes in this cluster (Allan et al., 1995).

1.4 GENETIC EVIDENCE OF LIPOPROTEIN-LIPID TRAITS

Lipoprotein-lipid traits have considerable genetic determination and their estimated heritability ranges between 40% and 80% (Wang and Paigen, 2005; Goode et al., 2007; Kronenberg al., 2002; Lusis et al., 2004; Beekman et al., 2003). Family-based linkage studies are more powerful in localization disease-causing mutations in monogenic disorders than in complex diseases. Mutations in *ABCA1*, *APOA1* and *LCAT* genes have been identified to be associated with hypoalphalipoproteinemia characterized with extremely low HDL-C, while mutations in *CETP* were associated with familial hyperalphalipoproteinemia (FHA) characterized with extremely high HDL-C (Miller et al., 2003). Although monogenic disorders causing low or high HDL-C, are rare and explain ~1% of the HDL-C variation in the general population (Strong and Rader, 2010; Miller and Zhan, 2004), they highlight the importance of genetic factors in affecting HDL-C and other lipid levels. A meta-analysis of genome-wide linkage studies of lipid traits had identified a linkage signal on chromosome 19q13.13-13.45 including the *APOE-C1-C4-C2* gene locus (19q13.32) (Beekman et al., 2003; Malhotra et al., 2007).

Genome-wide association studies (GWAS) had accelerated success in identifying ~100 loci associated with lipid traits, including the *APOE-C1-C4-C2* gene cluster (Teslovich et al., 2010). However, the identified common variation explains 25-30% of the genetic variance of each major lipid trait (LDL-C, HDL-C and TG) (Teslovich et al., 2010; Kathiresan et al., 2009; Weisglass-Volkov and Pajukanta, 2010).

APOE is the most frequently studied candidate gene and the influence of its common polymorphisms on lipid traits and CVD risk has been extensively investigated in different population groups (Bennet et al., 2007). Although the association of *APOE* polymorphisms with lipid traits is well established (Sing and Davignon, 1985; Davignon et al., 1988; Bennet et al., 2007), the contribution of other genes genetic variation on lipid traits and CVD risk remains uncertain.

Since common variants with small effect size explain ~25-30% of the lipid variation, additional common and rare variants in candidate genes could explain additional variation in plasma lipid levels. It has been shown that multiple rare and common variants interact with each other and modulate the risk of complex diseases (Anderson et al., 2011; Visscher et al., 2012). Therefore, sequencing candidate genes would provide insight into the role of common and rare variants in affecting plasma lipid variation.

1.5 HYPOTHESIS AND SPECIFIC AIMS

1.5.1 Hypothesis

Genetics plays an important role in influencing plasma lipid levels and more than 50% of lipid variation is believed to be genetically determined. Although lipid GWAS have identified ~100 loci, they explain only 25-30% of the plasma lipid variation. This emphasizes that in addition to common variation, multiple rare/uncommon variants with larger effect sizes may be responsible for part of the missing heritability of lipid traits. Genetic studies carried out on some lipid genes have confirmed the significant contribution of both common and rare variants in modulating lipid traits. Therefore, the objective of this study was to test both "common disease-common variant" (CDCV) and "common disease-rare variant" (CDRV) hypotheses by resequencing the *APOE-APOC1-APOC4-APOC2* gene cluster in selected individuals with extreme HDL-C/TG levels from two racial groups. **Figure 4** illustrates the study design and the objective of this study was fulfilled by carrying out the following aims:

1.5.2 Specific Aims

Aim 1:

Resequence the four apolipoprotein genes (*APOE, APOC1, APOC4,* and *APOC2)* and their two hepatic control regions *(HCR-1 and HCR-2)* in selected individuals falling in the upper (47 NHWs and 48 Blacks), and lower (48 NHWs and 47 Blacks) 10^{th} percentile distribution of HDL-C/TG to identify additional common (MAF≥5%) and potential rare variants (MAF<5%) that may affect plasma lipid levels.

Aim 2:

Screen the entire population samples of NHWs (n=623) and Blacks (n=788) for common tagSNPs and rare variants identified in Aim 1 plus HapMap tagSNPs covering the intergenic regions, that are not covered by the sequencing effort, to examine their association with plasma lipid traits.

Aim 3:

Evaluate the single and cumulative (haplotypes) effects of common variants on major plasma lipoprotein-lipid traits (LDL-C, HDL-C, TC, TG, apoB, and apoA1) to test the "common disease-common variant" hypothesis.

Aim 4:

Evaluate the cumulative effect of rare variants on major plasma lipoprotein-lipid levels (LDL-C, HDL-C, TC, TG, apoB, and apoA1) using Sequencing Kernel Association Test-Optimal (SKAT-O) approach to test the "common disease-rare variant" hypothesis.

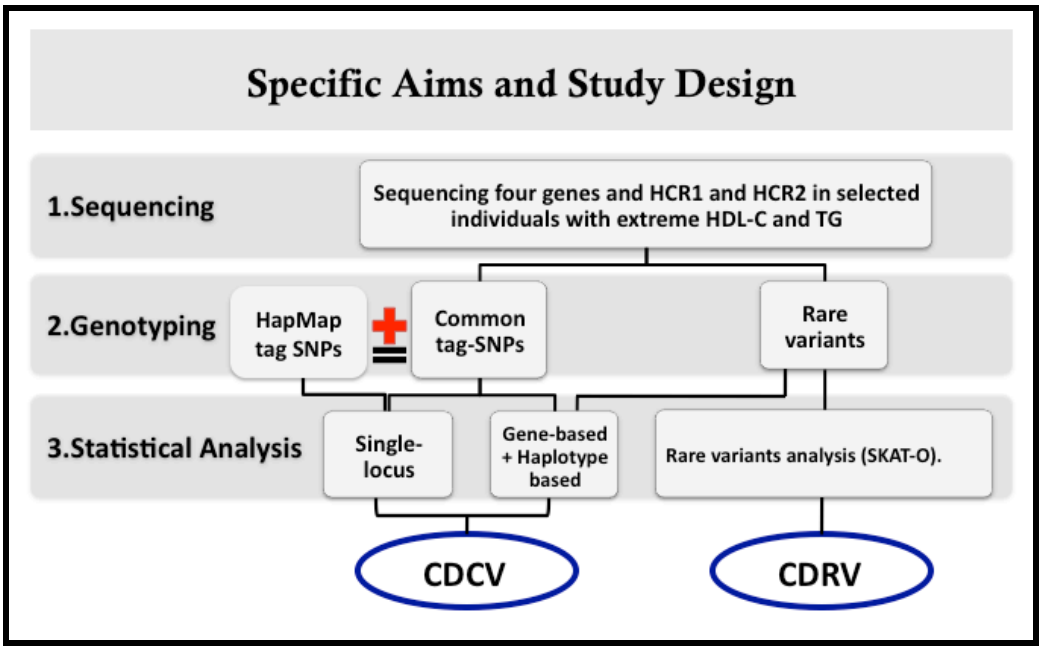

Figure 4. Flow chart of study design

2.0 METHODS AND MATERIALS

2.1 SUBJECTS

2.1.1 Study Population

The study was conducted on two well-characterized epidemiological samples, including 623 non-Hispanic whites (NHWs) and 788 African Blacks. NHW samples were collected as part of San Luis valley Diabetes Study (SLVDS). SLVDS was established as a geographical based case-control study of non-insulin dependant diabetes mellitus and cardiovascular disease in Alamosa and Conejos counties of south Colorado (Hamman et al., 1989). All NHWs used in this study were non-diabetics and the basic characteristic of this study are described elsewhere (Rewers et al., 1993; Hamman et al., 1989; Demirci et al., 2010). African Blacks were recruited from Benin City, Nigeria as part of study on CHD risk factors in Blacks and the study details have been described in Bunker et al. (1995, 1996). The demographic characteristics of both populations are summarized in **Table 1**.

Table 1. Demographic characteristic of study populations

Variable	NHWs (n=623)	African Blacks (n=788)
Males/Females (n)	295/328	495/293
Age (Yrs)	52.83 ± 0.46	40.95 ± 0.30
BMI (kg/m^2)	25.5 ± 4.1	22.87 ± 0.14
LDL-C (mg/dl) *	137.8 ± 1.51	109.25 ± 1.23
HDL-C (mg/dl) *	50.76 ± 0.57	47.88 ± 0.46
Triglycerides (mg/dl)*	139.45 ± 2.79	72.96 ± 1.40
Total cholesterol (mg/dl)*	216.11 ± 1.67	172.01 ± 1.37
ApoB (mg/dl) **	87.72 ± 1.16	66.98 ± 0.79
ApoA1(mg/dl)**	149.62 ± 1.59	137.03 ± 1.01

Data are unanadjusted means ± SE after outliers removal.
(*) the four lipid traits values were measured in the entire datasets.
(**) ApoB and ApoA1 were measured in subset of the samples (435 NHWs).
BMI: body mass index; LDL-C: low-density lipoprotein cholesterol; HDL-C: high-density lipoprotein cholesterol; ApoB; apolipoprotein B; ApoA1: apolipoprotein A1.

In NHWs, total cholesterol was measured using esterase-oxidase method (Richmond, 1973), HDL-C level was determined enzymatically following dextran sulfate magnesium precipitation (Wamick et al., 1982), and TG level was determined enzymatically by using Stavropoulous and Crouch procedure (Stavropoulous and Crouch, 1974). In Blacks, total cholesterol, HDL-C, and TG measurements were done at Heinz Nutrition laboratory, University of Pittsburgh, which is standardized for lipid measurement with US-Center for disease control and prevention (CDC), Atlanta, GA (Kamboh et al., 1999). LDL-C was estimated using Friedewald equation (Friedewald et al., 1972) when TG level was less than 400 mg/dl. ApoB and apoA1 were measured in subsets of the samples (435 NHWs, and 766 Blacks) using Boehringer Manneheim turbidmetric procedures (Kamboh et al., 1997). The DNA used for sequencing and TaqMan genotyping was extracted from clot sample in Blacks and from Buffy coats in NHWs using standard DNA extraction procedures.

2.1.2 Resequencing Samples

Ninety-five NHWs (47 individuals having high HDL-C/low TG and 48 having low HDL-C/high TG) and 95 African Blacks (48 individuals having high HDL-C/low TG and 47 having low HDL-C/high TG) were selected for resequencing the *APOE-APOC1-APOC4-APOC2* gene cluster and their hepatic control regions (*HCR-1*, and *HCR-2*) to detect both rare and common variants. The characteristics of subjects selected for resequencing are summarized in **Table 2**.

Table 2. Characteristics of the resequencing samples in NHWS and African Blacks

	NHWs (n=95)			African Blacks (n=95)		
	High HDL-C/low TG (n=47)	Low HDL–C/high TG (n=48)	p-value	High HDL-C/low TG (n=48)	Low HDL-C/high TG (n=47)	p-value
Sex (M/F)	24/23	24/24	1	24/24	23/24	1
Age (years)	55.45 ± 1.0	53.03 ± 1.08	0.25	41.29 ± 0.89	40.87 ± 0.73	0.80
BMI (kg/m2)	23.17 ± 0.32	27.35 ± 0.40	1.2E-07	22.06 ± 0.48	23.91 ± 0.56	0.08
TC (mg/dl)	22.734 ± 5.31	208.81± 4.58	0.07	201 ± 4.08	141.68 ± 3.18	2.4E-12
LDL-C(mg/dl)	126.84 ± 4.82	125.54 ± 5.64	0.90	112.55 ± 4.08	95.04 ± 2.9	0.02
HDL-C (mg/dl)	77.68 ± 1.36	31.81 ± 0.44	2.2E-16	76.05 ± 0.77	25.51 ± 0.58	2.2E-16
TG (mg/dl)	114.09 ± 6.25	240.21 ± 15.73	1.7E-06	61.98 ± 2.03	95.79 ± 7.51	0.004
ApoB(mg/dl)*	87.88 ± 2.61	89.61± 2.58	0.80	66.00 ± 2.07	69.64 ± 2.20	0.40
ApoA1(mg/dl)	174.08 ± 3.57	130.20 ± 2.78	1.4E-06	166.04 ± 2.89	103.84 ± 2.79	2.2E-16

Variables are presented in unadjusted mean ± SE.
***ApoB and apoA1 were measured in part of the NHWs (n=29).**

2.2 PCR AMPLIFICATION AND SEQUENCING

All four genes (*APOE, APOC1, APOC4, APOC2)* and their two hepatic control regions (*HCR-1*, and *HCR-2*), which represents 49% of the entire nucleotide sequence of this gene cluster (~22.2 kb of the total 45 kb sequence) were sequenced in 190 individuals with extreme HDL-C and TG levels from two ethnic groups (NHWs and African Blacks) using Sanger sequencing technique on the amplified DNA. DNA amplification of the target genomic regions was conducted in our lab using either M13 tagged forward and reverse primers that publicly available in SeattleSNPs

database (http://pga.mbt.washington.edu/) or designed primers using Primer3 software version 0.4 (http://frodo.wi.mit.edu/primer3/) for the complicated regions or expansion the amplified genomic regions.

We used seattleSNPs reference sequences for *APOE*, *APOC1*, *APOC4*, and *APOC2* and NCBI database (build 137) to locate *HCR-1* and *HCR-2* reference sequences according to Allan et al. (1995) and Dang et al. (1995). For some genes with insufficient coverage in either flanking regions, additional sequences were adopted from Chip bioinformatics database to extend the sequencing coverage in either 5' or 3' flanking region. The sequencing PCR primers are given in **Table 3**.

PCR primers generated 9, 13, 8 and 12 overlapping fragments for the amplification of the *APOE*, *APOC1*, *APOC4*, and *APOC2* gene sequences, respectively. We amplified 5.491 bp of *APOE* (1,180 bp of exons, 2,432 bp of introns, 1,034 bp in 5' flanking and 845 bp in 3' flanking region), 6,687 bp of *APOC1* (1,000 bp in 5' flanking region, 4,225 bp of introns, 462 bp of exons, and 1,000 bp in 3' flanking region), 5,086 bp of *APOC4* (956 bp in 5'flanking region, 614 bp of exons, 2,644 bp of introns, and 872 bp in 3'flanking region), and 6,438 bp of *APOC2* (1,400 bp in the 5' flanking region, 2855 bp of introns, 721 bp of exons, and 1,461 bp in the 3' flanking region). We sequenced 820 bp genomic region of *HCR-1* (ch19: 45427374 - ch19: 45428194) and 849 bp genomic region of *HCR-2* (ch19: 45438997- ch19: 45439846).

Both forward and reverse strands were sequenced for all the targeted sequencing genes. The PCR conditions are given in **Table 4**. The PCR conditions were optimized first at small scale before amplifying DNA from 190 individuals in 96-well plates. Necessary modifications to the standard PCR conditions were made for complicated regions either by changing the

annealing temperature, $MgCl_2$ concentration, or adding DMSO for the GC-rich regions. The quality of PCR was evaluated on agarose gel electrophoresis.

Table 3. PCR primers list of the sequenced regions

***APOE* Gene**			
Amplicon	**Amplified Region**	**Forward Primer Sequence (5'-3')**	**Reverse Primer Sequence (3'-5')**
SEQ-01	34-855	CTTGATGCTCAGAGAGGACAAG	GGCATAGAGGTCTTTTGACCA
SEQ-02	790-1515	GGTCAGGAAAGGAGGACTCT	GTCCCAGTCTCGCATTCCTC
SEQ-03	1445-2053	GGCAGCGACACGGTAGCTAG	AACCGAGGCCCAGAGAGCGT
SEQ-04	1930-2880	GTTGCTGGTCACATTCCTGG	GAGTCGGTTTAATCACTTG
SEQ-05	2560-3194	AGCCCTGCCTGGGGCACAC	GGACACTCACCTCAGTTCCT
SEQ-06	3100-3795	GAGTGGCAGAGCGGCCAGCG	CCTTCAACTCCTTCATGGTCTC
SEQ_07	3625-4360	CTAGCTCCTTCTTCGTCTCTG	GCTCGAACCAGCTCTTGAGG
SEQ-08	4250-4780	GCCAGCCGCTACAGGAGCG	CCAGCTACTGAGGCAGCAG
SEQ-09	4775-5430	GTGTGTATCTTTCTCTCTGCC	GGCAGGCCGCTCGGAGCCCAT
***APOC1* Gene**			
Amplicon	**Amplified Region**	**Forward Primer Sequence (5'-3')**	**Reverse Primer Sequence (3'-5')**
1**	380-947	CCAATTTCTGCCTCCAAAGA	GGGCAGGTTGATGTTGATCT
SEQ-01	845-1610	TCAGGAAGATTGAGAGGTGAGAG	GGAGGAATACTGGAGTGACCTG
2**	1480-1950	AGGTTCTCCCAGGCTCAGTC	ATTGGAACCCCCTTAGGTTG
SEQ-02	2025-2325	ATCTGCGCAGGAGAGCACTAGCA	GATGGGCAGGGGTTCAAAATTTG
3**	1960-2400	GCCATTCCTCCCCATTCTAA	GGCATGATCTCGGCCTAC
SQ-Sgap**	2025-2600	CTCTATCCATCCCGGTATCC	GCATCTTGGCAGAAAGTTCA
SEQ-03	2545-3150	ATTTTGAACCCCTGCCCATCTTC	TTACCTCACAAAACCATCTTTTT
5**	2815-3200	CAAGTCCTGGAGAGGCTGAC	GAGACAGGATCTCGCCATGT
6**	2976-3435	GGCTGATTGCCTGAGGTC	CCTGTAGGCCTGCTCCTTTA
SEQ-04	3915-3944	AAGATGGTTTTGTGAGGTAATGA	ATCTCTTGCTACCAATGCCTTCC
7**	3435-3850	CTGGAGTAGCACCCCTTCCT	GAATGCAGTGGCACAAACAT
SEQ-05	4975-5650	AGGCATTGGTAGCAAGAGATGGC	CTGGAAGCCCCTACCCTCTCCC
SQ-LAST**	5600-6260	GAGGACCTGAAGGGTGACAT	GATTGCTTAAGCCCAGGAGT
HCR-1			
Amplicon	**Amplified Region**	**Forward Primer Sequence (5'-3')**	**Reverse Primer Sequence (3'-5')**
SQ-1**	18-838	GAGGGGCTAGAGACACCAGA	AGGCTGAGGCTGACCAACAT
HCR-2			
Amplicon	**Amplified Region**	**Forward Primer Sequence (5'-3')**	**Reverse Primer Sequence (3'-5')**
SQ-1**	22-871	CCAGAAGATTAGCAGGGAGGA	GGTGGATCACAAGGTCAAGAG
APOC4			
Amplicon	**Amplified Region**	**Forward Primer Sequence (5'-3')**	**Reverse Primer Sequence (3'-5')**
SEQ-01	25-655	GAGACGGAGTCTTGCTCTTTCGC	TCAGTTTCCTCCTCCATAAAGTG
SEQ-02	489-1245	ATTACAGGCACGCATCACTACTT	CACACAGATGATCCCAGTTTGTA
SEQ-03	1108-1842	GTGAGAAGAAGTGGGTGGAGG	GTCAGGATATGGAGACCATCCTG

Cont. Table 3

SEQ-LAST**	1869-2147	CCAGGATGGTCTCCATATCC	GTGCCTGGCCCTGTATTAAA
SEQ-05	2165-2928	ATTCTAGATCAGCATTATCCAGTA	TCTTCACCTTGTGTCAGTAGTCC
SEQ-06	2819-3755	GTCCACAGAGGTAGCTCAGACAG	GCTCCTCTCTGTGACCTAGGAGT
SEQ-07	3537-4462	AAAGCTAAAGATGAGTCGCTGG	GGAGTCAGAGCTTGTAGGAGACA
SEQ-08**	4432-5022	CTTCAAGGCGTGTCAGTTTC	ATTTGTGGAGTGTGGTGGTG
		APOC2	
Amplicon	**Amplified Region**	**Forward Primer Sequence (5'-3')**	**Reverse Primer Sequence (3'-5')**
SEQ-01-1**	62-585	TTAGCGGTCAGGGGACACAT	CCCTCAGGTGGTCGTCATAG
SEQ-01-2**	478-997	CTAGGTCTGGGAGGAGTGGA	CAAGCCCACAATAGGGTGTT
SEQ-02	685-1555	AAGACAGCCTCTTGAAGAAGACC	GTCATGGTTCCAACACGGGCTT
SEQ-03	1455-2170	TGGGTCTCAACCACTATAAAGCC	GCTAGAGTACAGTGGCACGATCT
SEQ-04	1840-2734	GAACTGTAGACTATTTGAGCTTCT	CTAAGTCAGACCTCATGTCCCTG
SEQ-05**	2665-3338	TGCCGTACTTCCTCATCTCC	AGCTGGAATCACAAGCACCT
SEQ-06	3165-3909	TCACTTGAGGTTAGGAGTTCAAGA	TACCAGGAGGACAAGAAACAGAG
SEQ-07**	3810-4535	GAGCACACACAGAGCAGGAT	GTACAAGTCCCTGGGGAGAA
SEQ-08-1**	4390-4960	GCCCGCTGTAGATGAGAAAC	GAGAGAAAGCCGGACTTCAA
SEQ-08-2**	4860-5430	AGGACTCAAGGTGCCAAGAT	CTTGCTTTGTTTGTGCGTTT
SEQ-09	5350-6059	GCCAAAATCCAGCCTTCTCATTTGTA	CACGGGACCATTATACACTGATT
SEQ-10**	5920-6370	GCTCAAGAGATCCTCCCATC	CTATCTCCGCCTCCAGGGTA

(**) marked amplicons represent the PCR designed primers using Primer3 software, while the other remaining primers are M13-tag primers based on SeattleSNPs database.

Table 4. PCR reaction and cycling conditions

PCR Reaction Conditions (Reaction volume 25 µL)			PCR Cycle
Genomic DNA (1ng/dl)		3.0 µL	1. 95˚C for 5 minutes. 2. 95˚C for 45 sec. 3. 58-60˚C for 45 sec 4. 72˚C for 1 min. Repeats 2-4 for 40 cycles 5. 72˚C for 10 min. 6. Cool down to 4˚C
Master Mix (22µL)	d.H2O	11.75-13.25 µL	
	10x BufferGold	2.5 µL	
	$MgCl_2$ (25 mM)	1.5-3.0 µL	
	dNTPs (1.25 mM)	3.8 µL	
	Forward Primer (20 mM)	0.4 µL	
	Reverse Primer (20mM)	0.4 µL	
	Tag Polymerase enzyme Enzyme (5U/µL)	0.15 µL	

After PCR, gel electrophoresis was performed to confirm DNA amplification prior to DNA sequencing. Invitrogen TM E-Gel® 96 2% with SYBR® Safe precaste gels (Invitrogen corporation, Carlsbad, CA) was used for large scale PCR, while regular 2% agarose gel was used

for small scale PCR for samples that failed in the initial DNA amplification. The amplified DNA was sent to a commercial lab for automated fluorescence-based Sanger sequencing and capillary electrophoresis on ABI 3730x1DNA Analyzers (Genomic Services of Beckman Coulter Genomics, Denver, MA). Variant Reporter version 1.0 (Applied Biosystem, Foster City, CA) and Sequencher version 4.8 (Gene Codes Corporation, Ann Arbor, MI) were used to analyze the sequencing data. Variants calling were made by two independent reviewers to maximize the sequencing analysis accuracy.

The sequencing coverage was pretty good for the *APOE* and *APOC2* genes along with their hepatic control regions as compared to the other two genes (*APOC1*, and *APOC4*). Despite our repeated efforts we could not amplify the following sequences: 33 bp (nt: 1842-1875 bp) a repetitive region in intron 1 of *APOC4*, 16 bp (nt: 2147-2163) a repetitive region in intron 1 of *APOC4*, 75 bp gap (nt: 1950-2025) in intron 2 of *APOC1*, and 1,475 bp (nt: 3500-4975) in intron 3 of *APOC1*.

2.3 GENOTYPING

2.3.1 Selection of variants for genotyping

We genotyped tagSNPs (MAF≥5% and r^2=0.9) and all rare variants that were discovered in the sequencing subsets, in addition to the HapMap tagSNPs covering the intergenic unsequenced region based on HapMap data (CEPH Utah residents with ancestry from northern and western Europe [CEU], and Yoruba in Ibadan, Nigeria [YRI]).

2.3.2 Genotyping of *APOE-C1-C4-C2* gene cluster variation

Although we did not sequence the entire *APOE-C1-C4-C2* gene cluster, we genotyped common tagSNPs covering the intergenic regions based on HapMap genotype data of CEU and YRI population groups plus tagSNPs and rare variants identified in the sequencing region. Custom assays with masking population-specific sequencing variants and the database common variants with MAF≥5% in each racial group were ordered for genotyping. Either Sequenom iPLEX MassArray (Sequenom, San Diego, CA, USA) or TaqMan (Applied Biosystem, foster City, CA, USA) genotyping approach was used to genotype selected variants in the entire datasets (623 NHWs, and 788 Blacks). Upon genotyping completion, we compared the genotyping and sequencing results for those variants that were identified in the sequencing data and passed the genotyping process as a quality control measure. This step was done to check the concordance between sequencing and genotyping steps and also to increase the call for individuals that failed either sequencing or genotyping.

2.3.2.1 TaqMan Genotyping

TaqMan genotyping involves DNA amplification and end-point fluorescence reading using the ABI Prism 7900HT instrument. The TaqMan genotyping Master Mix and Assay were added to dried whole genome amplified DNA in 384-well plate. For TaqMan genotyping, we followed ABI manufactures protocol (Applied Biosystem, 2006) with some modifications on the DNA concentration and the number of cycle that are given in **Table 5**. TaqMan SNPs genotyping is based on 5'nuclease principle. Each TaqMan SNPs genotyping assay in a single tube consists of two primers to amplify the polymorphic sequence site, and two minor groove binder (MGB) probes for allele discrimination purpose. Each MGB probes contains three primary elements,

reporter dye (VIC or FAM) at the 5' end of the probe to label alleles at the polymorphic site, minor groove binder (MGB) at the 3' end of the probe to increase the melting temperature, and non-fluorescent quencher (NFQ) at the 3' end of the probe. Several steps are undertaken in the PCR process; MGB probes anneal specifically to the complementary sequences between the forward and reverse primers, once the probe attached to the complementary sequence, the ampli-tag gold enzyme cleaves the dye from the quencher resulting in increasing the fluorescence signal which indicates the allele change (Applied Biosystem, 2006). $SDS_{v2.4.1}$ and TaqMan Genotyper software were used to analyze the genotype calls.

Table 5. TaqMan SNPs Genotyping Condition

TaqMan Reaction total volume (5μL)		PCR condition
d.H2O	2.43 μL	1. 95˚ for 10 min. 2. 95˚ for 45 sec. 3. 60˚ for 1 min. -repeat 2-3 49x
Master Mix	2.5 μL	
Assay	0.06 μL	

2.3.2.2 Sequenom iPlex massarray Genotyping

Sequenom iPlex massarray genotyping technique is one of the high throughput genotyping massarrays and successful iPLEX reaction can take up to 40 multiplexed reactions. Whole genome amplification DNA was used for iPLEX Massarray genotyping. Sequenom Massarry designer software was used to design PCR and extension primers. Sequenom genotyping technique involved multiple steps, including locus-specific PCR reaction, followed by locus-specific primer extension in which the oligonucleotide primers anneal immediately upstream the target polymorphic site. The mass of the extended primer was determined by using MALDI-TOF spectrometry and the mass density indicates the sequence, which corresponds to the allele at the

target polymorphic site (Gabriel et al., 2009). SpectroTYPER software was used to translate the mass of the observed primer into a genotype.

2.4 STATISTICAL ANALYSES

2.4.1 Variants detection

After generating the sequencing data, variants call was made using Variant Reporter version 1.0 (Applied Biosystem, Foster City, CA) and Sequencher software version 4.8 (Gene Codes Corporation, Ann Arbor, MI).

2.4.2 Sequencing subset analysis

Haploview software (version 1.0: http://www.broadinstitute.org) was used to analyze the variant allele frequencies, their distributions between the two extreme lipid groups, and visualize their linkage disequilibrium (LD) patterns. Allele and genotype frequencies were determined by using direct counting. Chi squared test (X^2) was used to check concordance of genotype distribution to Hardy-Weinberg Equilibrium (HWE) and to compare allele frequencies between the two extreme lipid groups.

2.4.3 Phenotype trait and covariates detection

We used Box-Cox transformation (Box and Cox, 1964) for apoB, HDL-C and TG in NHWs and all lipid traits in Blacks such that the transformed lipid traits achieved normality. Significant

covariates for each trait were identified using stepwise regression method to select the most parsimonious set of covariates for each trait. In NHWs, gender, age, BMI (weight [kg]/height $[m]^2$), and smoking were included as covariates in the final analysis model. Among Blacks: gender, age, waist, BMI, smoking, Jobmin (minutes walking or bicycling to work each day [min]), and Staff (staff level [junior/senior]) covariates were included in the final analysis model.

2.4.4 Data cleaning

SNPs with extensive missing data (>15%) and/or deviating highly from HWE (P<0.01) were excluded from statistical analyses (call rate cut-off [85%], and HWE-p cut-off [0.01]). A total of seventy variants in NHWs and 108 variants in Blacks were included in the statistical association analyses.

2.4.5 Association analysis with major lipid traits

For SNPs genotyped in the entire datasets, R statistical package (version 2.3.1, http://www.r-project.org) was used to run the single-locus, haplotype-based and rare variants association analyses and versatile gene-based associations (VEGA) to perform gene-based analysis (Liu et al., 2010) with four major lipid traits (LDL-C, HDL-C, TC, and TG), apoB and apoA1.

2.4.5.1 Single-locus and gene-based association analyses

In the single-locus association analysis, additive linear regression model was used to test the association between SNPs and each lipid traits (HDL-C, LDL-C, TC and TG), apoB, and apoA1, and a p-value < 0.05 was considered as suggestive evidence of association. The versatile gene-

based associations (VEGA) were also performed to assess the relationship between traits and *APOE* gene cluster variation (Liu et al., 2010).

2.4.5.2 Haplotype-based association analysis

For haplotype association analysis, the generalized linear model (GLM) (Lake et al., 2003) was used. Including too many haplotypes can make above model inefficient and impractical. To reduce the number of haplotypes considered in association analysis, we used sliding window approach, 4-SNP per window, and assessed evidence for association within each window. Specifically, a global p-value for testing overall effects of the haplotypes with frequency greater than 0.01 was used to assess the association between the trait and haplotypes in each window. Sliding-window haplotype analysis was performed with the haplo.glm function in the Haplo.Stats R package (version 1.5.0). Haplotype sliding window approach resulted in 66 windows in NHWs and 104 windows in African Blacks.

2.4.5.3 Rare variants association analysis

We analyzed the cumulative effects of uncommon/rare variants (MAF<5%) by using the SKAT-O (Lee et al. 2012), which has been proposed to be the optimal test for rare variant analysis and exceeded the SKAT and burden tests in several ways. To date various methods have been developed and introduced for rare variants analysis but each method has its advantages and drawbacks depending on the data structure. In this study we used four methods; two burden-based approaches; rare variants test-1 (RVT1), rare variants test-2 (RVT2), and two kernel-based approaches; sequence kernel association test (SKAT), and sequence kernel association test-optimal (SKAT-O). Whereas RVT1 and RVT2 are two specific burden tests, SKAT and SKAT-O are kernel-based tests. Burden tests assume all variants affect the phenotypic traits on the same

direction with same effect and its power is affected by coexistence of multiple variants with different directions. SKAT has advantage over burden test and it is more powerful if the data has multiple variants with different effect directions. Since SKAT-O p-value combines both burden test and SKAT p-values, we rely on SKAT-O p-value. The analyses were performed by using three different minor allele frequency bin thresholds (<1%, <2% and <5%). The SKAT method was implemented using the “SKAT” R package.

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3.0 RESULTS

3.1 SEQUENCING *APOE-C1-C4-C2* GENE CLUSTER

Sequencing all the four genes and their two hepatic control regions in selected individuals with extreme HDL-C and TG levels from two ethnic groups (NHWs and African Blacks) revealed a total of 230 variants (215 substitutions, and 15 indels) of which 160 were reported and the remaining 70 were novel. We observed one dinucleotide microsatellite in *APOC4/APOC2* that mapped to (*APOC4*: 4929-4954), and (*APOC2*: 1625-1650). Of the 230 identified variants, 63 variants were shared in both populations, while 52 variants were NHW-specific and 115 variants were Black-specific (**Figure 5**).

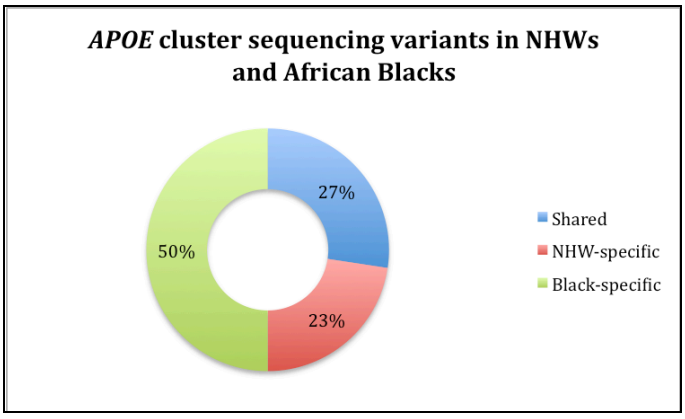

Figure 5. *APOE-C1-C4-C2* gene cluster sequencing-identified variants in NHWs and African Blacks

3.1.1 Sequencing variation in non-Hispanic Whites (NHWs)

A total of 115 variants were identified in NHW subset with extreme lipid traits (47 subjects with high HDL/low TG levels, and 48 subjects with low HDL-C/high TG levels), of which 105 variants were substitutions and 10 were indels. Of the 115 variants, 85 variants were reported, while the remaining 30 variants were novel. Of the 115 variants, 63 SNPs were present also in Blacks and the remaining 52 variants were NHW-specific (**Table 6**).

Of the 115 variants, 19 variants were mapped to *APOE* (17 reported, 2 novel), 29 variants were mapped to *APOC1* (20 reported, 9 novel), 5 variants were mapped to *HCR-1* (3 reported, 2 novel), 3 variants were mapped to *HCR-2* (2 reported, 1 novel), 21 variants were mapped to *APOC4* (13 reported, 8 novel), 2 variants were overlapped in *APOC4*/*APOC2* (both of them are reported), and 36 variants were mapped to *APOC2* (28 reported, 8 novel). **Figure 6** represents the distribution of sequencing variants in the sequenced regions and **Figure 7** summarizes the percentage of reported and novel variants in each gene in NHWs.

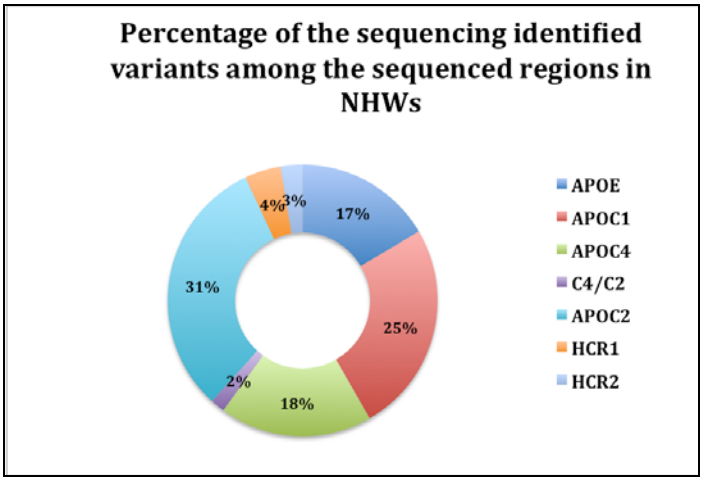

Figure 6. Percentage of the sequencing identified variants among the sequenced regions in NHWs

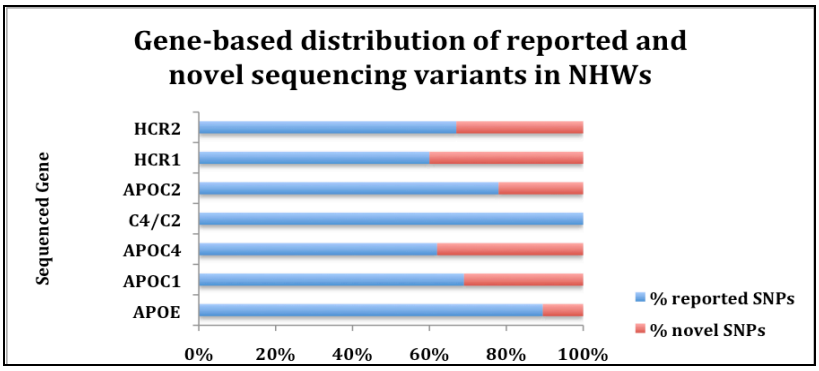

Figure 7. Gene-based distributions of reported and novel sequencing variants in NHWs

Gene-based distribution of the sequencing variants showed that 16% of *APOE* variants was located in the promoter region, 33% was in intronic region, 21% was in coding region, 5% was in UTR, and 26% was in 3' flanking region (**Figure 8**). For *APOC1* variation, 21% was in the promoter region, 52% was in intronic region, 7% was in coding region, 3% was in UTR, and 17% was in 3' flanking region. For *APOC4* variation, 29% was in promoter region, 52% was in introns, 14% was in coding region, and 5% was in UTR. For *APOC2*, 64% was in introns, 3% was in splice site, 5% was in 3'UTR, and 28% was in 3'flanking region.

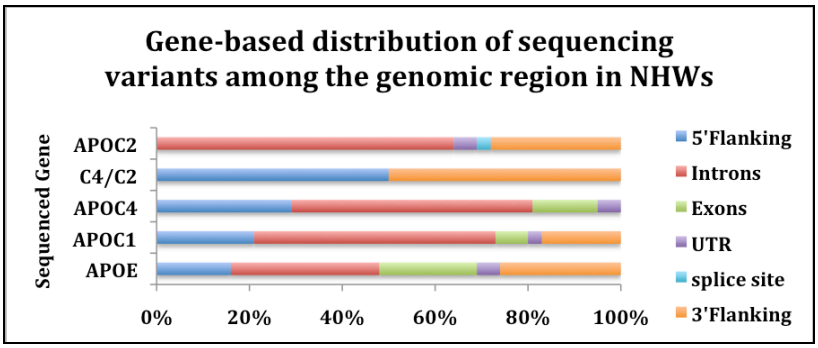

Figure 8. Gene-based distribution of sequencing variants (percentage) among the genomic regions in NHWs

Table 6. ***APOE-C1-C4-C2*** **gene cluster sequencing-identified variants in NHWs sequencing subset**

Name	Allele change	NCBI rs#	Function	Amino acid change	MAF	High HDL-C/low TG	Low HCL-C/high TG	HWE-P	%Geno
APOE-560	A>T	rs449647	5'flanking		0.126	0.085	0.167	0.379	100
APOE-624	T>C	rs769446	5'flanking		0.075	0.111	0.042	1.000	97.9
APOE-832	G>T	rs405509	5'flanking		0.484	0.479	0.490	1.000	100
APOE-1163	G>C	rs440446	intron1		0.358	0.340	0.375	0.108	100
APOE-1575	C>T	rs769448	intron1		0.021	0.043	0.000	1.000	100
APOE-1998	G>A	rs769449	intron 2		0.126	0.128	0.125	1.000	100
APOE-2294	C>T		intron 2		0.005	0.011	0.000	1.000	100
APOE-2440	G>A	rs769450	intron 2		0.400	0.404	0.396	0.855	100
APOE-2907	T>G	rs769451	intron 2		0.005	0.000	0.010	1.000	100
APOE-3038	G>A	rs111833428	exon 3	Ala 23 Ala	0.005	0.011	0.000	1.000	100
APOE-3937	T>C	rs429358	exon 4	Cys 130 Arg	0.168	0.160	0.177	1.000	100
APOE-4075	C>T	rs7412	exon 4	Arg 176 Cys	0.063	0.074	0.052	1.000	100
APOE-4310	T>A	rs199768005	exon 4	Val 254 Glu	0.005	0.011	0.000	1.000	100
APOE-4528	C>T		exon 4 (3' UTR)		0.005	0.011	0.000	1.000	100
APOE-4737	C>G	rs117656888	3'flanking		0.011	0.021	0.000	1.000	100
APOE-4951	A>C	rs1081105	3'flanking		0.042	0.032	0.052	1.000	100
APOE-5229	G>T	rs1065853	3'flanking		0.064	0.076	0.052	1.000	98.9
APOE-5230	INDEL	rs55729972	3'flanking		****	****	****	****	****
APOE-5361	T>C	rs1081106	3'flanking		0.105	0.117	0.094	1.000	100
APOC1-607	G>A	rs72654447	5'flanking		0.005	0.011	0.000	1.000	100
APOC1-655	A>T	rs66807996	5'flanking		0.016	0.021	0.011	1.000	98.9
APOC1-659	G>C	rs72654448	5'flanking		0.005	0.000	0.010	1.000	100
APOC1-698	C>A	rs72654449	5'flanking		0.011	0.011	0.010	1.000	100
APOC1-703	C>T	rs3207187	5'flanking		0.005	0.011	0.000	1.000	100
APOC1-720_721	ins4	HpaI	5'flanking		0.226	0.223	0.229	0.894	100
APOC1-1170	G>A		intron1		0.005	0.011	0.000	1.000	100
APOC1-1276	C>G	rs72654453	exon2	Ile 3 Met	0.011	0.021	0.000	1.000	100
APOC1-1294	T>G		intron2		0.005	0.011	0.000	1.000	100
APOC1-1317	G>A	rs12721048	intron2		0.011	0.021	0.000	1.000	100
APOC1-1422	G>A		intron2		0.005	0.011	0.000	1.000	100
APOC1-1566	G>A	rs12691088	intron2		0.026	0.011	0.042	1.000	100
APOC1-1669	T>C		intron2		0.005	0.011	0.000	1.000	100
APOC1-1870	T>C	rs5117	intron2		0.229	0.228	0.229	0.8701	98.9
APOC1-2041	C>T	rs3826688	intron2		0.370	0.337	0.402	0.674	96.8
APOC1-2629	G>A		exon3		0.005	0.011	0.000	1.000	100
APOC1-2817	C>T		intron3		0.005	0.011	0.000	1.000	100
APOC1-3423	G>A	rs389261	intron3		0.005	0.000	0.010	1.000	100
APOC1-3494	C>T		intron3		0.005	0.011	0.000	1.000	100
APOC1-4334	G>A	rs12721046	intron 3		0.181	0.202	0.160	0.288	98.9
APOC1-4957	G>A	rs484195	intron3		****	****	****	****	****
APOC1-5053_5054	del1	rs12721052	intron3		0.306	0.326	0.287	1.000	97.9
APOC1-5240	C>G	rs12721051	intron3		0.209	0.226	0.193	0.935	90.5
APOC1-5641	T>G	rs1064725	3'UTR		0.037	0.021	0.052	1.000	100
APOC1-5773	G>A		3'flanking		0.005	0.011	0.000	1.000	100
APOC1-5926	G>A	rs56131196	3'flanking		0.221	0.234	0.208	0.541	100

Cont. Table 6

APOC1-6026	A>G	rs4420638	3'flanking		0.221	0.234	0.208	0.541	100
APOC1-6122	G>C	rs142134314	3'flanking		0.005	0.000	0.010	1.000	100
APOC1-6213	G>A		3'flanking		0.005	0.011	0.000	1.000	100
HCR1-292	C>G	rs4803771	HCR-1		0.042	0.021	0.062	0.285	100
HCR1-362	C>A		HCR-1		0.011	0.011	0.010	1.000	100
HCR1-423	C>G		HCR-1		0.026	0.043	0.010	1.000	100
HCR1-575	A>G	rs157599	HCR-1		0.005	0.000	0.010	1.000	100
HCR1-727	T>G	rs149345	HCR-1		0.005	0.000	0.011	1.000	98.9
HCR2-188	C>G	rs35136575	HCR-2		0.242	0.277	0.208	0.263	100
HCR2-365	C>A		HCR-2		0.011	0.011	0.010	1.000	100
HCR2-523	C>T		HCR-2		0.026	0.021	0.031	1.000	100
APOC4-92_94	del3	rs12721101	5’ flanking		0.253	0.256	0.250	0.015	87.4
APOC4-108	G>A	rs112391061	5’flanking		0.253	0.256	0.250	0.015	87.4
APOC4-116	A>G		5’flanking		0.007	0.000	0.013	1.000	78.9
APOC4-150_152	ins114		5’flanking		0.256	0.262	0.250	0.022	88.4
APOC4-204	G>A	rs4803773	5’flanking		0.250	0.212	0.292	0.237	52.6
APOC4-636	C>T		5’flanking		0.005	0.000	0.010	1.000	100
APOC4-968	A>G	rs76214972	5’ UTR		0.037	0.011	0.062	1.000	100
APOC4-1150	A>G	rs148247675	Intron1		0.005	0.011	0.000	1.000	100
APOC4-1229	G>C		Intron1		0.011	0.000	0.021	1.000	100
APOC4-1325_1327	del3		Intron1		0.147	0.138	0.156	1.000	89.5
APOC4-1733	C>T	rs12721111	Intron1		0.263	0.276	0.250	0.016	82.1
APOC4-1823	C>G		Intron1		0.187	0.191	0.183	0.440	78.9
APOC4-2063	C>G		Intron1		0.005	0.000	0.011	1.000	98.9
APOC4-2557	C>A		Intron1		0.005	0.000	0.010	1.000	100
APOC4-2623	C>T	rs5157	Intron1		0.479	0.446	0.510	0.654	98.9
APOC4-2640	C>T	rs5158	Intron1		0.147	0.149	0.146	1.000	100
APOC4-2683	G>A	rs12721109	Intron1		0.011	0.011	0.010	1.000	100
APOC2-242	G>A	rs12691089	APOC4-exon2	Gly 52 Asp	0.005	0.000	0.010	1.000	100
APOC2-194C4-3498	C>T	rs1132899	APOC4-exon2	Pro 36 Leu	0.474	0.436	0.510	0.898	100
APOC2-543	T>C	rs186448850	APOC4-intron2		0.011	0.000	0.021	1.000	100
APOC2-623C4-3927	T>G	rs5167	APOC4-exon3	Leu 96 Arg	0.358	0.394	0.323	0.515	100
APOC2-1324	G>A	rs12721063	APOC4-3'FR/APOC2-5'FR		0.021	0.021	0.021	1.000	100
APOC2-1357C4-4661	G>C	rs2288912	APOC4-3'FR/APOC2-5'FR		0.484	0.457	0.510	0.885	100
APOC2-1442C4-4746	G>T	rs2288911	APOC2-splice site		0.495	0.479	0.510	0.878	100
APOC2-1591	G>A		APOC2-intron1		0.005	0.000	0.010	1.000	100
APOC2-1851	C>T	rs12709886	intron1		0.037	0.011	0.062	1.000	100
APOC2-2191	C>T	rs9304644	intron1		0.457	0.457	0.457	0.691	98.9
APOC2-2410	T>C	rs12721076	intron1		0.154	0.160	0.149	1.000	98.9
APOC2-2486	G>A	rs9304645	intron1		0.188	0.185	0.191	1.000	97.9
APOC2-2566	T>C	rs9304646	intron1		0.457	0.467	0.447	0.541	96.8
APOC2-2870	G>T		intron1		0.005	0.011	0.000	1.000	100
APOC2-2935	C>G	rs11879392	intron1		0.153	0.160	0.146	1.000	100
APOC2-2938	A>G		intron1		0.005	0.011	0.000	1.000	100

Cont. Table 6

APOC2-3010	A>G	rs10419086	intron1	0.063	0.085	0.042	1.000	100
APOC2-3030	A>G	rs4803774	intron1	0.453	0.457	0.448	0.630	100
APOC2-3086	C>T	rs4803775	intron1	0.484	0.543	0.490	0.885	100
APOC2-3348	G>A	rs10420434	intron1	0.063	0.085	0.042	1.000	100
APOC2-3409	T>C		intron1	0.005	0.000	0.010	1.000	100
APOC2-3600	A>G	rs7256684	intron1	0.453	0.457	0.448	0.630	100
APOC2-3778	A>T	rs5120	intron1	0.484	0.457	0.510	0.885	100
APOC2-3814	T>G	rs10422603	intron1	0.189	0.191	0.188	1.000	100
APOC2-4429	G>C	rs3745152	intron3	0.489	0.489	0.489	0.018	96.8
APOC2-4430_4431	ins3	rs35625559	intron3	0.489	0.489	0.489	0.018	96.8
APOC2-4477	G>A		intron3	0.005	0.011	0.000	1.000	95.8
APOC2-4493	C>T	rs4803776	intron3	0.483	0.543	0.489	0.800	94.7
APOC2-4532	C>T		intron3	0.075	0.098	0.054	1.000	91.6
APOC2-4534_4535	del1		intron3	0.075	0.098	0.054	1.000	91.6
APOC2-4853_4854	del1	rs150448996	3'flamking	0.261	0.261	0.260	1.000	98.9
APOC2-4971	C>T	rs1130742	3'flanking	0.295	0.713	0.698	0.100	100
APOC2-5004	G>A	rs10421404	3'flanking	0.189	0.191	0.188	1.000	100
APOC2-5018_5022	del5	rs78403558	3'flanking	0.153	0.160	0.146	1.000	100
APOC2-5303	C>T	rs7257468	3'flanking	0.458	0.468	0.448	0.480	100
APOC2-5310	T>G	rs7258345	3'flanking	0.457	0.543	0.543	0.614	97.9
APOC2-5324	C>T	rs7257476	3'flanking	0.458	0.468	0.448	0.480	100
APOC2-5398	G>A	rs12709889	3'flanking	0.268	0.277	0.260	1.000	100
APOC2-5644	G>A		3'flanking	0.011	0.011	0.010	1.000	100
APOC2-5815	G>A	rs10423208	3'flanking	0.453	0.457	0.448	0.630	100
APOC2-5922	A>G	rs10422888	3'flanking	0.149	0.160	0.138	1.000	98.9
APOC2-6037	G>A	rs10402642	3'flanking	0.453	0.457	0.448	0.630	100

Nucleotide position is according to the reference sequence; Ch. Position: chromosomal position is according to NCBI build 138; (***) Unavailable data for population-specific variants or not analyzed indels; HWE-P (hardy Weinberg equilibrium p-value); %Geno (call rate); Grey-highlighted variants represent shared variants in both populations.

3.1.2 Sequencing variation in African Blacks

A total of 178 variants were identified in 95 individuals from African Blacks with extreme lipid traits (48 subjects with high HDL/low TG levels, and 47 subjects with low HDL-C/high TG levels), of which 163 variants were substitutions and 15 variants were indels. Out of 178 variants, 133 variants were reported, while the remaining 45 variants were novel. Sixty-three of the 178 variants were found also in NHWs and the remaining 115 variants were Black-specific (**Table 7**).

Of the 178 SNPs, 31 variants were mapped to *APOE* (22 reported, 9 novel), 23 variants were mapped to *APOC1* (19 reported, 4 novel), 3 variants were mapped to *HCR-1* (all of the 3 variants were reported), 4 variants were mapped to *HCR-2* (2 reported, 2 novel), 46 variants were mapped to *APOC4* (32 reported, 14 novel), 5 variants were overlapped in *APOC4*/*APOC2* (all of them are reported), and 66 variants were mapped to *APOC2* (50 reported, 16 novel). **Figure 9** represents the distribution of sequencing variants in the sequenced regions and **Figure 10** summarizes the percentage of reported and novel variants in each gene in Blacks.

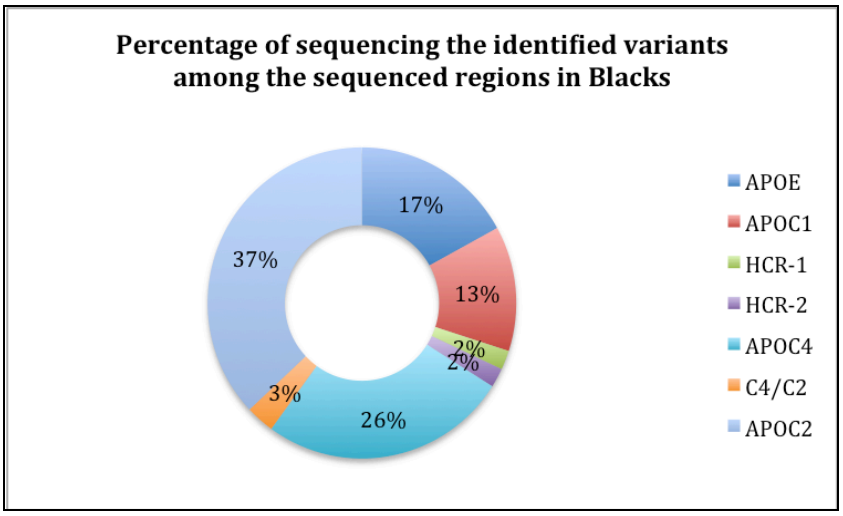

Figure 9. Percentage of the sequencing identified variants among the sequenced regions in Blacks

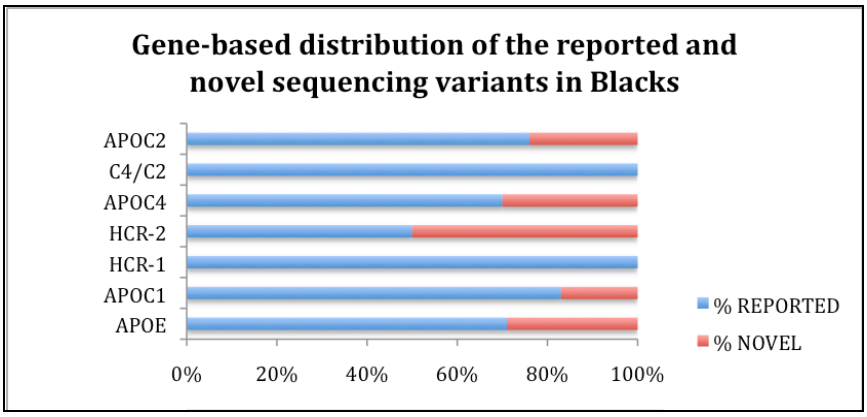

Figure 10. Gene-based distribution of the reported and novel sequencing variants in Blacks

Gene-based distribution of the sequencing variants among the genomic region (**Figure 11**) showed that 32% of *APOE* variants was located in promoter region, 36% was in intronic region, 10% was in coding region, 3% was in splice site, 3% was in UTR, and 15% was in 3" flanking region. For *APOC1* variation, 9% was in promoter region, 65% was in intronic region, 4% was in UTR, and 22% was in 3' flanking region. For *APOC4* variation, 26% was in promoter region, 54% was in introns, 15% was in coding regions, and 5% was in UTR. For *APOC2* variation, 60% was in introns, 8% was in exons, and 32% was in 3'flanking region.

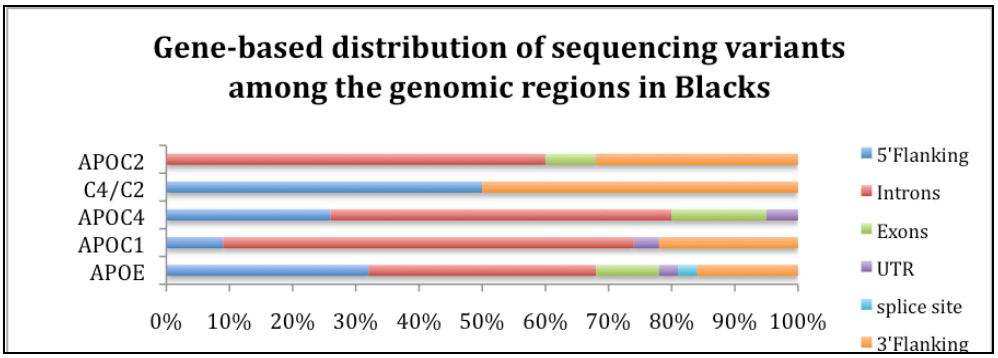

Figure 11. Gene-based distribution of sequencing variants (percentage) among the genomic regions in Blacks

Table 7. ***APOE-C1-C4-C2*** **gene cluster sequencing-identified variants in African Blacks sequencing subset**

Name	Alleles	NCBI ref ID	Function	Amino acid change	MAF	High HDL-C/low TG	Low HDL-C/high TG	HWE-P	%Geno
APOE-73	C>T	rs1081101	5'flanking		0.074	0.062	0.087	1.000	98.9
APOE-173	A>G		5'flanking		0.005	0.000	0.011	1.000	100
APOE-308	C>T	rs769445	5'flanking		0.005	0.000	0.011	1.000	100
APOE-471	A>G	rs439382	5'flanking		0.132	0.125	0.138	1.000	100
APOE-494	C>T		5'flanking		0.005	0.010	0.000	1.000	100
APOE-526	T>C		5'flanking		0.005	0.010	0.000	1.000	100
APOE-560	A>T	rs449647	5'flanking		0.395	0.385	0.404	0.169	100
APOE-618	G>C		5'flanking		0.005	0.000	0.011	1.000	100
APOE-624	T>C	rs769446	5'flanking		0.005	0.010	0.000	1.000	100
APOE-832	G>T	rs405509	5'flanking		0.261	0.260	0.261	0.337	98.9
APOE-1109	C>T	rs9282609	Splice site		0.053	0.052	0.054	1.000	98.9
APOE-1163	G>C	rs440446	intron1		0.124	0.115	0.133	0.822	97.9
APOE-1231	G>A		intron1		0.011	0.010	0.011	1.000	98.9
APOE-1279	C>A	rs877973	intron1		0.048	0.062	0.033	1.000	98.9
APOE-1539	A>G	rs184686013	intron1		0.011	0.021	0.000	1.000	100
APOE-1591	G>T	rs147236548	intron1		0.016	0.021	0.011	1.000	100
APOE-2072	G>A	rs189660912	intron 2		0.016	0.021	0.011	1.000	100
APOE-2269	G>A	rs61357706	intron 2		0.016	0.010	0.022	1.000	98.9
APOE-2440	G>A	rs769450	intron 2		0.394	0.383	0.404	0.978	98.9
APOE-2544	A>G	rs115299243	intron 2		0.016	0.010	0.022	1.000	98.9
APOE-2576	G>A		intron 2		0.005	0.010	0.000	1.000	100
APOE-3673	C>G	rs769453	intron 3		0.005	0.000	0.011	1.000	100
APOE-3937	T>C	rs429358	exon 4	Cys 130 Arg	0.237	0.240	0.234	0.201	100
APOE-4036	C>T	rs769455	exon 4	Arg 163 Cys	0.016	0.011	0.022	1.000	96.8
APOE-4075	G>A	rs7412	exon 4	Arg 176 Cys	0.042	0.062	0.021	1.000	100
APOE-4569	G>T		3'UTR		0.005	0.010	0.000	1.000	100
APOE-4951	A>C	rs1081105	3'flanking		0.042	0.042	0.043	1.000	100
APOE-5223	G>C		3'flanking		0.005	0.000	0.011	1.000	100
APOE-5229	G>T	rs1065853	3'flanking		0.059	0.074	0.043	1.000	98.9
APOE-5230	INDEL	rs55729972	3'flanking		****	****	****	****	****
APOE-5231	T>G		3'flanking		0.032	0.042	0.021	1.000	100
APOC1-720_721	ins4	rs72654451	5'flanking		0.237	0.260	0.213	1.000	100
APOC1-894	C>T	rs190454394	5'flanking		0.005	0.010	0.000	1.000	100
APOC1-1166	G>A	rs72654452	intron1		0.032	0.031	0.032	1.000	100
APOC1-1331	G>A	rs10408994	intron2		0.108	0.098	0.117	0.637	97.9
APOC1-1526	C>T	rs5114	intron2		0.047	0.062	0.032	1.000	100
APOC1-1642	C>T		intron2		0.011	0.010	0.011	1.000	98.9
APOC1-1684	G>A	rs12709881	intron2		0.075	0.083	0.067	1.000	97.9
APOC1-1870	T>C	rs5117	intron2		0.212	0.239	0.185	0.756	96.8
APOC1-2041	C>T	rs3826688	intron2		0.126	0.115	0.138	0.894	100
APOC1-2099	T>C		intron2		0.005	0.000	0.011	1.000	100
APOC1-2296	A>T	rs185495905	intron2		0.005	0.010	0.000	1.000	100

Cont. Table 7

APOC1-3358	A>G		intron3	0.005	0.010	0.000	1.000	100
APOC1-3423	G>A	rs389261	intron3	0.389	0.406	0.372	0.011	100
APOC1-3573	G>A	rs10424339	intron3	0.181	0.198	0.163	0.761	98.9
APOC1-5006	G>T	rs112528434	intron3	0.081	0.083	0.078	1.000	97.9
APOC1-5053_5054	del1	rs12721052	intron3	0.215	0.191	0.239	1.000	97.9
APOC1-5240	C>G	rs12721051	intron3	0.035	0.045	0.024	1.000	89.5
APOC1-5667	A>G	rs12721054	3'UTR	0.137	0.135	0.138	0.914	100
APOC1-5716	G>T	rs12721055	3'flanking	0.026	0.031	0.021	1.000	100
APOC1-5717	G>C	rs72654457	3'flanking	0.021	0.021	0.021	1.000	100
APOC1-5926	G>A	rs56131196	3'flanking	0.153	0.156	0.149	0.160	100
APOC1-6026	A>G	rs4420638	3'flanking	0.158	0.156	0.160	0.131	100
APOC1-6158	G>A		3'flanking	0.005	0.000	0.011	1.000	100
HCR1-424	G>A	rs117664574	HCR-1	0.011	0.021	0.000	1.000	100
HCR1-575	A>G	rs157599	HCR-1	0.424	0.448	0.398	0.034	96.8
HCR1-727	T>G	rs149345	HCR-1	0.392	0.404	0.380	0.012	97.9
HCR2-188	C>G	rs35136575	HCR-2	0.181	0.181	0.181	1.000	98.9
HCR2-286	G>A		HCR-2	0.059	0.032	0.085	1.000	98.9
HCR2-523	C>T	rs118004808	HCR-2	0.005	0.010	0.000	1.000	100
HCR2-632	T>C		HCR-2	0.083	0.033	0.136	0.940	94.7
APOC4-65	C>T		5’ flanking	0.007	0.000	0.015	1.000	77.9
APOC4-92_94	del3	rs12721101	5’ flanking	0.262	0.209	0.321	0.571	86.3
APOC4-108	G>A	rs112391061	5’ flanking	0.262	0.209	0.321	0.571	86.3
APOC4-150_151	ins114		5’ flanking	0.283	0.228	0.341	1.000	94.7
APOC4-204	G>A	rs4803773	5’ flanking	0.233	0.250	0.216	1.000	94.7
APOC4-233	C>T		5’ flanking	0.006	0.000	0.011	1.000	93.7
APOC4-245	G>T	rs192072159	5’ flanking	0.006	0.000	0.011	1.000	94.7
APOC4-368	A>G		5’ flanking	0.011	0.010	0.011	1.000	100
APOC4-438	G>A	rs146656012	5’ flanking	0.006	0.000	0.011	1.000	94.7
APOC4-489	C>T	rs140241604	5’ flanking	0.017	0.011	0.023	1.000	93.7
APOC4-637	G>T	rs113814026	5’ flanking	0.042	0.042	0.043	1.000	100
APOC4-757	C>A	rs12721105	5’ flanking	0.058	0.062	0.053	0.052	100
APOC4-1088	T>G		intron1	0.005	0.000	0.011	1.000	100
APOC4-1130	T>C		intron1	0.005	0.010	0.000	1.000	100
APOC4-1192	G>A	rs113745034	intron1	0.011	0.010	0.011	1.000	100
APOC4-1325_1327	del3		intron1	0.043	0.064	0.022	1.000	97.9
APOC4-1430_1431	insG		intron1	0.037	0.042	0.032	0.216	100
APOC4-1702	G>A	rs12721102	intron1	0.006	0.011	0.000	1.000	91.6
APOC4-1719	C>A		intron1	0.006	0.011	0.000	1.000	91.6
APOC4-1733	C>T	rs1271111	intron1	0.244	0.228	0.262	1.000	90.5
APOC4-1823	C>G		intron1	0.203	0.238	0.156	0.286	77.9
APOC4-2099	G>T	rs111339708	intron1	0.011	0.010	0.011	1.000	100
APOC4-2467	C>T	rs115225947	intron1	0.021	0.021	0.021	1.000	100
APOC4-2559	C>T	rs5155	intron1	0.09	0.074	0.106	1.000	98.9
APOC4-2607	G>A	rs5156	intron1	0.011	0.010	0.011	1.000	100
APOC4-2623	C>T	rs5157	intron1	0.163	0.167	0.160	1.000	100

Cont. Table 7

APOC4-2640	C>T	rs5158	intron1		0.032	0.042	0.021	1.000	100
APOC4-2641	G>A		intron1		0.005	0.000	0.011	1.000	97.9
APOC4-2678	G>C	rs148564866	intron1		0.005	0.000	0.011	1.000	100
APOC4-2767	G>T	rs12721107	intron1		0.021	0.031	0.011	1.000	100
APOC4-2971	A>G	rs5159	intron1		0.15	0.152	0.148	0.613	94.7
APOC4-3213	T>C	rs28616151	intron1		0.056	0.064	0.048	0.038	93.7
APOC4-3348	G>A		intron1		0.005	0.011	0.000	1.000	97.9
APOC2-59C4-3363	G>A	rs60170431	APOC4-intron1		0.043	0.053	0.032	1.000	98.9
APOC2-75C4-3380	G>A	rs12721104	APOC4-intron1		0.147	0.146	0.149	0.638	100
APOC2-194C4-3498	C>T	rs1132899	APOC4-exon2	Leu36Pro	0.232	0.240	0.223	1.000	100
APOC2-198C4-3502	C>T	rs10423683	APOC4-exon2	Ser37Ser	0.058	0.062	0.053	0.052	100
APOC2-228	G>A	rs5164	APOC4-exon2	Trp47Ter	0.005	0.000	0.011	1.000	100
APOC2-288C4-3592	C>T	rs12691090	APOC4-exon2	Asp67Asp	0.026	0.042	0.011	1.000	100
APOC2-396C4-3700	G>A		APOC4-intron2		0.005	0.010	0.000	1.000	100
APOC2-488C4-3792	G>A	rs5165	APOC4-intron2		0.016	0.021	0.011	1.000	100
APOC2-623C4-3927	T>G	rs5167	APOC4-exon3	Leu96Arg	0.011	0.010	0.011	1.000	100
APOC2-665C4-3969	A>C	rs138548797	APOC4-exon3	Lys110Thr	0.468	0.448	0.489	0.747	100
APOC2-708C4-4012	G>A		APOC4-exon3	Lys124Lys	0.005	0.000	0.011	1.000	100
APOC2-850C4-4154	G>A	rs12709884	APOC4-3' UTR		0.112	0.104	0.120	0.623	98.9
APOC2-853C4-4157	G>A	rs10425530	APOC4-3' UTR		0.101	0.104	0.098	1.000	98.9
APOC2-1042C4-4346	A>T	rs12709885	APOC4-3'FR/APOC2-5'FR		0.005	0.010	0.000	1.000	98.9
APOC2-1187C4-4491	G>A	rs111782345	APOC4-3'FR/APOC2-5'FR		0.005	0.000	0.011	1.000	97.9
APOC2-1229C4-4533	C>T	rs112698600	APOC4-3'FR/APOC2-5'FR		0.011	0.010	0.011	1.000	98.9
APOC2-1275C4-4579	G>A	rs111356234	APOC4-3'FR/APOC2-5'FR		0.053	0.031	0.076	1.000	98.9
APOC2-1357C4-4661	G>C	rs2288912	APOC4-3'FR/APOC2-5'FR		0.232	0.240	0.223	1.000	100
APOC2-1442C4-4746	G>T	rs2288911	APOC2-exon1/UTR		0.207	0.223	0.189	0.857	96.8
APOC2-1540C4-4844	G>A	rs75463753	APOC2-intron1		0.095	0.094	0.096	0.371	100
APOC2-1608C4-4912	G>C		APOC2-intron1		0.005	0.000	0.011	1.000	100
APOC2-2003	G>A	rs187834478	intron1		0.016	0.021	0.011	1.000	100
APOC2-2090	G>A	rs12721072	intron1		0.058	0.052	0.064	1.000	100
APOC2-2191	T>C	rs9304644	intron1		0.358	0.365	0.351	1.000	100
APOC2-2258	A>C	rs116489256	intron1		0.058	0.052	0.064	1.000	100
APOC2-2339	A>G	rs115943687	intron1		0.058	0.052	0.064	1.000	100
APOC2-2371	A>G		intron1		0.005	0.010	0.000	1.000	100
APOC2-2410	T>C	rs12721076	intron1		0.032	0.042	0.021	1.000	100
APOC2-2486	G>A	rs9304645	intron1		0.394	0.415	0.372	0.685	98.9
APOC2-2566	C>T	rs9304646	intron1		0.288	0.293	0.283	1.000	96.8
APOC2-2935	C>G	rs11879392	intron1		0.027	0.042	0.011	1.000	98.9
APOC2-3010	A>G	rs10419086	intron1		0.142	0.146	0.138	0.232	100
APOC2-3030	G>A	rs4803774	intron1		0.289	0.302	0.277	1.000	100
APOC2-3082_3083	ins3		intron1		0.058	0.052	0.064	1.000	100
APOC2-3086	C>T	rs4803775	intron1		0.158	0.167	0.149	0.343	100

Cont. Table 7

APOC2-3154	G>A	rs145931717	intron1		0.058	0.052	0.064	1.000	100
APOC2-3193	A>G	rs148616221	intron1		0.005	0.000	0.011	1.000	100
APOC2-3234	T>C		intron1		0.005	0.010	0.000	1.000	100
APOC2-3259	C>T	rs12721061	intron1		0.058	0.052	0.064	1.000	100
APOC2-3260	G>A	rs151176577	intron1		0.011	0.000	0.021	1.000	100
APOC2-3348	G>A	rs10420434	intron1		0.126	0.135	0.117	0.379	100
APOC2-3600	G>A	rs7256684	intron1		0.287	0.298	0.277	1.000	98.9
APOC2-3617	C>T		intron1		0.005	0.000	0.011	1.000	98.9
APOC2-3692	T>G	rs12721060	intron1		0.011	0.011	0.011	1.000	98.9
APOC2-3778	A>T	rs5120	intron1		0.158	0.167	0.149	0.343	100
APOC2-3805	C>G	rs7257095	intron1		0.163	0.138	0.189	0.524	96.8
APOC2-3806	C>G	rs12709887	intron1		0.043	0.053	0.032	1.000	98.9
APOC2-3814	T>G	rs10422603	intron1		0.306	0.340	0.272	0.588	97.9
APOC2-3892	C>T	rs5121	exon2/UTR		0.027	0.021	0.033	1.000	96.8
APOC2-4086	G>A	rs114780592	intron2		0.021	0.031	0.011	1.000	100
APOC2-4112	G>C	rs74500990	intron2		0.059	0.052	0.065	1.000	98.9
APOC2-4118	G>A	rs201709243	exon3	Val20 Ile	0.005	0.010	0.000	1.000	100
APOC2-4319	G>A	rs5123	intron3		0.055	0.044	0.065	1.000	95.8
APOC2-4429	C>G	rs3745152	intron3		0.259	0.293	0.226	0.545	87.4
APOC2-4430_4431	ins3	rs35625559	intron3		0.259	0.293	0.226	0.545	87.4
APOC2-4458	C>T		intron3		0.024	0.043	0.000	1.000	44.2
APOC2-4460_4461	del1		intron3		0.157	0.161	0.154	0.449	56.8
APOC2-4493	C>T	rs4803776	intron3		0.179	0.188	0.170	0.002	96.8
APOC2-4513	A>C	rs180809422	intron3		0.011	0.011	0.011	1.000	92.6
APOC2-4532	C>T		intron3		0.194	0.216	0.167	0.097	70.5
APOC2-4534_4535	del1		intron3		0.165	0.171	0.158	0.170	83.2
APOC2-4587	A>C	rs5126	exon4	Lys 77 Gln	0.044	0.044	0.043	1.000	95.8
APOC2-4754	C>T	rs7253690	exon4/UTR		0.065	0.062	0.067	1.000	97.9
APOC2-4853_4854	del1	rs150448996	3'flamking		0.272	0.255	0.289	0.659	96.8
APOC2-4971	C>T	rs1130742	3'flanking		0.279	0.740	0.702	0.529	100
APOC2-4973_4974	ins1	rs199828513	3'flamking		0.005	0.000	0.011	1.000	100
APOC2-5004	G>A	rs10421404	3'flanking		0.305	0.344	0.266	0.551	100
APOC2-5018_5022	del5	rs78403558	3'flanking		0.058	0.083	0.032	1.000	100
APOC2-5303	T>C	rs7257468	3'flanking		0.284	0.292	0.277	1.000	100
APOC2-5310	G>T	rs7258345	3'flanking		0.285	0.302	0.267	1.000	97.9
APOC2-5324	T>C	rs7257476	3'flanking		0.295	0.302	0.287	1.000	100
APOC2-5398	G>A	rs12709889	3'flanking		0.25	0.240	0.261	1.000	98.9
APOC2-5491	C>T		3’flanking		0.005	0.010	0.000	1.000	100
APOC2-5512	G>A	rs12721064	3'flanking		0.005	0.010	0.000	1.000	100
APOC2-5562	G>C		3'flanking		0.021	0.010	0.032	1.000	100
APOC2-5586	T>G	rs73558127	3'flanking		0.089	0.104	0.074	1.000	100
APOC2-5612	A>G		3'flanking		0.063	0.062	0.064	1.000	100
APOC2-5771_5775	del5		3'flanking		0.005	0.011	0.000	1.000	97.9
APOC2-5815	A>G	rs10423208	3'flanking		0.293	0.302	0.283	1.000	98.9
APOC2-5922	A>G	rs10422888	3'flanking		0.121	0.156	0.085	0.258	100

Cont. Table 7

APOC2-5965	G>A		3'flanking	0.005	0.010	0.000	1.000	100
APOC2-6037	A>G	rs10402642	3'flanking	0.295	0.302	0.287	1.000	100
APOC2-6222	G>C		3'flanking	0.011	0.010	0.989	1.000	100
APOC2-6334	G>A		3'flanking	0.026	0.031	0.021	1.000	100

Nucleotide position is according to the reference sequence; Ch. Position: chromosomal position is according to NCBI build 138; (***) Unavailable data for population-specific variants or not analyzed indels; HWE-P (hardy Weinberg equilibrium p-value); %Geno (call rate); Grey-highlighted variants represent shared variants in both populations.

3.2 ANNOTATED COLORED FASTA

The colored FASTA adopted from SeattleSNPs database with some modifications have been made by adding color-coded sequencing discovered variants in each population. **Red**-colored variants represent NHW-specific variants, while **blue**-colored variants represent Black-specific variants, and **black**-colored variants represent overlapped variants in both populations. All variants that identified previously in database but not in our study are depicted with **Dark green** font. Yellow highlight is used for deletion and blue highlight is used for bases flank the insertion with population-specific colored-font. Variants identified in database (comparing to NCBI build 138) and in our study include reference SNPs ID in addition to its position according to the annotated reference sequence and the corresponding allele change. The color code used in SeattleSNPs reference sequence is as follows: light grey for flanking regions and introns, green for UTR, dark blue for exons, purple for repeat regions, and light blue for regions not scanned in SeattleSNPs database.

For all these four genes (*APOE, APOC1, APOC4,* and *APOC2),* we used SeattleSNPs database reference sequence, while we used NCBI (build 137) for their two hepatic control regions (*HCR-1* and *HCR-2*). For some genes with no sufficient coverage in either flanking regions, additional sequences were adopted from chip bioinformatics or gene bank database to

extend the sequencing coverage in the 5’ and 3’ flanking region. For *APOC1* gene we adopted 803 bp in the 5’flanking region and 942 bp in the 3’ flanking region from Chip bioinformatics. For *APOC4*, we adopted 546 bp in the 3’flanking region from Chip bioinformatics.

We noticed two issues in *APOC2* SeattleSNPs reference sequence where all subjects in the sequencing subsets had (P.65_66insC) and (P.178_179delG) similar to what we found in *APOC2* reference sequence from other databases (NCBI build 138, and Chip Bioinformatics). Additional issues were found in *APOC4* SeattleSNPs reference sequence where all subjects had C>G change at position 1722 (rs10409424) and G>C change at position 1723 (rs10409808). Since all subjects are homozygote for these two allele changes, we assumed that these two (C4-1722/rs10409424, and C4-1723/rs10409808) are errors in the reference sequence and thus are not polymorphisms. Moreover, we noticed some difference in *APOC1* reference sequence from SeattleSNPs database and that from genebank database where there is deletion T at position 1673, and position 4697 in SeattleSNPs reference sequence and insertion A at position 3173. Since we used genebank reference sequence in variant reporter software for variant detection, the nucleotide position of our data corresponds to the genebank reference sequence.

We observed that reference allele is the minor allele for couple of variants. For these overlapped variants in *APOC4/APOC2* genes, C2-1357/C4-4661 (rs22889120), and C2-1442/C4-4746 (rs2288911), seattleSNPs reference allele is the major allele (*APOC2* annotated FASTA), while Chip Bioinformatics reference allele is the minor allele (*APOC4* annotated FASTA). Additionally, reference allele was the minor allele for these two variants; C2-3600/rs7256684 and C2-4429/rs3745152. Moreover, reference allele is the minor allele for one deletion in *APOC2* at position C2-4853_4854delT, which is insertion not deletion. **Figure 12**

represents the annotated colored FASTA of all the sequenced four genes along with their two hepatic control regions (HCR1 and HCR2).

APOE annotated colored FASTA (Accession # AF261279.1)

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CTTGATGCTC AGAGAGGACA AGTCATTTGC CCAAGGTCAC ACAGCTGGCA 50  | REPEAT
ACTGGCAGAG CCAGGATTCA CGCCCTGGCA ATTTGACTCC AGAATCCTAA 100 | P.73/rs1081101[C>T]
CCTTAACCCA GAAGCACGGC TTCAAGCCCC TGGAAACCAC AATACCTGTG 150
GCAGCCAGGG GGAGGTGCTG GAATCTCATT TCACATGTGG GGAGGGGGCT 200 | P.173[A>G]
CCCCTGTGCT CAAGGTCACA ACCAAAGAGG AAGCTGTGAT TAAAACCCAG 250 | REPEAT
GTCCCATTTG CAAAGCCTCG ACTTTTAGCA GGTGCATCAT ACTGTTCCCA 300
CCCCTCCCAT CCCACTTCTG TCCAGCCGCC TAGCCCCACT TTCTTTTTTT 350 | P.308/rs769445[C>T] | REPEAT
TCTTTTTTTG AGACAGTCTC CCTCTTGCTG AGGCTGGAGT GCAGTGGCGA 400
GATCTCGGCT CACTGTAACC TCCGCCTCCC GGGTTCAAGC GATTCTCCTG 450
CCTCAGCCTC CCAAGTAGCT AGGATTACAG GCGCCCGCCA CCACGCCTGG 500 | P.471/rs439382[A>G] | P.494[C>T]
CTAACTTTTG TATTTTTAGT AGAGATGGGG TTTCACCATG TTGGCCAGGC 550 | P.526[T>C]| P.545/rs1081103[C>T]
TGGTCTCAAA CTCCTGACCT TAAGTGATTC GCCCACTGTG GCCTCCCAAA 600 | P.560/rs449647[A>T]
GTGCTGGGAT TACAGGCGTG AGCTACCGCC CCCAGCCCCT CCCATCCCAC 650 | P.618[G>C]| P.624/rs769446[T>C]
TTCTGTCCAG CCCCCTAGCC CTACTTTCTT TCTGGGATCC AGGAGTCCAG 700
ATCCCCAGCC CCCTCTCCAG ATTACATTCA TCCAGGCACA GGAAAGGACA 750
GGGTCAGGAA AGGAGGACTC TGGGCGGCAG CCTCCACATT CCCCTTCCAC 800
GCTTGGCCCC CAGAATGGAG GAGGGTGTCT GGATTACTGG GCGAGGTGTC 850 | P.832/rs405509[G>T]
CTCCCTTCCT GGGGACTGTG GGGGGTGGTC AAAAGACCTC TATGCCCCAC 900
CTCCTTCCTC CCTCTGCCCT GCTGTGCCTG GGGCAGGGGG AGAACAGCCC 950
ACCTCGTGAC TGGGGGCTGG CCCAGCCCGC CCTATCCCTG GGGGAGGGGG 1000
CGGGACAGGG GGAGCCCTAT AATTGGACAA GTCTGGGATC CTTGAGTCCT 1050 | Exon 1 | UTR
ACTCAGCCCC AGCGGAGGTG AAGGACGTCC TTCCCCAGGA GCCGGTGAGA 1100
AGCGCAGTCG GGGGCACGGG GATGAGCTCA GGGGCCTCTA GAAAGAGCTG 1150 | P.1109/rs9282609[C>T]
GGACCCTGGG AAGCCCTGGC CTCCAGGTAG TCTCAGGAGA GCTACTCGGG 1200 | P.1163/rs440446[G>C]
GTCGGGCTTG GGGAGAGGAG GAGCGGGGGT GAGGCAAGCA GCAGGGGACT 1250 | P.1231[G>A]
GGACCTGGGA AGGGCTGGGC AGCAGAGACG ACCCGACCCG CTAGAAGGTG 1300 | P.1279/rs877973[C>A]
GGGTGGGGAG AGCAGCTGGA CTGGGATGTA AGCCATAGCA GGACTCCACG 1350
AGTTGTCACT ATCATTTATC GAGCACCTAC TGGGTGTCCC CAGTGTCCTC 1400
AGATCTCCAT AACTGGGGAG CCAGGGGCAG CGACACGGTA GCTAGCCGTC 1450
GATTGGAGAA CTTTAAAATG AGGACTGAAT TAGCTCATAA ATGGAACACG 1500
GCGCTTAACT GTGAGGTTGG AGCTTAGAAT GTGAAGGGAG AATGAGGAAT 1550 | P.1522/rs769447[G>A]|
P.1539/rs184686013[A>G]
GCGAGACTGG GACTGAGATG GAACCGGCGG TGGGGAGGGG GTGGGGGGAT 1600 | P.1575/rs769448[C>T]|
P.1591/rs147236548[G>T]
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TGGGGATGGG GAGATAAGAG AAGACCAGGA GGGAGTTAAA TAGGGAATGG 1700
GTTGGGGGCG GCTTGGTAAA TGTGCTGGGA TTAGGCTGTT GCAGATAATG 1750
CAACAAGGCT TGGAAGGCTA ACCTGGGGTG AGGCCGGGTT GGGGCCGGGC 1800
TGGGGGTGGG AGGAGTCCTC ACTGGCGGTT GATTGACAGT TTCTCCTTCC 1850
CCAGACTGGC CAATCACAGG CAGGAAGATG AAGGTTCTGT GGGCTGCGTT 1900 | Exon 2 | UTR
                           M   K  V  L   W  A  A  L 8
GCTGGTCACA TTCCTGGCAG GTATGGGGGC GGGGCTTGCT CGGTTCCCCC 1950
  L  V  T   F  L  A                                   14
CGCTCCTCCC CCTCTCATCC TCACCTCAAC CTCCTGGCCC CATTCAGGCA 2000 | P.1998/rs769449[G>A]
GACCCTGGGC CCCCTCTTCT GAGGCTTCTG TGCTGCTTCC TGGCTCTGAA 2050
CAGCGATTTG ACGCTCTCTG GGCCTCGGTT TCCCCCATCC TTGAGATAGG 2100 | P.2072/rs189660912[G>A]
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TGAGATGAAG TCTCGCTCTG TCGCCCAGGC TGGAGTGCAG TGGCGGGATC 2200
TCGGCTCACT GCAAGCTCCG CCTCCCAGGT CCACGCCATT CTCCTGCCTC 2250
AGCCTCCCAA GTAGCTGGGA CTACAGGCAC ATGCCACCAC ACCCGACTAA 2300 | P.2269/rs6135770[G>A]| P.2294[C>T]
CTTTTTTGTA TTTTCAGTAG AGACGGGGTT TCACCATGTT GGCCAGGCTG 2350
GTCTGGAACT CCTGACCTCA GGTGATCTGC CCGTTTCGAT CTCCCAAAGT 2400
GCTGGGATTA CAGGCGTGAG CCACCGCACC TGGCTGGGAG TTAGAGGTTT 2450 | P.2440/rs769450[G>A]
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CTTTATTCTC CATCACCCCC ACACAGCCCT GCCTGGGGCA CACAAGGACA 2550 | P.2544/rs115299243[A>G]
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GCACTTTGGG AGGCCAAGGT GGGAGGATCA CTTGAGCCCA GGAGTTCAAC 2650
ACCAGCCTGG GCAACATAGT GAGACCCTGT CTCTACTAAA AATACAAAAA 2700
TTAGCCAGGC ATGGTGCCAC ACACCTGTGC TCTCAGCTAC TCAGGAGGCT 2750
GAGGCAGGAG GATCGCTTGA GCCCAGAAGG TCAAGGTTGC AGTGAACCAT 2800
GTTCAGGCCG CTGCACTCCA GCCTGGGTGA CAGAGCAAGA CCCTGTTTAT 2850
AAATACATAA TGCTTTCCAA GTGATTAAAC CGACTCCCCC CTCACCCTGC 2900
CCACCATGGC TCCAAAGAAG CATTTGTGGA GCACCTTCTG TGTGCCCCTA 2950 | P.2907/rs769451[T>G]
GGTACTAGAT GCCTGGACGG GGTCAGAAGG ACCCTGACCC ACCTTGAACT 3000
TGTTCCACAC AGGATGCCAG GCCAAGGTGG AGCAAGCGGT GGAGACAGAG 3050 | Exon 3| P.3038/rs111833428[G>A]
             G  C  Q   A  K  V   E  Q  A  V   E  T  E  27
CCGGAGCCCG AGCTGCGCCA GCAGACCGAG TGGCAGAGCG GCCAGCGCTG 3100
 P  E  P   E  L  R  Q   Q  T  E   W  Q  S   G  Q  R  W 44
GGAACTGGCA CTGGGTCGCT TTTGGGATTA CCTGCGCTGG GTGCAGACAC 3150 | P.3106/rs769452[T>C]
  E  L  A   L  G  R   F  W  D  Y   L  R  W   V  Q  T   60
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L  S  E  Q   V  Q  E   E  L  L   S  S  Q  V   T  Q  E  77
CTGAGGTGAG TGTCCCCATC CTGGCCCTTG ACCCTCCTGG TGGGCGGCTA 3250
 L  R                                                  79
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GGCCTGGGTC TCTGCTGGTT CTAGCTTCCT CTTCCCATTT CTGACTCCTG 3350
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TTCTGACTCA GTCTCTCACA CTCGTCCTGG CTCTGTCTCT GTCCTTCCCT 3450
AGCTCTTTTA TATAGAGACA GAGAGATGGG GTCTCACTGT GTTGCCCAGG 3500 | REPEAT
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AGTGCTGGGA TTAGAGGCAT GAGCCACCTT GCCCGGCCTC CTAGCTCCTT 3600
CTTCGTCTCT GCCTCTGCCC TCTGCATCTG CTCTCTGCAT CTGTCTCTGT 3650
CTCCTTCTCT CGGCCTCTGC CCCGTTCCTT CTCTCCCTCT TGGGTCTCTC 3700 | P.3673/rs769453[C>G]
TGGCTCATCC CCATCTCGCC CGCCCCATCC CAGCCCTTCT CCCCGCCTCC 3750
CACTGTGCGA CACCCTCCCG CCCTCTCGGC CGCAGGGCGC TGATGGACGA 3800 | Exon 4
                                        A  L  M  D  E  84
GACCATGAAG GAGTTGAAGG CCTACAAATC GGAACTGGAG GAACAACTGA 3850
  T  M  K   E  L  K   A  Y  K  S   E  L  E   E  Q  L   100
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T  P  V  A   E  E  T   R  A  R   L  S  K  E   L  Q  A  117
GCGCAGGCCC GGCTGGGCGC GGACATGGAG GACGTGTGCG GCCGCCTGGT 3950 | P.3937/rs429358[T>C]
 A  Q  A   R  L  G  A   D  M  E   D  V  C   G  R  L  V 134
GCAGTACCGC GGCGAGGTGC AGGCCATGCT CGGCCAGAGC ACCGAGGAGC 4000
  Q  Y  R   G  E  V   Q  A  M  L   G  Q  S   T  E  E   150
TGCGGGTGCG CCTCGCCTCC CACCTGCGCA AGCTGCGTAA GCGGCTCCTC 4050 | P.4036/rs769455[C>T]
L  R  V  R   L  A  S   H  L  R   K  L  R  K   R  L  L  167
CGCGATGCCG ATGACCTGCA GAAGCGCCTG GCAGTGTACC AGGCCGGGGC 4100 | P.4075/rs7412[C>T]
 R  D  A   D  D  L  Q   K  R  L   A  V  Y   Q  A  G  A 184
CCGCGAGGGC GCCGAGCGCG GCCTCAGCGC CATCCGCGAG CGCCTGGGGC 4150
  R  E  G   A  E  R   G  L  S  A   I  R  E   R  L  G   200
CCCTGGTGGA ACAGGGCCGC GTGCGGGCCG CCACTGTGGG CTCCCTGGCC 4200
P  L  V  E   Q  G  R   V  R  A   A  T  V  G   S  L  A  217
GGCCAGCCGC TACAGGAGCG GGCCCAGGCC TGGGGCGAGC GGCTGCGCGC 4250
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GCGGATGGAG GAGATGGGCA GCCGGACCCG CGACCGCCTG GACGAGGTGA 4300
  R  M  E   E  M  G   S  R  T  R   D  R  L   D  E  V   250
AGGAGCAGGT GGCGGAGGTG CGCGCCAAGC TGGAGGAGCA GGCCCAGCAG 4350 | P.4310/rs199768005[T>A]
K  E  Q  V   A  E  V   R  A  K   L  E  E  Q   A  Q  Q  267
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GCCCCTGGTG GAAGACATGC AGCGCCAGTG GGCCGGGCTG GTGGAGAAGG 4450
  P  L  V   E  D  M   Q  R  Q  W   A  G  L   V  E  K   300
TGCAGGCTGC CGTGGGCACC AGCGCCGCCC CTGTGCCCAG CGACAATCAC 4500
V  Q  A  A   V  G  T   S  A  A   P  V  P  S   D  N  H  317
TGAACGCCGA AGCCTGCAGC CATGCGACCC CACGCCACCC CGTGCCTCCT 4550 | UTR| P.4528[C>T]
GCCTCCGCGC AGCCTGCAGC GGGAGACCCT GTCCCCGCCC CAGCCGTCCT 4600 | P.4569[G>T]
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CTGGCCTCCC CCTGTGATTT CCTCTAAGCC CCAGCCTCAG TTTCTCTTTC 4700
TGCCCACATA CTGGCCACAC AATTCTCAGC CCCCTCCTCT CCATCTGTGT 4750 | P.4737/rs117656888[C>G]
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CCTCTGCCTC TTGGGTTCAA GCGATTCTGC TGCCTCAGTA GCTGGGATTA 4900
CAGGCTCACA CCACCACACC CGGCTAATTT TTGTATTTTT AGTAGAGACG 4950
AGCTTTCACC ATGTTGGCCA GGCAGGTCTC AAACTCCTGA CCAAGTGATC 5000 | P.4951/rs1081105[A>C]
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CCGGCCTCTG CCCCTCTTTC TTTTTTAGGG GGCAGGGAAA GGTCTCACCC 5100 | REPEAT
TGTCACCCGC CATCACAGCT CACTGCAGCC TCCACCTCCT GGACTCAAGT 5150
GATAAGTGAT CCTCCCGCCT CAGCCTTTCC AGTAGCTGAG ACTACAGGCG 5200
CATACCACTA GGATTAATTT GGGGGGGGGG TGGTGTGTGT GGAGATGGGG 5250 | P.5223[G>C] | P.5229/rs80125357
[G>T]| P.5230/rs55729972[delG/insG]| P.5231[T>G]
TCTGGCTTTG TTGGCCAGGC TGATGTGGAA TTCCTGGGCT CAAGCGATAC 5300
TCCCACCTTG GCCTCCTGAG TAGCTGAGAC TACTGGCTAG CACCACCACA 5350
CCCAGCTTTT TATTATTATT TGTAGAGACA AGGTCTCAAT ATGTTGCCCA 5400 | P.5361/rs1081106[T>C]
GGCTAGTCTC AAACCCCTGG GCTCAAGAGA TCCTCCGCCA TCGGCCTCCC 5450
AAAGTGCTGG GATTCCAGGC ATGGGCTCCG AGCGGCCTGC C          5491
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APOC1 ANNOTATED COLORED FASTA

```
CAAAAAAGGG AGACTGAGAA CCATGAAGTT AAGAGCCCAG AGAATATCAC 50
GGTGGTCTGG GGTGCTTCAA GGGCTGGTCT GGAATAAATT GGAGGTGGCA 100
CGCAGGGTAG GAGCGCCGGG CCAACTGGGA GACCCAGCAA CATAAAGGAA 150
AAGTTGTTGG GGCTGAGGAG GCTTGCTGAG AGAGGGGAAG TGAGGGAAAG 200
AGGTGATCTA GGGACACGGT GTGAATGAGG GGGGGATGAG ATCACAGGGT 250
TATTACTGGG AGACCCCTGA GGGAAGATGG CCACAGGGAC AGGACAAGGC 300
TGTCTTCTTA AGGGAGGAGA CCACCCCTCA TATTGTCTTA TGCCCAATTT 350
CTGCCTCCAA AGAAAGAAAA AGTAAAAACT AAAAGGCAGA AATGAAATCC 400
ACAAGCAGAC AGCCCGCGCC ACACCCTGGG CCTGGTGGTT AAAGATTGAC 450
CCCTGACCTA ATCCGTTAGG TTATCTATAG ATTACAGACA TTGTATAGAA 500
AAGCACTGTG AAAATCCCTA TTCTGTTTTG TTCCGATCTA ATTACCGGTG 550
CATGCAGCCC CCAGTCACGC ATCCCCTGCT TGTTCAATCG ATCACGACCC 600
TCTCACGTGC ACCCACTTAG AGTTGTGAGC CCTTAAAAGG AACAGGGATT 650 | P.607/rs72654447[G/A]
GCTCACTCGG GGAGCTCGGC TCTTGAGACA GGAATCTTGC CCATTCCCCG 700 | P.655/rs66807996[A/T] |
P.659/rs72654448[G/C] | P.698/rs72654449[C/A]
AACGAATAAA CCCCTTCCTT AACTCAGCGT CTGAGGAATT TTGTCTGCGG 750 | P.703/rs3207187[C/T] |
P.720_721/rs72654451 [insCGTT]
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CCCCACAGAG TCAGGAAGAT TGAGAGGTGA GAGTGCTGAA CGGGGAGGGG 850
CTTTGGGGCT AAGGGAAGTG CCCGGGACCC CACCTGACCC CAACGCTCAC 900 | P.894/rs190454394[C/T]
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TCAGGGGAAG GCTCAGGAGG AGGGAGATCA ACATCAACCT GCCCCGCCCC 1000
CTCCCCAGCC TGATAAAGGT CCTGCGGGCA GGACAGGACC TCCCAACCAA 1050
GCCCTCCAGC AAGGATTCAG GTTGGTGCTG AGTGCCTGGG AGGGACACCC 1100 | Exon 1 | UTR
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GGAGGTAGGG AGGGAGGAGG GTGCCACTGA TCCCCTGAAC CCCTGCCTCT 1200 | P.1166/rs72654452[G/A]| P.1170[G/A]
GCCTCCAGAG TGCCCCTCCG GCCTCGCCAT GAGGCTCTTC CTGTCGCTCC 1250 | Exon 2 | UTR |
                           M   R  L  F   L  S  L   7
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P.1249/rs12721047[C/T]
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P  V  L  V   V  V  L   S  I  V   L  E                 19
 GGAGAATTGC GGAGTTGGAG ATTTGGAAGA GTGAAGGTGG CTACAGGCCT 1350 | P.1317/rs12721048[G/A]|
 P.1331/rs10408994[G/A]
GGGGTCCCGG CTTAGAGGAC CTCTGAGAGC TCCGGGGCCC CTTCTGGGTC 1400
GTGGTTGCCT CATCGTGGTC GGGTGGGTCT CCAGGTTCTC CCAGGCTCAG 1450 | P.1422[G/A]
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TTGAGGCCCA CACCTCTGGG ATTGGCTGTC CTGCTTCGAC AGCCTTGAAA 1550 | P.1526/rs5114[C/T]
GTGGGTAAGC TGGGTGGGGG GCTCTGGGAG AGGTCAGTGC TGAGTAAGGC 1600 | P.1566/rs12691088[G/A]
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CCGCGCCCGG CTAATTTTTT GTATTTTCAG TAGAGACAGG GTTTCACCGT 1850
GGTCTCGATC TCCTGACTTT GTGATCCGCC TGCCTCGACC TCCCAAAGTG 1900 | P.1870/rs5117[T/C]
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GCTACAGAGC AAGACTCCAT CTCCAAAAAA AAAAAAAAAA AAACAAATTT 2500
TGAACCCCTG CCCATCTTCC TGGCAGGCCC AGCCCCAGCC CAGGGGACCC 2550 | Exon 3
                          G  P   A  P  A   Q  G  T   27
CAGACGTCTC CAGTGCCTTG GATAAGCTGA AGGAGTTTGG AAACACACTG 2600
P  D  V  S   S  A  L   D  K  L   K  E  F  G   N  T  L  44
GAGGACAAGG CTCGGGAACT CATCAGCCGC ATCAAACAGA GTGAACTTTC 2650 | P.2629[G/A]
 E  D  K   A  R  E  L   I  S  R   I  K  Q   S  E  L  S 61
TGCCAAGATG CGGTTAGAAC CCTTCCCAGG GCACGGGAGA GCTGGGGTGT 2700
  A  K  M   R                                        65
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AGAAAGACAG GGAGGGAGGG AGGAAGGAAG GGAGGGAGGG AGGGAAAATA 4000
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CAGTGAGCCG AGATCATGCC ACTGCACTCC AGCCTGGGCG ACAAGGCGAG 4300 | P.4298/rs12721044[insA]
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TCGAGACTAG CCTGCTCAAC ATAATGAAAC CCTCTCTGTA CTAAAAATAC 4450
AAAAATTAGC TGGGTGTGGT GGCAGGCACC TGTAGTCCCA GCTACTCGGG 4500
AGGCTGAGGC AGGAGAATGG CTTGAACCTG GGAGGCAGAG GTTGCAGTGA 4550
GCCGAGACAG TGCCATTGCA CTCCAGTCCA GGTGACAGAG CGAAACTCCA 4600
TCTCAAAAAA AAAAGGAAGG CATTGGTAGC AAGAGATGGC AGGCCTTGAA 4650
AGCCAGGCCA GGGTGAAGTG TTTCTTTTTT TTTTTTTTTT TTTTTTCTTT 4700 | REPEAT
TTAAATTTTT TTTTTTGAGA CGGAGTCTCG CTCTGTCACC CAGGCTGGAT 4750
TGCAGTGGCC TGATCTCGGC TCACTGCAAG TTCCGCCTCC CGGGTTCATG 4800
CCATTCTCCT GCCTCACCCT CCCGAGTAGC TGGGACTACA GGCACCTGCC 4850 | P.4824/rs12721056[G/T]
ACCACGCCAG CTAATTTTTT GTATTCTTAG TAGAATGTAG AATTTACTTA 4900
GTAGAATTTT TTGTATTCTT AGCCAGCATG GTCTCGATCT CCTGACCTGG 4950
TGATCCGCCC GCCTCGGCCT CCCAAAGTGC TGGGATTACA GGCGTGAGCC 5000 | P.4957/rs484195[G/A]
ACGGCGCCCG GCCTTATTTT TTCTTTTTGA GATGTACCCA GACTGGAGTA 5050 | P.5006/rs112528434[G/T]
CAGTGGTGCG ATCTCGGCTT ACTGGAACCT CCACCTCCCG GGTTCAGGCA 5100 | REPEAT| P.5053_5054/rs12721052[del1]
ATTCTCCTGC CTCAGCCTCA TGAGTACTTG GAACTACAGG TGTGTGACAC 5150
CACACATGGT ATTTTTTGTA TTTTTAGTGA AGATGACATT TCACCATGTT 5200
GCCCAGGTTG GTCTCGAACT CCTGACCTCA AGTGATCAGC CTACCTCGGC 5250 | P.5240/rs12721051[C/G]
CTCCCAAAGT GTTGGGATTA CAGGCGTGAG CCAAATGCCC AGCCAAGGGT 5300
AAAGTGTTTA GACTTCAACG TGCTTTGGTC CATCTGGGAA ACTGAGGCAC 5350 | P.5338/rs12721050[G>A]
AGAAGTTGGC CCACCCAGCC CAGCGGTCCT CCTAATCCCA CAGACAGTGG 5400
GGATGGAGAT TCTGCAAGGG GAAGAGGTGG GAGTCAGGTA GCAGGCAGAA 5450
TTTGGACAGC CTGGGAGGTA GCTGCACACA GTGACCCCCT TCCTTATTCC 5500
TCCCCACAGG GAGTGGTTTT CAGAGACATT TCAGAAAGTG AAGGAGAAAC 5550 | Exon 4
            E  W  F   S  E  T  F   Q  K  V   K  E  K   78
 TCAAGATTGA CTCATGAGGA CCTGAAGGGT GACATCCCAG GAGGGGCCTC 5600 | UTR
L  K  I  D  S                                           83
TGAAATTTCC CACACCCCAG CGCCTGTGCT GAGGACTCCC TCCATGTGGC 5650 | P.5641/rs1084725[T/G]
CCCAGGTGCC ACCAATAAAA ATCCTACAGA AAATTCTCTC CTGAGTGCTT 5700 | P.5667/rs12721054[A/G]
CTTTACTCTG GGGAAGGGGC TGCGGGAGAG GGTAGGGGCT TCCAGAGAGG 5750 | P.5716/rs12721055[G/T]|
 P.5717/rs72654457[G/C]
GCAGGGTCTG CAGGAGAGGG CAGGGGCTAA ACCTTAGGTA CTCCTCACAA 5800 | P.5773[G/A]
GCCCTCCAAT GCCCTATCTA CTTGCCCTGT GCTGAGGATG TTTTAACTCC 5850
ATGGTCTCAA AAGAGTCTTC CTAAGAACCC TGCAAACTGG GCCTTATTAA 5900
TCCCATAAGG GCATTGAGGC CCAGAGAGGT GAAGTTACTT GTATAAGGTC 5950 | P.5926/rs56131196[G/A]
ACACAGCCAG GAAGTAGAGA ACTGGAACTA GATTGAACCC TCAGCCTAGC 6000
AATGTCACTA TGCTACACTT TTCCTAGTGT GGTCTACCCG AGATGAGGGG 6050 | P.6026/rs4420638[A/G]
CTGAGGTTTT TTTTTGTTTT TGTTTCTGTT TTGAGGCAGA CTCACTCTCT 6100
CCCCCAGGAT GGAGTACAGT GGTGCGATCT CAGCTCACTG CAACCTCCAC 6150 | P.6122/rs142134314[G/C]
CTCCCAGGTT CAAGAGATTA TCCTGCCTCA GCCTCCCAAG TAGCTGGGAT 6200 | P.6158[G/A]
TTACAGGTGT GCGCCACCAC ACCCAGCTAA TTTTTGTATT TTTAGTAGAG 6250 | P.6213[G/A]
ACAGGGTTTC ATCATGTTGG CCAGGCTGGT CTCCAACTCC TGGGCTTAAG 6300
CAATCCTCCT GCCTTGGCCT CCCAAAGTAT TAGAATTACA GGCGTGAGCC 6350
ACTGTGCCTG GCTCTTATGT AAAATTAAAC CACATACACA TGAGAAACAA 6400
CCCTATGTAA TTAAGATTTC TTTCTTTTTT TTTTTTTTTT TAAGAGATGG 6450
AGTCACCCAG GCTGGAGTGC AGTTGCACAA TCTCCATTCA CTGCAGCCTT 6500
GCAACCTCCA CCACCTGAGT TCAAGGGATT CTCCTGCCTC AGCCTCCTGA 6550
GTAGCTGGGA TTATAGGCAT GTGCCACCAC GCCCAGCTAA TTTTTTTGTA 6600
TTTTTAGTAG AGACGGAATT TCCCCATGTT GGCCAGGCTG GTCTCAAACT 6650
CCTGGCCTTA AATGATCCAC CCGTCCTGGC CTCCCAA              6687
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HCR-I ANNOTATED COLORED FASTA

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GTATCCAGCC AGGAGGGGAG GGGCTAGAGA CACCAGAAGT TTAGCAGGGA  50
GGAGGGCGTA GGGATTCGGG GAATGAAGGG ATGGGATTCA GACTAGGGCC  100
AGGACCCAGG GATGGAGAGA AAGAGATGAG AGTGGTTTGG GGGCTTGGTG  150
ACTTAGAGAA CAGAGCTGCA GGCTCAGAGG CACACAGGAG TTTCTGGGCT  200
CACCCTGCCC CCTTCCAACC CCTCAGTTCC CATCCTCCAG CAGCTGTTTG  250
TGTGCTGCCT CTGAAGTCCA CACTGAACAA ACTTCAGCCT ACTCATGTCC  300 | P.292/rs4803771[C>G]
CTAAAATGGG CAAACATTGC AAGCAGCAAA CAGCAAACAC ACAGCCCTCC  350
CTGCCTGCTG ACCTTGGAGC TGGGGCAGAG GTCAGAGACC TCTCTGGGCC  400 | P.362[C>A]
CATGCCACCT CCAACATCCA CTCGACCCCT TGGAATTTCG GTGGAGAGGA  450 | P.423[C>G]| P.424/rs117664574[G>A]
GCAGAGGTTG TCCTGGCGTG GTTTAGGTAG TGTGAGAGGG TCCGGGTTCA  500
AAACCACTTG CTGGGTGGGG AGTCGTCAGT AAGTGGCTAT GCCCCGACCC  550
CGAAGCCTGT TTCCCCATCT GTACAATGGA AATGATAAAG ACGCCCATCT  600 | P.575/rs157599[A>G]
GATAGGGTTT TTGTGGCAAA TAAACATTTG GTTTTTTTGT TTTGTTTTGT  650
TTTGTTTTTT GAGATGGAGG TTTGCTCTGT CGCCCAGGCT GGAGTGCAGT  700
GACACAATCT CATCTCACCA CAACCTTCCC CTGCCTCAGC CTCCCAAGTA  750 | P.727/rs149345[T>G]
GCTGGGATTA CAAGCATGTG CCACCACACC TGGCTAATTT TCTATTTTTA  800
GTAGAGACGG GTTTCTCCAT GTTGGTCAGC CTCAGCCTCC CAAGTAACTG  850
GGATTACAGG CCTGTGCCAC CACACCCGGC TAATTTTTTC TATTTTTGAC  900
AGGGACGGGG TTTCACCATG TTGGTCAGGC TGGTCTAGA              939
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****Yellow-highlighted sequences represent the 325bp functional domain**

HCR-II ANNOTATED COLORED FASTA

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GGAGGGGAGT GGCTAGAGAC ACCAGAAGAT TAGCAGGGAG GAGGGTGCAG 50
GGTTTCGGGG GATGAGGGGA TGGGATTCAG ACCAGGGTAA GGATCCAGGG 100
GTAGAGAGAA AGATTTGAGA GTGGTTTTGG GGCTTGGTGA CTTAGAGAAC 150
AGAGTTGCAG GCTCTGTTTT TGGGCCCGCC CTGCCCCCTT CCGACCTCTT 200 | P.188/rs35136575[C>G]
AGTTCCTATC CTCCAGCAGC TGTTTGTGTG CTGCCTCTGA AGTCCACCCT 250
GAATGACCTT CAGCCTGTTC CCGTCCCTGA TATGGGCAAA CATTGCAAGC 300 | P.286[G>A]
AGCAAACAGC AAACACATAG CCCTCCCTGC GTGCTGACCT TGGAGCTGCG 350
GCAGAGGTCA GAGACCTCTC AGGGCCCATA CCACTTCCAA CATCCCCTTG 400 | P.365[C>A]
ATCTCTTGGA TTTTGGTGGA GAGGGGCAGA GGTTGTCCTG GCCTGGTTAG 450
GTAGTGTGAG AGGGTCCCGG TTCAAAACCA CCACTTGCTG GTTGAGGAGT 500
CGTCAGTAAG TGGCTGCGCC CCCACCCTGA GGCTTGTTTC TCCATCTGTA 550 | P.523/rs118004808[C>T]
CAATGGAAAT GATGAAGATG CCCACCTGAT AGGGTTTTTG TGGCAAATAA 600
GTAAGTAGTT TTTTTGTTTT TCTTTTTCTT TTTTTTTTTT TTTTTTTGAG 650 | P.632[T>C]
ATGGAGTCTC ACTCTGTCAC CAGGCTGGAG CGCAGTGGCG TGATCTCGGC 700
TCACTGCCAA CTCCACCTCC CGGGTTCAAG CGATTCTCCT GCCTCAGCCT 750
CTGAGTAGCT AGGACTACAG GCGCCCGCCA CCACACCCAG CTAATTTTTG 800
CATTTTTAGT AGAGATGGGG TTTCACCATG TTGGCCAGGA TGGTCTCAAT 850
CTCTTGACCT TGTGATCCAC CTGCCTCGGC CTCCCAAAGT GCTG       894
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****Yellow-highlighted sequences represent the sequences of 85% homology with the 325bp functional domain of HCR-I.**

APOC4 ANNOTATED COLORED FASTA

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GAGACGGAGT CTTGCTCTTT CGCCCAGGCT GGACTGCAGT GGCGCGATCT 50  | REPEAT
CGGCTCAATG CAAGCTCCAC CTCCCAGGTT CACGCCATTC TCCTGCCTCA 100 | p.65[C>T]| p.92_94/rs12721101[delCCT]
GCCTCCCGAG TAGCTAGGAC TACAGGCGCC TGCCACCACG CCTGGCTAAT 150 | p.108[G>A]/rs112391061| p.116[A>G]
TTTTCATATT TTTAGTAGAG ATGGGGTTTC ACCGTGTTAG CCAAGATGGT 200 | P.150_151[ins114]
CTCAATCTCC TGACCTCGTG ATCCGCCTGC CTCGGCCTCC CAAAGTGTTG 250 | p.204/rs4803773[A>G]| p.233[C>T]|
p.245/rs192072159[G>T]
GGGTTACAGG CATGAGCCAC CGCGCCTGGC CAACAGCAAT GATCTTTGAG 300 | REPEAT
CACCTATATT GCCAGTCTCC ACGGTAAGAG CTTTCTTCAT TTTTTGTTTT 350 | REPEAT
GTTTTGTTTC AAGACAGAGT CTTGCTCTGT CACCCAGGCT GGAGTGCAGT 400 | p.368[A>G]
GGTGTGATCG CGGCTCACTG CAGCCTTCAC TTCCCGGGTT CAAGCCATTC 450 | p.438/rs146656012 [G>A]
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TCCTGCCTCA GCCTCCCAAG TAGCTGGGAT TACAGGCACG CATCACTACT 500 | p.489/rs140241604 [C>T]
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GCCAGGTTGG TCTCAAACTC CTGGCCTCAT ATGATCTGCC CACCTCGGCC 600
TCCCAAAGTG CTGGGATTAC AGGCGTGAGC CACTGCGCCT TTCTTTGTAT 650 | REPEAT| p.636[C>T]|
p.637/rs73558107[G>T]
TTGTTCAAGT AATATACTGA AATATGTACT GTGCCTCCCA CTTTATGGAG 700
GAGGAAACTG AGGCCAGCAA ATGAGGCTGT CATGGGAGGT GGAGACAGGA 750
TTTGAACCTG CCTCAGTGCA GGAGGCTCAA GAGCCTCTGT CTTCTCTCAG 800 | p.757/rs12721105[C>A]
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CTGATTGCCA CTGTCACCTG GGCCCTGCTC TCTGAAGTCT CTGCCAAGCG 900
GGGAGGTGGC CGGGGGAGGG CCCTGCTCTG TGCAGCCTCC CCTCCCCCGG 950
CCCGCAGAGT TGAGCACAGA GGGACAGAGG CACGGAACCC CCAGAAATGT 1000 | Exon 1 | UTR| p.968/rs76214972[A>G]
                                                  M   1
CCCTCCTCAG AAACAGGCTC CAGGCCCTGC CTGCCCTGTG CCTCTGCGTG 1050
S  L  L  R   N  R  L   Q  A  L   P  A  L  C   L  C  V  18
CTGGTCCTGG CCTGCATTGG GGGTGAGAAG AAGTGGGTGG AGGGATGTGG 1100 | p.1088[T>G]
 L  V  L   A  C  I  G                                  25
GGCCCACACC TGGTGGGTGT GAGTGTGGCT GTGTGTCCTG TGGCTCTGTA 1150 | p.1130[T>C]| P.1150/rs148247675[A>G]
GCCACGTGAG ACATGAGTAC GGAGTGTGTG CGTTTCATGG CGTGCGTATG 1200 | p.1192/rs113745034[G>A]
CATGTGCGTG TCGGGGAGTG TGTGTGTCGG TGGCTGAGAG TGAAGTGTGA 1250 | p.1229[G>C]
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GTGGAAGTGG GAGTATGCAG TCGTGGTAAA AAAGTGCATG TCTGTGTGCA 1350 | p.1325_1327[delGGT]
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TATTTGAGTG TGTGGACATG TGTGAGGGGG TGAGTGTGTG CTGGTGTGTA 1450 | p.1430_1431[insG]
CGTCTGTGTT TTGCATATGC ATTTTTTTTT TTTTTTTTGA GACGGAGTCT 1500 | REPEAT
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CTCACTGCAT CATCCGCCTA CCCGTTTCAA GGGATTCTCC TGCCTCAGTC 1600
TTCAGAGTAT TTGGGACTAC AGACACACGC CACCATGCCT GGCTAATTTT 1650 | REPEAT
TTTTTTTTGA GACGGAGTCT CGCTCTGTTA CCCAGGCTGG AGTGCAGTGG 1700
CGTGATCTTG GCTCACTGCA ACGTCCGCCT CCCGGGTTCA CGCCATTCTC 1750 | p.1702/rs12721102[G>A]| p.1719[C>A]|
p.1733/rs12721111[C>T]
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TGGCTAATTT TTTGTATTTT TACTAGAGAC GGGGTTTCGC CGTGTTAGCC 1850 | p.1823[C>G]
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AATTTTTTTA TATTTTTGGT AGAGACAGGG TTTTGCCATG TTGCCCAGGC 2000
TGGTCTTGAA ATCCTGACCT CAGGTGATCC GCCCGCCTTG GCCTCCCAAA 2050
GTGCTGGGAT TACAGGCATG AGCCACCACG CCCGGCCATG TACTTTATGT 2100 | p.2063[C>G]| p.2099/rs111339708[G>T]
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TTTAATACAG GGCCAGGCAC GGTGGCTCAT GCCTGTAATC CCAGCACTTT 2200 | REPEAT
CGGAGGCCGA GGCGGGTGGA TCGCAAGGTC AGGAGATTTG AGATCATCCT 2250
GGCTAACAGA TGGGTAAAAA CCCATCTCTA CTAAAAATAC AAAAAATTAG 2300
CCATGCATGG TGGCATGCGC CTGTAGTCCC AGCTACTCGG GAGGCTGAGG 2350
CCGGAGAATC ACTTGAACCC GGGAGGCAGA GGTTGCAGTG AGCCGAGATC 2400
GCGCCACTGC ATTCCAACCT GGGTGACAGA GCGAGACTCC GTCTGAAAAA 2450
AAAAAAAAAT TTAACACGTA TGTAGACAAT GTGCAAGGCA CCATTCCATG 2500 | p.2467/rs115225947[C>T]| REPEAT
TGCATCGTAT GTAGTAACTC TTAATTCTCA CGATAACCCT GAGGTAGATA 2550
TTATTACCCC GTTCTACAAA AGGAGAAACA GTCCTGGGGA GACAGGATAA 2600 | p.2557[C>A]| p.2559/rs5155[C>T]
GTCACCGGCC AAGGCACACA GCCAGCTACA TGTGGCCCCC GCGTGACGGC 2650 | p.2607/rs5156[G>A]|
p.2623/rs5157[C>T] | p.2640/rs5158[C>T]| p.2641[G>A]
TGGTCTCTGT AGGCGAGGCT TTGTCCAGAT GCGTGGGTAG AAGGTCTGGC 2700 | p.2678/rs148564866[G>C]|
p.2683/rs12721109[G>A]
CCGGAAAGAG GAACTGACAG CAAGGCTAAG CCAATGTCTG CCCCTGGGGG 2750 | p.2703/rs12721108[G>T]
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p.2767/rs12721107[G>T]
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AGCAAAATCA GGTGGTGAAG GGAGGCATCA GAGGATGGCA ATTAGAGAGG 2900 | p.2886/rs12709883[T<C]
CCATTAGAGG GGAACCACAG GCAGACAGGG TGACAGGAGG GACTACTGAC 2950
ACAAGGTGAA GAGATGGCCC AGCCGGACGG GGTGGCTCAC ATCTGTAATC 3000 | REPEAT | p.2971/rs5159[A>G]
CCAGCATTTT GGGAGCCCGA GGTGGGTGGA TCACTTGAGG TCAGGAGTTC 3050
GAGGCCCCAA CATGGCAAAA CCCCATCTCT TCTAAAAATA CAAAAATTAG 3100
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CAGGAAAATT GCCTGAATCC AGGAGGTGGA GGTTGCAATG AGACGAGATC 3200
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ATGACACTGC ACTCCACCCT GGGCAACAGA GCAAGAGACT GACTCTGTCT 3250 | p.3213/rs28616151[T>C]
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GAGGGGTTAG CGGTCAGGGG ACACATAAGG GTAAAGGCAG GAGGCAAGAG 3350 | p.3348[G>A]
GACTGGCAGG GGGCTGCCCC TGGGCCACCG GGAGCGACAC AGGATGAGCA 3400 | p.3363/rs60170431[G>A]|
p.3380/rs12721104[G>A]
TGGAGGGAAA GGGAGAAGGG GATTCTAGGG TCCCAGCCTA CCCAAGTTGC 3450
CCTCTGGTTC CACCTAGCAT GCCAGCCAGA GGCCCAGGAA GGAACCCCGA 3500 | Exon 2 | p.3498/rs1132899[C>T]
                  A   C  Q  P  E   A  Q  E   G  T  P   36
GCCCCCCACC AAAGCTAAAG ATGAGTCGCT GGAGCCTGGT GAGGGGCAGG 3550 | p.3502/rs10423683[C>T]|
p.3546/rs12691089[G>A]
S  P  P  P   K  L  K   M  S  R   W  S  L  V   R  G  R  53
ATGAAGGAGC TGCTGGAGAC AGTGGTGAAC AGGACCAGAG ACGGGTGGCA 3600 | p.3592/rs12691090[C>T]
 M  K  E   L  L  E  T   V  V  N   R  T  R   D  G  W  Q 70
ATGGTTCTGG TGAGGGTGTG CTGGGCTGGG TGGTGGGAGG GGACTCCTGG 3650 | REPEAT
  W  F  W                                              73
GTCTGAGGGA GGAGGGGCTG GGGCCTGGAC CCCTGAGTCT CAGGGAGGAG 3700 | p.3700[G>A]
GAAAGGGTGG GAGTGGGGCT GTGACCCCTA GGTCTGGGAG GAGTGGAGGG 3750
TTAGAGCTGA GAGCAGGAAC TCCTAGGTCA CAGAGAGGAG CGGATAAATG 3800 | p.3792/rs5165[G>A]
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TCCTGTAGGA GCCCGAGCAC CTTCCGGGGC TTCATGCAGA CCTACTATGA 3900 | Exon 3
           S  P  S  T   F  R  G   F  M  Q   T  Y  Y  D 87
CGACCACCTG AGGGACCTGG GTCCGCTCAC CAAGGCCTGG TTCCTCGAAT 3950 | p.3927/rs5167[T>G]
  D  H  L   R  D  L   G  P  L  T   K  A  W   F  L  E   103
CCAAAGACAG CCTCTTGAAG AAGACCCACA GCCTGTGCCC CAGGCTTGTC 4000 | p.3969/rs138548797[A>C]
S  K  D  S   L  L  K   K  T  H   S  L  C  P   R  L  V  120
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 C  G  D   K  D  Q  G                                  127
GTGGCGGGTG CCTGTAGTCC CAGCTACTCA GGAGGCTGAG GTAGGATGAT 4100
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GCCCTCACTG AGAGCTTCGC CCTTGTCTCC TACAAGCTCT GACTCCATTC 4500
CCAGTGGGCA CCCAGCACCT CCAACCCCTC CACAGCCCCC AACCCAGCCT 4550 | p.4533/rs112698600[C>T]
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GGGGGTTGTG GCTGTGGAGC GGAAGTGGGT CTCAACCACT ATAAATCCTC 4750 | p.4746/rs2288911[T>G]
TCTGTGCCCG TCCGGAGCTG GTGAGGACAG CCTGCCAGAG TCTGGTAAGA 4800
AAGGGACTCA GGGTGCGGGG ACAGGGGGGC GTCAGCAGGG AGAGGGCAAA 4850 | p.4844/rs75463753[G>A]
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GAACCATGAC TGTGTGTGTG TGTGTGTGTG TGTGTGTGTG TGTGTGTGTG 4950 | p.4912[G>C]
TGTGAGAGAG AGAGAGAGGG AGATGGAGTC TCGCTATGTA GCCCAGGCTA 5000
GACTCAAACT CCTGGGCTCA AGCAATCCTC CTGCCTCAGC CTCCCCAGTA 5050
GCTGGGACTA CAGGTGCACC ACCACACTCC ACAAAT                5086
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APOC2 ANNOTATED COLORED FASTA

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GGTTAGCGGT CAGGGGACAC ATAAGGGTAA AGGCAGGAGG CAAGAGGACT 50
GGCAGGGGGC TGCCCTGGGC CACCGGGAGC GACACAGGAT GAGCATGGAG 100 | P.59/rs60170431[G>A]| P.65_66insC|
P.75/rs12721104[G>A]
GGAAAGGGAG AAGGGGATTC TAGGGTCCCA GCCTACCCAA GTTGCCCTCT 150
GGTTCCACCT AGCATGCCAG CCAGAGGGCC CAGGAAGGAA CCCCGAGCCC 200| p.178_179delG| P.194/rs1132899[C>T]|
P.198/rs10423683[C>T]
CCCACCAAAG CTAAAGATGA GTCGCTGGAG CCTGGTGAGG GGCAGGATGA 250 | P.228/rs5164[G>A]|
P.242/rs12691089[G/A]
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AGGAGCTGCT GGAGACAGTG GTGAACAGGA CCAGAGACGG GTGGCAATGG 300 | P.288/rs12691090[C>T]
TTCTGGTGAG GGTGTGCTGG GCTGGGTGGT GGGAGGGGAC TCCTGGGTCT 350 | REPEAT
GAGGGAGGAG GGGCTGGGGC CTGGACCCCT GAGTCTCAGG GAGGAGGAAA 400 | P.396[G>A]
GGGTGGGAGT GGGGCTGTGA CCCCTAGGTC TGGGAGGAGT GGAGGGTTAG 450
AGCTGAGAGC AGGAACTCCT AGGTCACAGA GAGGAGCGGA TAAATGGGGC 500 | P.488/rs5165[G>A]
AGAGAACACC TGGGGAGAGC TGGGGCCTCC ACTGTGATGT CCTCTCTCCT 550 | P.543/rs186448850[T>C]
GTAGGAGCCC GAGCACCTTC CGGGGCTTCA TGCAGACCTA CTATGACGAC 600
CACCTGAGGG ACCTGGGTCC GCTCACCAAG GCCTGGTTCC TCGAATCCAA 650 | P.623/rs5167[T>G]
AGACAGCCTC TTGAAGAAGA CCCACAGCCT GTGCCCCAGG CTTGTCTGTG 700 | P.665/rs138548797[A>C]
GGGACAAGGA CCAGGGTTAA AATGTTCATA AAAGCCAGGT GTGGTTGTGG 750 | P.708[G>A]| REPEAT
CGGGTGCCTG TAGTCCCAGC TACTCAGGAG GCTGAGGTAG GATGATGGCT 800
TGAGCCCAGG AGTTCGAGAC CAGCCTGGGC AACACAGCGA GATCTCTTGG 850 | P.850/rs12709884[G>A]
GGGTAAAACA AAAAGAAAAA AAAAAGTTCA TACTTCTCCA ATAAATAAAG 900 | P.853/rs10425530[G>A]
TCTCACCTGT GTCCCTGTCT GGATCCTTCC CCAGTGTGGC CAGAAAAAAA 950
CCCACCCCAC TGCCTCCCAG GAATCAATGA GTAGAAGAGG TGACACCTGA 1000
TGGGGAAGGA AGAGTAGGGA GGTCGGGAAG GGTATCAAGG AATAACACCC 1050 | P.1042/rs12709885[A>T]
TATTGTGGGC TTGCGGAGAA TGGGGGACTT CAAGGCGTGT CAGTTTCAGG 1100
AGGGTGAGGG CAGGAGCGTG GGTGGAGTCA GCAGGTCCCC ATGATGGCCC 1150
TCACTGAGAG CTTCGCCCTT GTCTCCTACA AGCTCTGACT CCATTCCCAG 1200 | P.1187/rs111782345[G>A]
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CGGAGGCGAA TTCTCAGAGT GAGGGTTCCC TGTCACTTGA GAGAAGGTTC 1300 | P.1275/rs111356234[G>A]
CCTGTGACGT GACCTTGGGG GACGTCATTG CCCTTTCTGT CCCCACCCAC 1350 | P.1324/rs12721063[G/A]
CCCCTCGGCA GTTCTGTTGG CCAGGACTTT GGCCTAGACA AAGGATGGGG 1400 | P.1357/rs2288912[G>C]
GTTGTGGCTG TGGAGCGGAA GTGGGTCTCA ACCACTATAA AGCCTCTCTG 1450 | P.1442/rs2288911[G>T]| Exon 1| UTR
TGCCCGTCCG GAGCTGGTGA GGACAGCCTG CCAGAGTCTG GTAAGAAAGG 1500
GACTCAGGGT GCGGGGACAG GGGGGCGTCA GCAGGGAGAG GGCAAAGATC 1550 | P.1540/rs75463753[G>A]
GATAAAGCAG GAATTTTAAG AGGCACAATA TTAGAAGCCC GTGTTGGAAC 1600 | P.1591/rs9304644[G>A]
CATGACTGTG TGTGTGTGTG TGTGTGTGTG TGTGTGTGTG TGTGTGTGTG 1650 | P.1608[G>C]
AGAGAGAGAG AGAGGGAGAT GGAGTCTCGC TATGTAGCCC AGGCTAGACT 1700 | REPEAT
CAAACTCCTG GGCTCAAGCA ATCCTCCTGC CTCAGCCTCC CCAGTAGCTG 1750
GGACTACAGG TGCACCACCA CACTCCACAA ATCACAGAAT TTAGAACTGT 1800
AGACTATTTG AGCTTCTGCT TAGAGTTAGG GTGGCTGAGG TGGGGAGGAT 1850 | REPEAT
CCCTTGAGCC CAGGAGTTTG AGGATGCAGT GAGCTGTGAT CTTGCCACCG 1900 | P.1851/rs12709886[C>T]
TGTTCCAGCC TGGGTGACAG AGAAACCCCA TTTCTAAAAA AGAGAAAGAA 1950
AAAGGGATAG GTACAATGGC TCATGCCTGT AATCCCAGCA CTCTGGGAGG 2000 | REPEAT
CCGAGGCGGG TGGATCACTT GAGGTCAGGA GTTCGACACC AGCCTTACCA 2050 | P.2003/rs187834478[G>A]
GCATGGTGAA ACCGCATCTA TACTAAAAAT ACAAAAATTG GCCGGGTGTG 2100 | P.2090/rs12721072[G>A]
GTAGCATATG CCTGTAATCC CAGCTATTCC AGAGGCTGAG ACAGGAGAAT 2150
TGCTTGAACC CAGGAAGCGG AGGTTGCAGT GAGCCCAGAT CGTGCCACTG 2200 | P.2191/rs9304644[C>T]
TACTCTAGCC TGGGTGACAG AGCAAGACTC AGTCTTGGCG GAAAAAAAGA 2250
ATGAAAAAAT TTAAAAAACT AAAAAAGAAC TGTAGGCTGG GCGTGGTGGC 2300 | REPEAT| P.2258/rs116489256[A>C]
TTACACTTGT AATCCAAACG CTTTGGGAGG CCAAGGCAAA CGGATCACTT 2350 | P.2339/rs115943687[A>G]
GATGTCAGGA GTTGGAGACC AGCCTGGCCA ACATGGTGAA ACCCCGTCTC 2400 | P.2371[A>G]
TACTAAAAAT ACAAAAATTA GACAGGCATG GTGGTGCATG CTTGTATTTC 2450 | P.2410/rs12721076[T>C]
CAGTTACTCA GGAGGCTGAG GCAGGAGAAT CGCTCGAACC CGGAAGACAG 2500 | P.2486/rs9304645[G>A]
AGGTTGCGGT GAGCCAAAAT TGCGCCATCG CACTCCAGCC TGGGCGAGAG 2550
AACAAGACCT TGTCTTGGAA AAAAAAAAAG AATTGTAGAC CATTTGCTTG 2600 | P.2566/rs9304646[T>C]
TGTTCTTTCT CCGGGGATCA GATCTCACCC TCTTTCTGCC GTACTTCCTC 2650
ATCTCCTACG TGTGGATGAT GATATTGTGC CCTGTGCATG TTCTTCGTCA 2700
CCAAAAGTGC CTCTCTCATA GAGCAGGTGA GAACTCAGTG AGGAGATGCA 2750
GGGACATGAG GTCTGACTTA GGGCAGAGCC CTAAGGTAAC ACATTTGATC 2800
TACTGTAGGT CCTTAATGGT GTCTGCAGAG CACCTCCCTG CACTGACTCA 2850
GCCTTAGCAA AGGGCAGAGG CTTTGCTGTG TTCCCTGCTG GGCCCAGAAC 2900 | P.2870[G/T]
TGTTTAGGTG CTCAAGAAAG CCTTCTAGGC TGGGCTCAGT GGCTCACACC 2950 | REPEAT | P.2935/rs11879392[C>G] |
P.2938[A>G]
TGTACTCCCA GCACCCTGGG GAGGCCGAGA TGGGAGGATC GCTTGAGCCC 3000
AGGAGTTCCA GACCAGCCTG GGCAACAAAA CAAGTCTCCC ATCTCTACAA 3050 | P.3010/rs10419086[A>G]|
P.3030/rs4803774[A>G]
AAGAATAAAA ATTAGCAGCT GGGCATGGTG GCTCACGCCT GTAATTCCAG 3100 | REPEAT | P.3082_3083[insTGG]|
P.3086/rs4803775[C>T]
CACTTTGGGA GGCCAAGGCA GGCAAATCAC TTGAGGTTAG GAGTTCAAGA 3150
CCAGCCTGGC CAACATGGTG AAACCCCATC TCTACTAAAA ATACAAAAAT 3200 | P.3154/rs145931717[G>A]|
P.3193/rs148616221[A>G]

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CAGGTGGGGC ACAGTGGCTC AAGCCTGTAA TCCTAGCACT TTGGGAGGCC 3250 | REPEAT| P.3234[T>C]
AAGGTGGGCG GATCACGAGG TCAGAAGTTC GAGACCAGCC TGGCCAGCAT 3300 | P.3259/rs12721061[C>T]|
P.3260/rs151176577[G>A]| P.3289/rs12721058[C>G]
GGTGAAACCC CATCTCTACT AAAAATACAA AATATTAGCC GGGCATGGTG 3350 | P.3348/rs10420434[G>A]
GCAGGTGCTT GTGATTCCAG CTCCTTGGGA GGCTGAGGCA GAAGAATTGC 3400
TAGAACCCTG GAGGCAGAGG TTGCAGTGAG CCGAGAACAC GCCACTGCAC 3450 | P.3409[T>C]
TCCAGCCTGG GTGACAGAGC GAGACTCCAT CTCAAAAAAT ACGAAAACAA 3500 | P.3459/rs12721062[G>C]
AAATCAGCCG GGTGGTGGCG GGTGCCTGTA ATCCCAGCTA CTGGGGAGGC 3550 | REPEAT
TGAGGCAGGA GAATTGCTTG AACCTGGGAG GTGGGGGTTG CAGTGAGCCA 3600 | P.3600/rs7256684[A>G]
AGATTGCACC ACTGCACTCC AGCCTGGGCA ACAGAGTGAG ATTCCATCTC 3650 | P.3617[C>T]
AAAAAAGAAA AAAATAATAA TTAAAATGTT AAAATCAGGA GTAGAATCAC 3700 | P.3692/rs12721060[T>G]
AGAATGTTGG AAAGTGAGGC CCAAGAAGGG GGCTGTGTCC AAGTCCATGC 3750
ATGGGAAACT TGACTGGGAC ACCGAGCACA CACAGAGCAG GATCTCAGTC 3800 | P.3778/rs5120[A>T]
CCCCCCACCA GAGTGGGGCG TGACCACAGG AACAGCCGCC TCCAGTCAGC 3850 | P.3805/rs7257095[C>G]|
P.3806/rs12709887[C>G]| P.3814/rs10422603[T>G]| P.3820/rs12709888[G>A]
CTGCCACATG ACACCCCCTC AATGTTCCAG GTCTCTGGAC ACTATGGGCA 3900 | Exon 2 | UTR|
                                                M  G   2
P.3892/rs5121[C>T]
CACGACTCCT CCCAGCTCTG TTTCTTGTCC TCCTGGTATT GGGATTTGGT 3950
T  R  L  L   P  A  L   F  L  V   L  L  V  L   G  F     18
GAGTGTGGGC TTCCGGGGAG GGAAGCCTTG GGGAGGGGAA TGAGCTCCAA 4000
GCATCTTCCC AGCCCAGGCC CTTCTTACCT CTGCCTCTGC CCTCTCCTCT 4050
TCTTCCTTCC TCCTTTCCCC CTGCTGCAGC CCCACGGGCT CTCCTGACAC 4100 | P.4086/rs114780592[G>A]
ACTCTCCCCC TGCAGAGGTC CAGGGGACCC AACAGCCCCA GCAAGATGAG 4150 | P.4112/rs74500990[G>C]|
             E  V   Q  G  T   Q  Q  P  Q   Q  D  E  30
Exon 3 | P.4118/rs201709243[G>A]
ATGCCTAGCC CGACCTTCCT CACCCAGGTG AAGGAATCTC TCTCCAGTTA 4200
 M  P  S   P  T  F  L   T  Q  V   K  E  S   L  S  S  Y 47
CTGGGAGTCA GCAAAGACAG CCGCCCAGAA CCTGTACGAG AAGACATACC 4250
  W  E  S   A  K  T   A  A  Q  N   L  Y  E   K  T  Y   63
TGCCCGCTGT AGATGAGAAA CTCAGGTAGC ACCTGCCCCT GGAGAAATGG 4300
L  P  A  V   D  E  K   L  R                           72
GGTCTGGCCC ATACCACCGA CTGCATCCAG GACCCAGAAG TTCAGGCCCC 4350 | P.4319/rs5123[G>A]| REPEAT
AGCCCCTCCT CCCTCAGACC CAGGAGTCCA GGCCTCAGCC CCTCCTCCCT 4400
CAGACCCAGG AGTCCAGGCC CCCAGCCCGT CCTCCCTCAG ACCCAGGAGT 4450 | P.4429/rs3745152[G>C]|
P.4430_4431/rs35625559[insCTT]
CCAGGCCCCC AGCCCCTCCT CCCTCAGACC CAGGAGTCCA GGTCCCCAGA 4500 | P.4458[C>T]| P.4460_4461[del1]|
P.4477[G>A] | P.4493/rs4803776[T>C]
CCCTCCTCCC TCAGACCCAG GAGTCCAGGC CCCCAGCCCC TCCTCCCTCT 4550 | P.4513[A>C]| P.4532[C>T]|
P.4534_4535[del1]
AACCATCTGT GCTTTCTCCC CAGGGACTTG TACAGCAAAA GCACAGCAGC 4600 | Exon 4| P.4587/rs5126[A>C]
                          D  L   Y  S  K   S  T  A  A 81
CATGAGCACT TACACAGGCA TTTTTACTGA CCAAGTTCTT TCTGTGCTGA 4650
  M  S  T   Y  T  G   I  F  T  D   Q  V  L   S  V  L   97
AGGGAGAGGA GTAACAGCCA GACCCCCCAT CAGTGGACAA GGGGAGAGTC 4700 | UTR
K  G  E  E                                            101
CCCTACTCCC CTGATCCCCC AGGTTCAGAC TGAGCTCCCC CTTCCCAGTA 4750
GCTCTTGCAT CCTCCTCCCA ACTCTAGCCT GAATTCTTTT CAATAAAAAA 4800 | P.4754/rs7253690[C>T]
TACAATTCAA GTTGCTTCTC ATGGATGGCA CTGCTTTTCT GAGGACTCAA 4850
GGTGCCAAGA TGGAGGGGCT GACTCAGTCC AGCCAACATT TAATGAGCAC 4900 | P.4852/rs5127[G>T]|
P.4853_4854/rs150448996[delT]| REPEAT
CTACTTTATG TATGGAGCTC TAACCCATGG GTCCATGGGA ATAAAGCAGT 4950
GAATAGTAAC AATAAATAAT CGTAACAGCA ATTAGAGACT AATCTTTATT 5000 | P.4971/rs1130742[C>T]|
P.4973_4974/rs199828513[insT]
GAAGTCCGGC TTTCTCTCTT TTATTTTTTT ATTTTTTGAG ACAGGGTTTC 5050 | P.5004/rs10421404[G>A]| REPEAT|
P.5018_5022/rs78403558[del5]
ACTCTGTCAC CCAGGCTGGA CAGCAGTGGT GCAATCTCGG CTCACTGCAC 5100
CCTCCGCCTC CCAGGTTCCA GCGATTCTGT GTGCCTCAGC CTCTGGAGTA 5150
GCTGGGATTA TGGGCATGTG CCACTGTGCA CGGCTAATGT TTGTATTTTT 5200
AGTAGGGTTT TGCCAGTTGG CTAGGCTGGT CTCAAACTTC TGACCTCAAG 5250
TGATCCACCC GCCTCAGCCT CCCAAAGTAC TGGGGTGACA GGCATGAGCC 5300
ACCGCGCCAT GCCAAAATCC AGCCTTCTCA TTTGTAAAAT AACAAATCAT 5350 | P.5303/rs7257488[C>T]|
P.5310/rs7258345[T>G]| P.5324/rs7257476[C>T]
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AGACACAGCT AGTCCACAGT GGCCTCTGAC AGTCTCCAGT TGTTAACGGT 5400 | REPEAT | P.5398/rs12709889[G>A]
GAATGGTGTC CAGGTTTTTG GCGTCCTGAA CAAAGAACTG GACAAAACGC 5450
ACAAACAAAG CAAGGAAGGA ATGAAGGGAT TTATTGAAAA CGAACATACA 5500 | P.5491[C>T]
CTAAACAGTG TGGGAGCGGG CCCAAGCATA TGGGTTCAAA AGCCCTGTTA 5550 | P.5512/rs12721064[G>A]
CAGAATTTTT GGGAGTTTAA ATTCCCCCTA GAGGATTCCC CTTCCACTGG 5600 | P.5562[G>C]| P.5586/rs73558127[T>G]
TTACTTCTGG TACACCCTAT GTAAATGGAG AGGATGAAGA AAAGTTACAA 5650 | P.5612[A>G] | P.5644[G>A]
AGTCATTTAT GGCCTACCGG AGAGGATGTT TCCTGTTATA GCTGAAGTGA 5700
ATTGGCCTTA TGTTCCCTGC CTCCCTATTT TCCTGCCTTA CAGTTGCTGG 5750
ACTGACACAT TTTTTATTTT ATTTATTTTG TTTTGAGATA AGGTCTTGCT 5800 | REPEAT| P.5771_5775[del5]
CTGTCGCCCA GGCTGAAGTG CAGTGGTGAG ATCTTGGCTT ACTGTAGCCT 5850 | P.5815/rs10423208[G>A]
TGACCTTTTG GGCTCAAGAG ATCCTCCCAT CTCAGCCTCC CAAGTAGTTG 5900
GGACTAGGGA TGCCCACTGC CACACCTGGC TAATTTTTTG TATTTTTAGT 5950 | P.5922/rs10422888[A>G]
AGAGACGGGG TTTCGTCAAG TTGCCTAGGC TAGTCTCCAA TTCCTGGGCT 6000 | P.5965[G>A]
CAAGCGATCT GCCCACCTTG CCCTTCCAAA GTGTTGGGAT TACGGGTGTG 6050 | P.6037/rs10402642[G>A]
AACCACCGCA CCAGGCCTGG GCTGACACTT TAAACGTGCC ATTGCAATCA 6100
GTGTATAATG GTCCCGTGGC AGAGGGAGAA TGGTGCCCAA GTCAGTACTT 6150
CTTGGCTGGG ACCCAAGAAG ACAAACCTCT AGGGCCGGCG TGGTGGCTCA 6200 | REPEAT
CGCCTGTAAT CCCAGCACTT TGGTTGGCTG AGGTGGGCAG ATCATCTGAG 6250 | P.6222[G>C]
GTCAGGAGTT CAAGACCAGC CTGGCCAACA TGGTGAAACC TTGTCTCTAA 6300
TAAAAACACA AAAATTAGCT AGGGGTGGCC CGCGCCTGTA ATCCCAGTTA 6350 | P.6334[G>A]
CCTGGAGGCT GAGGCAGGAG AATTGCTTGT ACCCTGGAGG CGGAGATAGT 6400
GCCACTGCAC TCCAGCCTGG GCAGCAGAGT GAGACTCC
```

Figure 12. Annotated colored FASTA

Red-color represents the NHW-specific variants, Blue-color represents the Black-specific variants, and Black-color represents the shared variants in the two populations.

3.3 SEQUENCING ANALYSIS

Open-access software, haploview software, was used to analyze sequencing data, examine their MAF, select tagSNPs and visualize their LD structure.

3.3.1 Common and rare variants

3.3.1.1 NHWs

A total of 113 sequencing variants were included in haploview analysis (excluding *APOE*-5230, and *APOC1*-4975). Out of 113 variants, 60 variants had MAF≥5% and were considered common, 21 variants had MAF 1-5% and were considered relatively less common, and 32 variants had MAF<1% and were considered rare. Ninety-two percent of the common variants were reported (55 reported vs. 5 novel), while 53% of the rare variants were reported (28 reported vs. 25 novel). Eighty-three percent (25/30) of the novel variation is rare as compared to the common novel variation (5/30=17%).

3.3.1.2 Blacks

A total of 174 variants were included in the haploview analysis (excluding *APOE*-5230, *APOC2*-4458, *APOC2*-4460_4461, and *APOC2*-4532). Out of the 174 variants, 84 variants were considered common (MAF≥5%), 47 SNPs were considered less common (1%≤MAF<5%), and the remaining 43 SNPs were considered rare (MAF<1%). Ninety-two percent of the common variants were reported (77 reported, and 7 novel), while 61% of the rare variants were reported

(55 reported, and 35 novel). Similar to NHWs, eighty percent of the novel variation in Blacks is rare while the remaining twenty percent is common.

3.3.2 Selection of variants for genotyping

We selected sequencing-identified tagSNPs, all sequencing-identified rare variants and HapMap tagSNPs covering the intergenic region to be genotyped in the entire datasets (623 NHWs and 788 Blacks) for genotype-phenotype association analysis.

3.3.2.1 Selection of sequencing-identified variants

Haploview software was used to run tagger analysis on sequencing-identified variants that were discovered in the sequencing subsets and tagSNPs were selected in the two racial groups separately using MAF≥5% and r^2=0.9 as a cut-off parameters.

NHWs: Tagger results in NHWs are presented in **Table 8** and **Figure 13** illustrates their LD structure. In NHWs, 33 variants were selected as tagSNPs to capture 60 common variants in the sequenced regions in addition to 53 rare/less common variants with MAF<5% (see **Table 9**), and 4 suspicious variants (*APOE*-4489, *APOE*-4490, *APOC4*-870, *HCR2*-801) were selected to be genotyped in 623 NHWs.

Table 8. Tagger analysis results of *APOE* gene cluster sequencing variants in NHWs

TagSNPs	Alleles Captured
APOC2-5303	APOC2-5324, APOC2-3600, APOC2-6037, APOC2-2191, APOC2-5310, APOC2-5815, APOC2-5303, APOC2-3030, APOC2-2566
APOC2-194APOC4-3498	APOC2-3086, APOC2-1357APOC4-4661, APOC4-2623, APOC2-1442APOC4-4746, APOC2-4493, APOC2-194APOC4-3498, APOC4-204, APOC2-3778
APOC2-5018	APOC4-1325del3, APOC2-2935, APOC4-2640, APOC2-5922, APOC2-2410, APOC2-5018
**APOC4-108	APOC4-92del3, APOC4-108, APOC4-150ins114
APOC2-3814	APOC2-5004, APOC2-3814, APOC2-2486rs9304645
APOC1-6026	APOC1-5926, APOC1-5240, APOC1-6026
**APOC2-4534	APOC2-4534, APOC2-4532
**APOC2-4429	APOC2-4429, APOC2-4430ins
APOC1-720	APOC1-1870, APOC1-720
APOC2-4853	APOC2-5398rs12709889, APOC2-4853
APOC2-3348	APOC2-3010, APOC2-3348
APOE-5229	APOE-4075, APOE-5229
APOE-1163	APOE-1163
APOC1-4334	APOC1-4334
APOE-560	APOE-560
APOE-2440	APOE-2440
APOC2-623APOC4-3927	APOC2-623APOC4-3927
**APOC4-1733	APOC4-1733
**APOC4-1823	APOC4-1823
APOC1-2041	APOC1-2041
APOE-5361	APOE-5361
**APOC1-5053	APOC1-5053
HR2-188rs35136575	HCR2-188rs35136575
APOE-1998	APOE-1998
**APOE-624	APOE-624
APOE-3937	APOE-3937
**APOC2-4971	APOC2-4971
APOE-832	APOE-832

Yellow-highlighted variants represent variants that were genotyped successfully.
**** represent variants that failed genotyping, and red-color variants were out of HWE or had low call rate.**

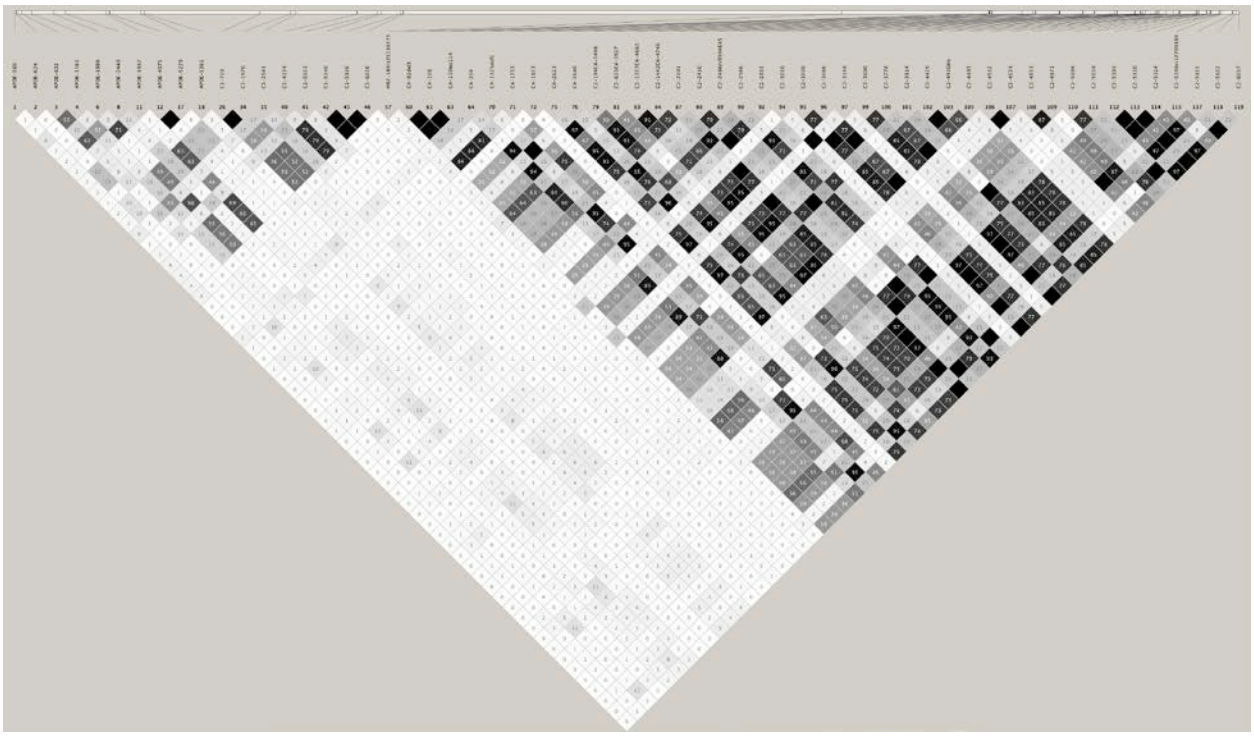

Figure 13. LD plot of the *APOE* gene cluster sequencing common variants in NHWs

Table 9. Sequencing-identified less common/rare variants (MAF<5%) in NHWs sequencing subset

Name	Alleles	NCBI rs no.	Function	Amino acid change	MAF	High HDL/ low TG (MAF)	Low HDL/ high TG (MAF)
APOE-1575	C>T	rs769448	Intron1		0.021	0.043	0.000
APOE-2294	C>T		Intron 2		0.005	0.011	0.000
**APOE-2907	T>G	rs769451	Intron 2		0.005	0.000	0.010
APOE-3038	G>A	rs111833428	Exon 3	Ala 23 Ala	0.005	0.011	0.000
APOE-4310	T>A	rs199768005	Exon 4	Val 254 Glu	0.005	0.011	0.000
APOE-4528	C>T		3' UTR		0.005	0.011	0.000
APOE-4737	C>G	rs117656888	3'flanking		0.011	0.021	0.000
**APOE-4951	A>C	rs1081105	3'flanking		0.042	0.032	0.052
**APOC1-607	G>A	rs72654447	5'flanking		0.005	0.011	0.000
**APOC1-655	A>T	rs66807996	5'flanking		0.016	0.021	0.011
**APOC1-659	G>C	rs72654448	5'flanking		0.005	0.000	0.010
APOC1-698	C>A	rs72654449	5'flanking		0.011	0.011	0.010
APOC1-703	C>T	rs3207187	5'flanking		0.005	0.011	0.000
APOC1-1170	G>A		intron1		0.005	0.011	0.000
**APOC1-1276	C>G	rs72654453	Exon2	Ile 16 Met	0.011	0.021	0.000
APOC1-1294	T>G		intron2		0.005	0.011	0.000
APOC1-1317	G>A	rs12721048	intron2		0.011	0.021	0.000
APOC1-1422	G>A		intron2		0.005	0.011	0.000
APOC1-1566	G>A	rs12691088	intron2		0.026	0.011	0.042
**APOC1-1669	T>C		intron2		0.005	0.011	0.000
APOC1-2629	G>A		Exon3	Arg 44 His	0.005	0.011	0.000

Cont. Table 9

APOC1-2817	C>T		intron3		0.005	0.011	0.000
APOC1-3423	G>A	rs389261	intron3		0.005	0.000	0.010
APOC1-3494	C>T		intron3		0.005	0.011	0.000
APOC1-5641	T>G	rs1064725	3'UTR		0.037	0.021	0.052
APOC1-5773	G>A		3'flanking		0.005	0.011	0.000
**APOC1-6122	G>C	rs142134314	3'flanking		0.005	0.000	0.010
**APOC1-6213	G>A		3'flanking		0.005	0.011	0.000
HR1-292	C>G	rs4803771	HCR-1		0.042	0.021	0.062
HR1-362	C>A		HCR-1		0.011	0.011	0.010
HR1-423	C>G		HCR-1		0.026	0.043	0.010
HR1-575	A>G	rs157599	HCR-1		0.005	0.000	0.010
HR1-727	T>G	rs149345	HCR-1		0.005	0.000	0.011
HR2-365	C>A		HCR-2		0.011	0.011	0.010
HR2-523	C>T	rs118004808	HCR-2		0.026	0.021	0.031
**APOC4-116	A>G		5'flanking		0.007	0.000	0.013
APOC4-636	C>T		5' flanking		0.005	0.000	0.010
APOC4-968	A>G	rs76214972	5' UTR		0.037	0.011	0.062
APOC4-1150	A>G	rs148247675	Intron1		0.005	0.011	0.000
APOC4-1229	G>C		Intron1		0.011	0.000	0.021
**APOC4-2063	C>G		Intron1		0.005	0.000	0.011
APOC4-2557	C>A		Intron1		0.005	0.000	0.010
APOC4-2683	G>A	rs12721109	Intron1		0.011	0.011	0.010
APOC2-242C4-3546	G>A	rs12691089	APOC4-exon2 (non-synonymous)	Glycine 52 Aspartate	0.005	0.000	0.010
APOC2-543C4-3847	T>C	rs186448850	APOC4-intron2		0.011	0.000	0.021
**APOC2-1324C4-4628	G>A	rs12721063	APOC4-3'flanking/APOC2-5'flanking		0.021	0.021	0.021
APOC2-1591	G>A		APOC2-intron1		0.005	0.000	0.010
APOC2-1851	C>T	rs12709886	intron1		0.037	0.011	0.062
APOC2-2870	G>T		intron1		0.005	0.011	0.000
**APOC2-2938	A>G		intron1		0.005	0.011	0.000
**APOC2-3409	T>C		intron1		0.005	0.000	0.010
**APOC2-4477	G>A		intron3		0.005	0.011	0.000
APOC2-5644	G>A		3'flanking		0.011	0.011	0.010

Blue-highlighted variants represent unique SNPs to the high HDL-C/low TG group, while red-highlighted variants represent unique SNPs to the low HDL-C/high TG group, (**) represent SNPs failed genotyping.

African Blacks: In African Blacks, 58 SNPs were selected as tagSNPs to capture information of 84 common variants (excluding *APOC2*-4458, and *APOC2*-4460 with low call rates) using MAF≥5%, r^2=0.9 as cut-off values in addition to 90 rare variants with MAF<5%, and 4 suspicious variants (*APOC2*-4458, *APOC2*-4460, *APOC2*-4532, and *HCR2*p801). **Table 10** summarizes tagger results and **Figure 14** represents LD pattern of the common variants, and **Table 11** summarizes less common/rare sequencing-identified variants.

Table 10. Tagger analysis results of the *APOE* gene cluster sequencing common variants in African Blacks

Test	Alleles Captured
APOC2-2090	APOC2-2258, APOC2-4754, APOC2-3154, APOC2-3259, APOC2-4319, APOC2-2339, APOC2-4112, APOC2-2090, APOC2-5612, APOC2-3082
APOC2-5310	APOC2-5303, APOC2-5310, APOC2-6037, APOC2-5324, APOC2-4430, APOC2-5815, APOC2-3600, APOC2-4429
**APOC4-92	APOC4-92, APOC4-150, APOC4-108
APOC2-198APOC4-3502	APOC4-3213, APOC4-757, APOC2-198APOC4-3502
APOC1-1684	APOC1-1684, APOC1-5006
APOC2-194APOC4-3498	APOC2-194APOC4-3498, APOC4-204
APOC2-3778	APOC2-3778, APOC2-3086
APOC1-2041	APOC1-2041, APOE-1163
HCR1-727	HCR1-727, APOC1-3423
APOC1-6026	APOC1-6026, APOC1-5926
APOC2-75C4-3380	APOC2-75APOC4-3380, APOC4-2971
APOC2-5004	APOC2-5004, APOC2-3814
APOC4-2559	APOC4-2559
APOC2-5398	APOC2-5398
APOC2-623C4-3927	APOC2-623C4-3927
APOC2-1275APOC4-4579	APOC2-1275C4-4579
APOC2-5018	APOC2-5018
APOE-73	APOE-73
APOC2-1357C4-4661	APOC2-1357C4-4661
APOE-1109	APOE-1109
APOC2-5586	APOC2-5586
APOC2-1442C4-4746	APOC2-1442C4-4746
APOC1-5667	APOC1-5667
APOE-3937	APOE-3937
**APOC2-4971	APOC2-4971
APOC2-853C4-4157	APOC2-853C4-4157
**APOE-471	APOE-471
**APOC2-2566	APOC2-2566, APOC2-3030
**APOC1-1870	APOC1-1870

Cont. Table 10

APOE-2440	APOE-2440
APOC2-5922	APOC2-5922
APOC2-1540C4-4844	APOC2-1540C4-4844
APOC2-3010	APOC2-3010
**APOC2-2191	APOC2-2191
HCR2-286	HCR2-286
APOC1-720	APOC1-720
HCR2-188	HCR2-188
APOC2-4853	APOC2-4853
APOC1-1331	APOC1-1331
**APOC2-4493	APOC2-4493
**APOE-5229	APOE-5229
**APOC4-1823	APOC4-1823
**APOC2-850C4-4154	APOC2-850C4-4154
APOC2-2486	APOC2-2486
**APOC2-3348	APOC2-3348
APOE-832	APOE-832
APOC1-3573	APOC1-3573
APOC4-2623	APOC4-2623
APOE-560	APOE-560
**HCR2-632	HCR2-632
HCR1-575	HCR1-575
APOC2-3805	APOC2-3805
APOC1-5053	APOC1-5053
**APOC4-1733	APOC4-1733
**APOC2-4534	APOC2-4534

(**) tagSNPs failed genotyping, yellow-highlighted SNPs represent the successfully genotyped variants.

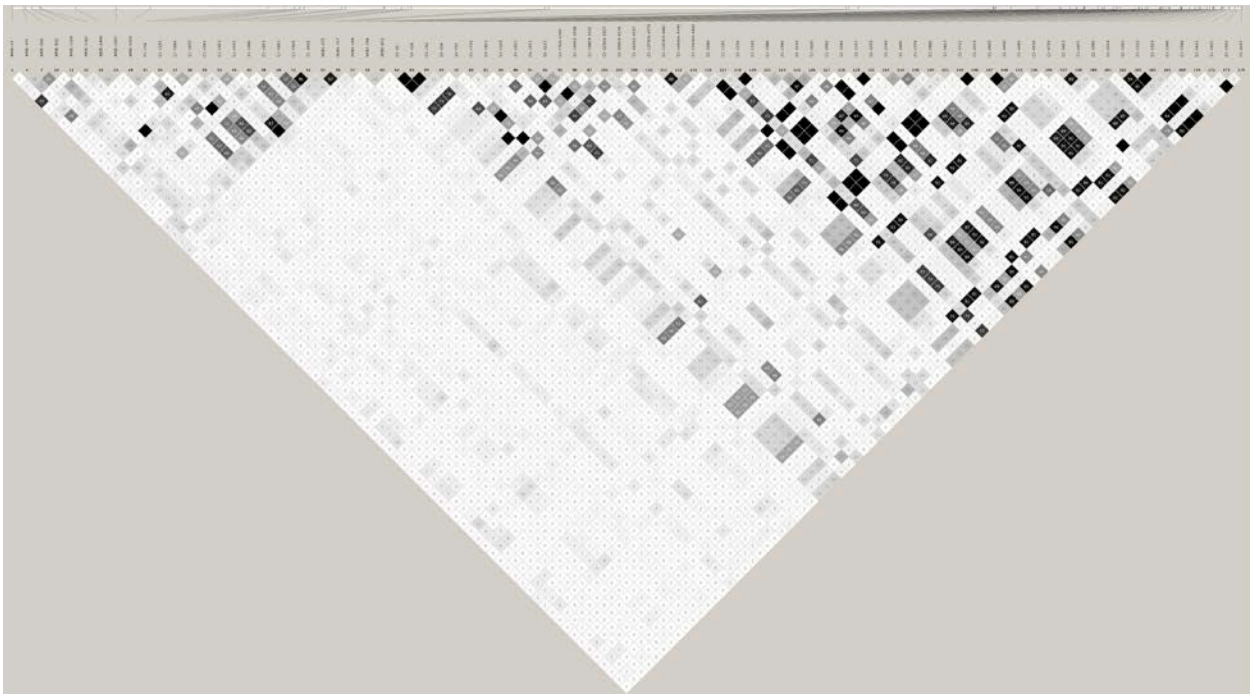

Figure 14. LD plot of the *APOE* gene cluster sequencing common variants in Blacks

Table 11. Sequencing-identified less common/rare variants (MAF<5%) in Blacks sequencing subset

	Alleles	NCBI ref no.	Function	Amino Acid Change	MAF	High HDL-C/low TG (MAF)	Low HDL-C/high TG (MAF)
APOE-173	A>G		5'flanking		0.005	0.000	0.011
APOE-308	C>T	rs769445	5'flanking		0.005	0.000	0.011
**APOE-494	C>T		5'flanking		0.005	0.010	0.000
**APOE-526	T>C		5'flanking		0.005	0.010	0.000
APOE-618	G>C		5'flanking		0.005	0.000	0.011
APOE-624	T>C	rs769446	5'flanking		0.005	0.010	0.000
APOE-1231	G>A		intron1		0.011	0.010	0.011
APOE-1279	C>A	rs877973	intron1		0.048	0.062	0.033
APOE-1539	A>G	rs184686013	intron1		0.011	0.021	0.000
**APOE-1591	G>T	rs147236548	intron1		0.016	0.021	0.011
APOE-2072	G>A	rs189660912	intron 2		0.016	0.021	0.011
APOE-2269	G>A	rs61357706	intron 2		0.016	0.010	0.022
APOE-2544	A>G	rs115299243	intron 2		0.016	0.010	0.022
**APOE-2576	G>A		intron 2		0.005	0.010	0.000
APOE-3673	C>G	rs769453	intron 3		0.005	0.000	0.011
APOE-4036	C>T	rs769455	exon 4	Arg 163 Cys	0.016	0.011	0.022
APOE-4075	G>A	rs7412	exon 4	Arg 176 Cys	0.042	0.062	0.021
APOE-4569	G>T		3'UTR		0.005	0.010	0.000
**APOE-4951	A>C	rs1081105	3'flanking		0.042	0.042	0.043

Cont. Table 11

APOE-5223	G>C		3'flanking		0.005	0.000	0.011
APOE-5231	T>G		3'flanking		0.032	0.042	0.021
APOC1-894	C>T	rs190454394	5'flanking region		0.005	0.010	0.000
APOC1-1166	G>A	rs72654452	intron1		0.032	0.031	0.032
APOC1-1526	C>T	rs5114	intron2		0.047	0.062	0.032
APOC1-1642	C>T		intron2		0.011	0.010	0.011
**APOC1-2099	T>C		intron2		0.005	0.000	0.011
**APOC1-2296	A>T	rs185495905	intron2		0.005	0.010	0.000
APOC1-3358	A>G		intron3		0.005	0.010	0.000
APOC1-5240	C>G	rs12721051	intron3		0.035	0.045	0.024
**APOC1-5716	G>T	rs12721055	3'flanking		0.026	0.031	0.021
**APOC1-5717	G>C	rs72654457	3'flanking		0.021	0.021	0.021
**APOC1-6158	G>A		3'flanking		0.005	0.000	0.011
HCR1-424	G>A	rs117664574	HCR-1		0.011	0.021	0.000
HCR2-523	C>T	rs118004808	HCR-2		0.005	0.010	0.000
**APOC4-65	C>T		5’ flanking		0.007	0.000	0.015
**APOC4-233	C>T		5’ flanking		0.006	0.000	0.011
**APOC4-245	G>T	rs192072159	5’ flanking		0.006	0.000	0.011
APOC4-368	A>G		5’ flanking		0.011	0.010	0.011
**APOC4-438	G>A	rs146656012	5’ flanking		0.006	0.000	0.011
**APOC4-489	C>T	rs140241604	5’ flanking		0.017	0.011	0.023
APOC4-637	G>T	rs113814026	5’ flanking		0.042	0.042	0.043
APOC4-1088	T>G		intron1		0.005	0.000	0.011
APOC4-1130	T>C		intron1		0.005	0.010	0.000
APOC4-1192	G>A	rs113745034	intron1		0.011	0.010	0.011
APOC4-1325_1327	del3		intron1		0.043	0.064	0.022
APOC4-1430_1431	insG		intron1		0.037	0.042	0.032
**APOC4-1702	G>A	rs12721102	intron1		0.006	0.011	0.000
**APOC4-1719	C>A		intron1		0.006	0.011	0.000
APOC4-2099	G>T	rs111339708	intron1		0.011	0.010	0.011
APOC4-2467	C>T	rs115225947	intron1		0.021	0.021	0.021
APOC4-2607	G>A	rs5156	intron1		0.011	0.010	0.011
APOC4-2640	C>T	rs5158	intron1		0.032	0.042	0.021
**APOC4-2641	G>A		intron1		0.005	0.000	0.011
APOC4-2678	G>C	rs148564866	intron1		0.005	0.000	0.011
APOC4-2767	G>T	rs12721107	intron1		0.021	0.031	0.011
APOC4-3348	G>A		intron1		0.005	0.011	0.000
**APOC2-59C4-3363	G>A	rs60170431	APOC4-intron1		0.043	0.053	0.032
APOC2-228	G>A	rs5164	APOC4-exon2	Trp47Ter	0.005	0.000	0.011
APOC2-288C4-3592	C>T	rs12691090	APOC4-exon2	Asp67Asp	0.026	0.042	0.011
APOC2-396C4-3700	G>A		APOC4-intron2		0.005	0.010	0.000
APOC2-488C4-3792	G>A	rs5165	APOC4-intron2		0.016	0.021	0.011
APOC2-623C4-3927	T>G	rs5167	APOC4-exon3	Leu96Arg	0.011	0.010	0.011

Cont. Table 11

APOC2-708C4-4012	G>A		APOC4-exon3	Lys124Lys	0.005	0.000	0.011
APOC2-1042C4-4346	A>T	rs12709885	APOC4-3'/APOC2-5'		0.005	0.010	0.000
APOC2-1187C4-4491	G>A	rs111782345	APOC4-3'/APOC2-5'		0.005	0.000	0.011
APOC2-1229C4-4533	C>T	rs112698600	APOC4-3'/APOC2-5'		0.011	0.010	0.011
**APOC2-1608C4-4912	G>C		APOC2-intron1		0.005	0.000	0.011
**APOC2-2003	G>A	rs187834478	intron1		0.016	0.021	0.011
**APOC2-2371	A>G		intron1		0.005	0.010	0.000
APOC2-2410	T>C	rs12721076	intron1		0.032	0.042	0.021
APOC2-2935	C>G	rs11879392	intron1		0.027	0.042	0.011
**APOC2-3193	A>G	rs148616221	intron1		0.005	0.000	0.011
APOC2-3234	T>C		intron1		0.005	0.010	0.000
**APOC2-3260	G>A	rs151176577	intron1		0.011	0.000	0.021
**APOC2-3617	C>T		intron1		0.005	0.000	0.011
APOC2-3692	T>G	rs12721060	intron1		0.011	0.011	0.011
**APOC2-3806	C>G	rs12709887	intron1		0.043	0.053	0.032
APOC2-3892	C>T	rs5121	5'UTR		0.027	0.021	0.033
APOC2-4086	G>A	rs114780592	intron2		0.021	0.031	0.011
APOC2-4118	G>A	rs201709243	exon3	Val20 Ile	0.005	0.010	0.000
APOC2-4513	A>C	rs180809422	intron3		0.011	0.011	0.011
APOC2-4587	A>C	rs5126	exon4	Lys 77 Gln	0.044	0.044	0.043
APOC2-4973_4974	insT	rs199828513	3'flanking		0.005	0.000	0.011
APOC2-5491	C>T		3'flanking		0.005	0.010	0.000
APOC2-5512	G>A	rs12721064	3'flanking		0.005	0.010	0.000
APOC2-5562	G>C		3'flanking		0.021	0.010	0.032
APOC2-5771_5775	delATTTA		3'flanking		0.005	0.011	0.000
APOC2-5965	G>A		3'flanking		0.005	0.010	0.000
**APOC2-6222	G>C		3'flanking		0.011	0.010	0.989
APOC2-6334	G>A		3'flanking		0.026	0.031	0.021

**** SNPs that failed genotyping, blue-highlighted variants represent unique SNPs to the high HDL-C/low TG group, red-highlighted SNPs represent unique SNPs to the low HDL-C/high TG group.**

3.3.2.2 Selection of HapMap tagSNPs covering the intergenic regions

HapMap genotypes data covering the entire 45.8 kb of *APOE-C1-C4-C2* gene cluster mapping to (Ch19: 50,099,879 - 50,145,657) from two populations CEU and YRI were used to select tagSNPs. The tagSNPs results in CEU and YRI populations are summarized in **Table 12** and

Table 13, respectively and their corresponding LD structures are illustrated in **Figure 15** and **Figure 16,** respectively.

Using cutoffs of MAF≥5%, r^2=0.9, resulted in the selection of 15 tagSNPs in CEU to capture information for a total of 23 SNPs. Likewise 30 tagSNPs in YRI were selected to capture information for 35 SNPs. HapMap tagSNPs represent small portion of our sequencing-identified tagSNPs and only 7 tagSNPs out of the 15 HapMap tagSNPs in CEU and 7 HapMap tagSNPs out of 23 tagSNPs in YRI were mapped to the unsequenced intergenic regions and were added to the genotyping list.

Table 12. Tagger analysis results of *APOE* gene cluster based on HapMap data of CEU

TagSNPs in CEU	Alleles Captured
rs2288912(C4-4661)	rs2288912(C4-4661),rs7257476(C2-5324),rs1132899(C4-3498),rs2288911(C4-4746), rs5157(C4-2623),rs5120(3778)
****rs5127**	rs12709889(C2-5398),rs1130742(C2-4971),rs5127
rs584007	**rs439401**,rs584007
****rs11083751**	rs11083751
rs769450(APOE-2440)	rs769450(APOE-2440)
rs445925	rs445925
rs1064725(C1-5641)	rs1064725(C1-5641)
rs10421404(C2-5004)	rs10421404(C2-5004)
rs405509(APOE-832)	rs405509
rs4420638(C1-6026)	rs4420638
rs5112	rs5112
rs7259004	rs7259004
rs5167(C4-3927)	rs5167
rs5158(C4-2640)	rs5158
rs4803770	rs4803770

Yellow highlighted variants represent SNPs that located in the sequenced regions.
(**) represent intergenic SNPs; red-colored: represent SNPs that failed genotyping and black bolded SNPs represent genotyped intergenic variants.

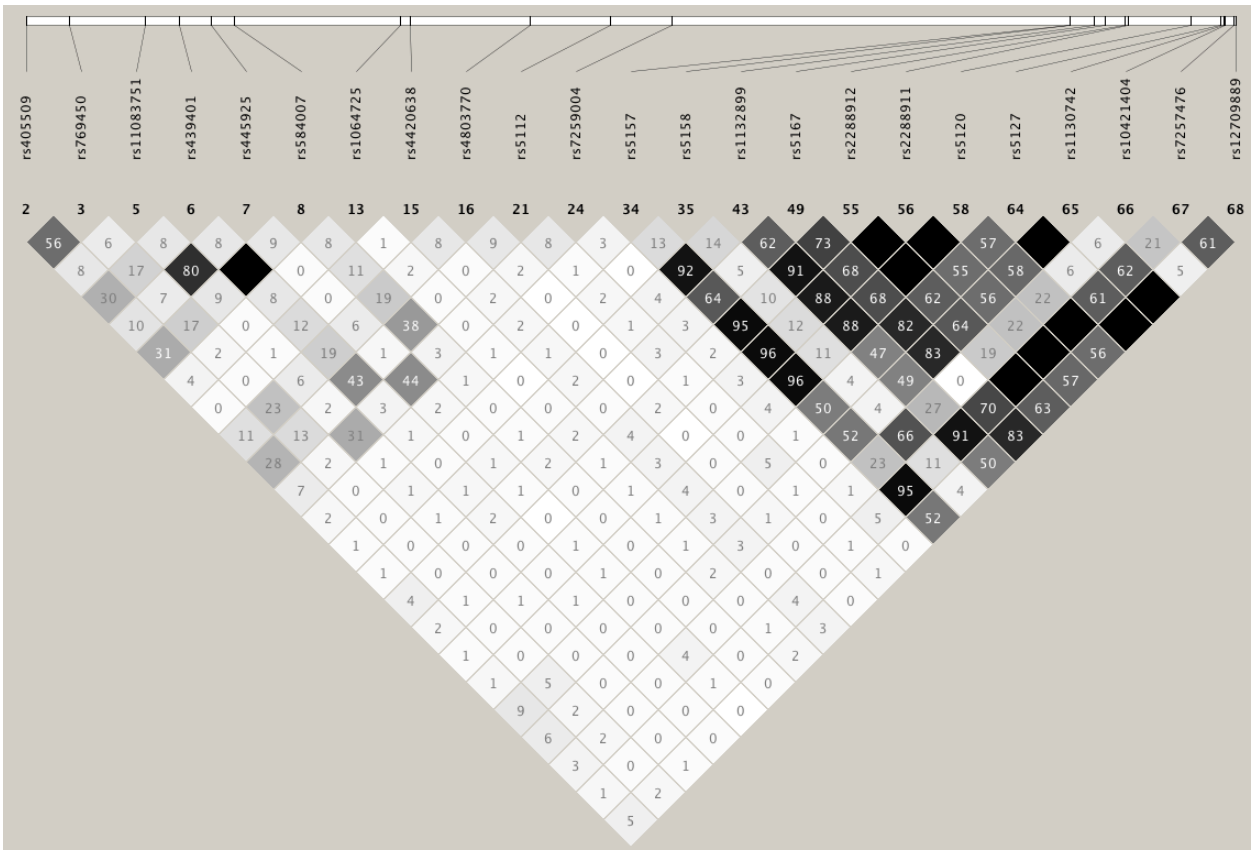

Figure 15. LD plot of the *APOE* gene cluster HapMap common variants in CEU

Table 13. Tagger analysis results of *APOE* gene cluster HapMap common variants in YRI

Test	Alleles Captured
rs5127	rs12709889(C2-5398), rs5127, rs1130742(C2-4971)
rs5159(C4-2971)	rs12721104(C2-75/C4-3380), rs5159
rs584007	rs584007, **rs439401**
rs2288911(C4-4746)	rs2288912 (C4-4661), rs2288911
****rs7259004**	rs7259004
rs5114(C1-1526)	rs5114
rs1132899(C2-194)	rs1132899
rs10421404(C2-5004)	rs10421404
rs4420638(C1-6026)	rs4420638
rs5126 (C2-4587)	rs5126
rs769450(APOE-2440)	rs769450
**rs11878790	rs11878790
rs405509(APOE-832)	rs405509
rs10424339(C1-3573)	rs10424339
rs5167(C2-623)	rs5167
****rs445925**	rs445925
rs5157(C4-2623)	rs5157
rs10425530(C2-853)	rs10425530
rs389261(C1-3423)	rs389261
****rs5112**	rs5112
rs12709884(C2-850)	rs12709884
rs157599(HCR1-575)	rs157599
rs5155(C4-2559)	rs5155
rs5120(C2-3778)	rs5120
rs7257476(C2-5324)	rs7257476
rs7412(APOE-4075)	rs7412
**rs10424663	rs10424663
rs1081101(APOE-73)	rs1081101
rs12721054(C1-5667)	rs12721054
****rs4803770**	rs4803770

Yellow highlighted variants represent SNPs that located in the sequenced regions. (**) represent intergenic variants; red-colored SNPs represent SNPs that failed genotyping and black bolded SNPs represent successfully genotyped variants.

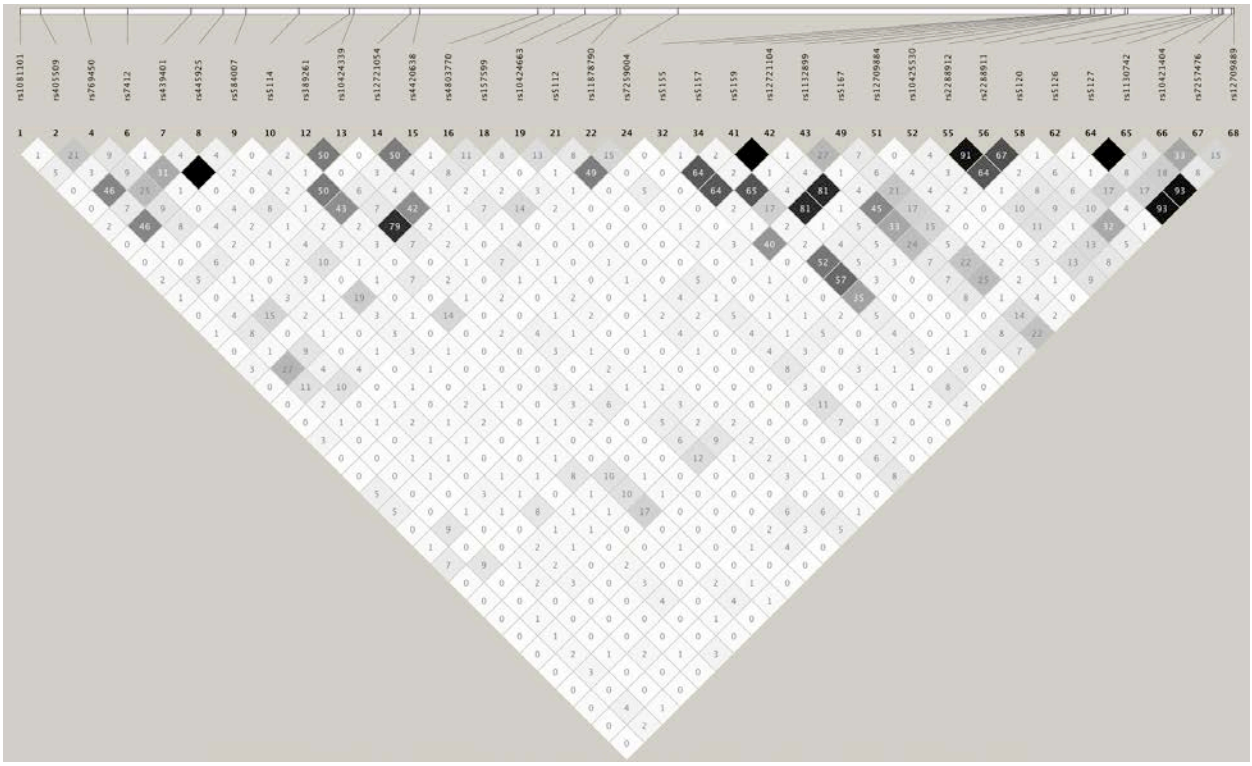

Figure 16. LD plot of *APOE* gene cluster HapMap common variants in YRI

3.4 GENOTYPING

Initially, 103 variants were selected to be genotyped in the entire NHW dataset consisting of 90 sequencing variants (33 tagSNPs, 53 rare variants, and 4 suspicious variants), 7 HapMap tagSNPs covering the intergenic regions, and 6 database common variants (according to Chip Bioinformatics and SeattleSNPs database) mapped to the sequenced regions. Because of the high degree of sequencing homology between the member genes in this cluster, we encountered high degree of nonspecific bindings in the sequencing and genotyping stages that resulted in

sequencing gaps (1550 bp in *APOC1*, and 49 bp in *APOC4*) and failing of 22 variants in the genotyping.

In NHWs, a total of 22 variants were failed genotyping, including 6 tagSNPs (*APOC4*-108, *APOC2*-4534, *APOC2*-4429, *APOC4*-1733, *APOC4*-1823, *APOC2*-4971), 15 rare variants (*APOE*-2907, *APOE*-4951, *APOC1*-607, *APOC1*-655, *APOC1*-659, *APOC1*-1276, *APOC1*-1669, *APOC1*-6122, *APOC1*-6213, *APOC4*-116, *APOC4*-2063, *APOC2*-1324, *APOC2*-2938, *APOC2*-3409, *APOC2*-4477), and one HapMap intergenic variant (rs11083751). Eleven genotyped variants were excluded from the final statistical analyses, including 4 suspicious sequencing variants (*APOE*-4489, *APOE*-4490, *APOC4*-870, *HCR2*-801) that turned out to be not genuine, four common database SNPs [according to Chip Bioinformatics and SeattleSNPs database]; *APOC1*p1249/rs12721047, *APOC2*p3820/rs12709888, *APOC2*p4596/rs76186107, *APOC2*p228/rs5164 and one HapMap intergenic SNP; rs5127 turned out to be non-polymorphics in NHWs, *APOE*624 had low call rate and one variant (*APOC1*p5053) was out of HWE. Therefore, in NHWs a total of 70 variants were included in the association analyses.

In Blacks, initially 160 variants were selected for genotyping: 152 sequencing variants (58 tagSNPs, 90 rare variants, and 4 suspicious sequencing variants), one common database variant (according to Chip Bioinformatics and SeattleSNPs database) mapped to the sequenced regions, and 7 HapMap intergenic tagSNPs. Since genotyping variants in this gene region is challenging, we ended up with the following 42 genotyping failures: 12 tag SNPs (*APOC4*-92, *APOC2*-4971, *APOC2*-2566, *APOC1*-1870, *APOC2*-2191, *APOE*-5229, *APOC4*-1823, *APOC2*-850/C4-4154, *APOC2*-1442/C4-4746, *APOC4*-1733, *APOC2*-4534, *APOC2*-4971), 27 rare variants (*APOE*-494, *APOE*-526, *APOE*-1591, *APOE*-2576, *APOE*-4951, *APOC1*-2099, *APOC1*-2296, *APOC1*-5716, *APOC1*-5717, *APOC1*-6158, *APOC4*-65, *APOC4*-233, *APOC4*-

245, *APOC4*-438, *APOC4*-489, *APOC4*-1702, *APOC4*-1719, *APOC4*-2641, *APOC2*-59/C4-3363, *APOC2*-1608/C4-4912, *APOC2*-2003, *APOC2*-2371, *APOC2*-3193, *APOC2*-3260, *APOC2*-3617, *APOC2*-3806, and *APOC2*-6222), and the 4 suspicious sequencing variants (*APOC2*-4458, *APOC2*-4460, *APOC2*-4532, and *HCR2*p801). Nine variants were excluded from the final statistical analyses either because they were monopolymorphics (*APOC1*p5572), out of HWE (*APOE*1591, *HCR2*p632, *APOC2*p4493, rs11878790, *APOC2*p3348, rs10424663) or had low call rates (*APOC2*p2339 and *APOE*2544). Thus, a total of 108 successfully genotyped variants were considered for the association analyses in African Blacks.

3.5 LD STRUCTURE AND TAGGER ANALYSIS OF THE GENOTYPED VARIANTS

3.5.1 NHWs

A total of 70 variants were successfully genotyped and considered for the genotype-phenotype association analyses (**Table 14**). Out of the 70 variants 65 were mapped to the sequenced regions, and the remaining 5 variants were HapMap variants mapped to the intergenic regions. Out of the 70 genotyped variants, 29 variants had MAF≥5% and were considered common, 10 variants had 1%≤ MAF<5% and were considered relatively less common, and the remaining 31 variants had MAF<1% and were considered rare.

Table 14. Quality parameters of the 70 genotyped variants in 623 NHWs

Common Variants (MAF≥5%)									
#	Variant Name	Position	Alleles	MAF	HWE-P	%Geno	Regulomedb score	Function	GENE
1	APOE560/rs449647	45408564	A>T	0.162	0.27	99.70	5	5'flanking	APOE
2	APOE832/rs405509	45408836	G>T	0.478	1.00	99.80	1f	5'flanking	APOE
3	APOE1163/rs440446	45409167	G>C	0.360	0.47	100.00	4	intron1	APOE
4	APOE1998rs769449	45410002	G>A	0.117	0.46	99.20	4	intron 2	APOE
5	APOE2440/rs769450	45410444	G>A	0.401	0.51	99.40	5	intron 2	APOE
6	APOE3937/rs429358	45411941	T>C	0.153	1.00	98.40	5	exon 4	APOE
7	APOE4075/rs7412	45412079	C>T	0.081	0.81	99.50	5	exon 4	APOE
8	APOE5361/rs1081106	45413365	T>C	0.085	1.00	99.80	3a	3'flanking	APOE
9	rs439401	45414451	C>T	0.359	0.38	97.80	1b	Intergenic	APOE (+6447bp)
10	APOC1rs445925	45415640	G>A	0.110	1.00	99.00	No Data	Intergenic	APOC1(-1281bp)
11	APOC1p720/rs72654451	45417640	insCGTT	0.231	0.88	99.80	4	5'flanking	APOC1
12	APOC1p2041/rs3826688	45418961	G>A	0.342	0.76	97.30	5	intron2	APOC1
13	APOC1p4334/rs12721046	45421254	G>A	0.153	0.84	98.10	6	intron3	APOC1
14	APOC1p5926/rs56131196	45422846	G>A	0.189	0.51	99.20	No Data	3'flanking	APOC1
15	APOC1p6026/rs4420638	45422946	A>G	0.156	0.01	89.30	No Data	3'flanking	APOC1
16	rs4803770	45427353	C>G	0.377	0.99	95.40	5	Intergenic	HCR1(-4bp)
17	rs5112	45430280	G>C	0.464	0.98	91.80	4	APOAPOC1P1	HCR1(+2931 bp)
18	rs7259004	45432557	C>G	0.117	1.00	98.20	6	APOAPOC1P1	HCR2 (-6419bp)
19	HR2p188/rs35136575	45439163	C>G	0.227	0.24	97.80	2a	HCR2	HCR2
20	APOC4p2623/rs5157	45447161	C>T	0.497	0.86	99.80	4	Intron1	APOC4
21	APOC4p2640/rs5158	45447178	C>T	0.139	0.92	99.40	2b	Intron1	APOC4
22	APOC2p194C4p3498/rs1132899	45448036	C>T	0.486	0.66	99.50	5	APOC4-exon2	APOC4
23	APOC2p623C4p3927/rs5167	45448465	T>G	0.360	0.28	100.00	5	exon3	APOAPOC4
24	APOC2p1357C4p4661/rs2288912	45449199	C>G	0.498	0.79	99.80	1a	APOC4-3'/APOC2-5'	APOC4/APOC2
25	APOC2p3778/rs5120	45451620	T>A	0.498	0.82	98.90	4	intron1	APOC2
26	APOC2p4853/rs199828513	45452695	insT	0.279	0.27	99.20	No Data	3'flanking	APOC2
27	APOC2p5004/rs10421404	45452845	C>T	0.183	0.43	99.00	No Data	3'flanking	APOC2
28	APOC2p5310/rs7258345	45453151	T>G	0.466	0.92	98.20	No Data	3'flanking	APOC2
29	APOC2p5398/rs12709889	45453240	G>A	0.276	0.34	97.10	6	3'flanking	APOC2
Rare and less common variants (MAF<5%)									
#	Variant Name	Position	Alleles	MAF	HWE-P	%Geno	Regulomedb score	Function	GENE
1	APOE1575/rs769448	45409579	C>T	0.021	0.47	99.50	4	intron1	APOE
2	APOE2907/rs769451	45410911	T>G	0.011	1.00	100.00	5	intron 2	APOE
3	APOE3038/rs111833428	45411042	G>A	0.002	1.00	99.20	5	exon 3	APOE
4	APOE3106/rs769452	45411110	T>C	0.001	1.00	99.70	5	exon 3	APOE
5	APOE4310/rs199768005	45412314	T>A	0.004	1.00	99.80	5	exon 4	APOE
6	APOE4528	45412532	C>T	0.001	1.00	100.00	5	3' UTR	APOE
7	APOE4737/rs117656888	45412741	C>G	0.008	1.00	99.50	5	3'flanking	APOE
8	APOC1p698/rs72654449	45417618	C>A	0.004	1.00	99.20	4	5'flanking	APOC1
9	APOC1p703/rs3207187	45417623	C>T	0.001	1.00	99.50	4	5'flanking	APOC1

Cont. Table 14

10	APOC1p1170	45418090	G>A	0.001	1.00	97.90	2b	intron1	APOC1
11	APOC1p1294	45418214	A>C	0.001	1.00	99.40	4	intron2	APOC1
12	APOC1p1317/rs12721048	45418237	G>A	0.002	1.00	97.80	4	intron2	APOC1
13	APOC1p1422	45418342	G>A	0.002	1.00	100.00	4	intron2	APOC1
14	APOC1p1566/rs12691088	45418486	G>A	0.006	1.00	97.10	2b	intron2	APOC1
15	APOC1p2629	45419549	G>A	0.001	1.00	99.40	4	exon3	APOC1
16	APOC1p2817	45419737	C>T	0.003	1.00	97.40	2b	intron3	APOC1
17	APOC1p3423/rs389261	45420343	G>A	0.002	1.00	97.60	No Data	intron3	APOC1
18	APOC1p3494	45420414	C>T	0.002	1.00	99.70	No Data	intron3	APOC1
19	APOC1p5641/rs1064725	45422561	T>G	0.039	1.00	99.20	No Data	3'UTR	APOC1
20	APOC1p5773	45422693	G>A	0.001	1.00	97.10	No Data	3'flanking	APOC1
21	HCR1p292/rs4803771	45427648	C>G	0.024	0.61	98.20	4	HCR1	HCR1
22	HCR1p362	45427718	C>A	0.002	1.00	97.60	2a	HCR1	HCR1
23	HCR1p423	45427779	C>G	0.026	0.67	99.50	4	HCR1	HCR1
24	HCR1p575/rs157599	45427931	A>G	0.002	1.00	99.70	3a	HCR1	HCR1
25	HCR1p727/rs149345	45428083	T>G	0.002	1.00	98.60	3a	HCR1	HCR1
26	HCR2p365	45439340	C>A	0.004	1.00	98.10	2b	HCR2	HCR2
27	HCR2p523	45439498	C>T	0.023	1.00	96.00	2b	HCR2	HCR2
28	APOC4p636	45445174	C>T	0.001	1.00	96.60	No Data	5’ flanking	APOC4
29	APOC4p968/rs76214972	45445506	A>G	0.036	0.88	99.70	4	5’ UTR	APOC4
30	APOC4p1150/rs148247675	45445688	A>G	0.002	1.00	96.80	5	Intron1	APOC4
31	APOC4p1229	45445767	G>C	0.002	1.00	99.70	2b	Intron1	APOC4
32	APOC4p2557	45447095	C>A	0.001	1.00	99.50	4	Intron1	APOC4
33	APOC4p2683/rs12721109	45447221	G>A	0.024	0.61	98.20	2b	Intron1	APOC4
34	APOC4p2703/rs12721108	45447241	G>T	0.008	1.00	99.40	2a	Intron1	APOC4
35	APOC2p242C4p3546/rs12691089	45448084	G>A	0.003	1.00	99.70	5	APOC4-exon2	APOC4
36	APOC2p543C4p3847C/rs186448850	45448385	T>C	0.002	1.00	98.10	5	APOC4-intron2	APOC4
37	APOC2p1591C4p4895	45449433	G>A	0.001	1.00	99.70	4	APOC2-intron1	APOC2
38	APOC2p1851/rs12709886	45449693	G>A	0.037	0.84	99.20	6	intron1	APOC2
39	APOC2p2870	45450712	G>T	0.004	1.00	99.70	4	intron1	APOC2
40	APOC2p3348/rs10420434	45451190	G>A	0.037	0.84	99.50	No Data	intron1	APOC2
41	APOC2p5644	45453486	G>A	0.009	1.00	95.70	6	3'flanking	APOC2

Red-colored variants represent database and HapMap intergenic variants. HWE-P (Hardy Weinberg equilibrium), MAF (minor allele frequency), Position (chromosomal position corresponds to NCBI db SNPs build 138).

Tagger analysis of the genotyped variants in NHWs using cut-off MAF≥0.048, and r^2=0.9 selected 23 tagSNPs to capture 29 SNPs. Results of Tagger analysis were shown in **Table 15** and their LD structure was shown in **Figure 17**.

Table 15. Tagger results of the 29 genotyped common variants in NHWs (MAF≥0.048, r^2=0.9)

Bin	Test	**Alleles Captured**
1	APOC4p2623/rs5157	APOC4p2623/rs5157, APOC2p194APOC4p3498/rs1132899, APOC2p3778/rs5120, APOC2p1357APOC4p4661/rs2288912
2	APOC2p4853/rs199828513	APOC2p5398/rs12709889, APOC2p4853/rs199828513
3	APOC1p2041/rs3826688	APOC1p2041/rs3826688, rs439401
4	APOC1p5926/rs56131196	APOC1p6026/rs4420638, APOC1p5926/rs56131196
5	APOE2440/rs769450	APOE2440/rs769450
6	APOE3937/rs429358	APOE3937/rs429358
7	APOE5361/rs1081106	APOE5361/rs1081106
8	APOC1rs445925	APOC1rs445925
9	APOE1163/rs440446	APOE1163/rs440446
10	APOC2p5310/rs7258345	APOC2p5310/rs7258345
11	APOC1p720/rs72654451	APOC1p720/rs72654451
12	APOC2p5004/rs10421404	APOC2p5004/rs10421404
13	APOE560/rs449647	APOE560/rs449647
14	APOC4p2640/rs5158	APOC4p2640/rs5158
15	HCR2p188/rs35136575	HCR2p188/rs35136575
16	rs5112	rs5112
17	APOE832/rs405509	APOE832/rs405509
18	APOE4075/rs7412	APOE4075/rs7412
19	APOE1998/rs769449	APOE1998/rs769449
20	APOC2p623C4p3927/rs5167	APOC2p623C4p3927/rs5167
21	APOC1p4334/rs12721046	APOC1p4334/rs12721046
22	rs4803770	rs4803770
23	rs7259004	rs7259004

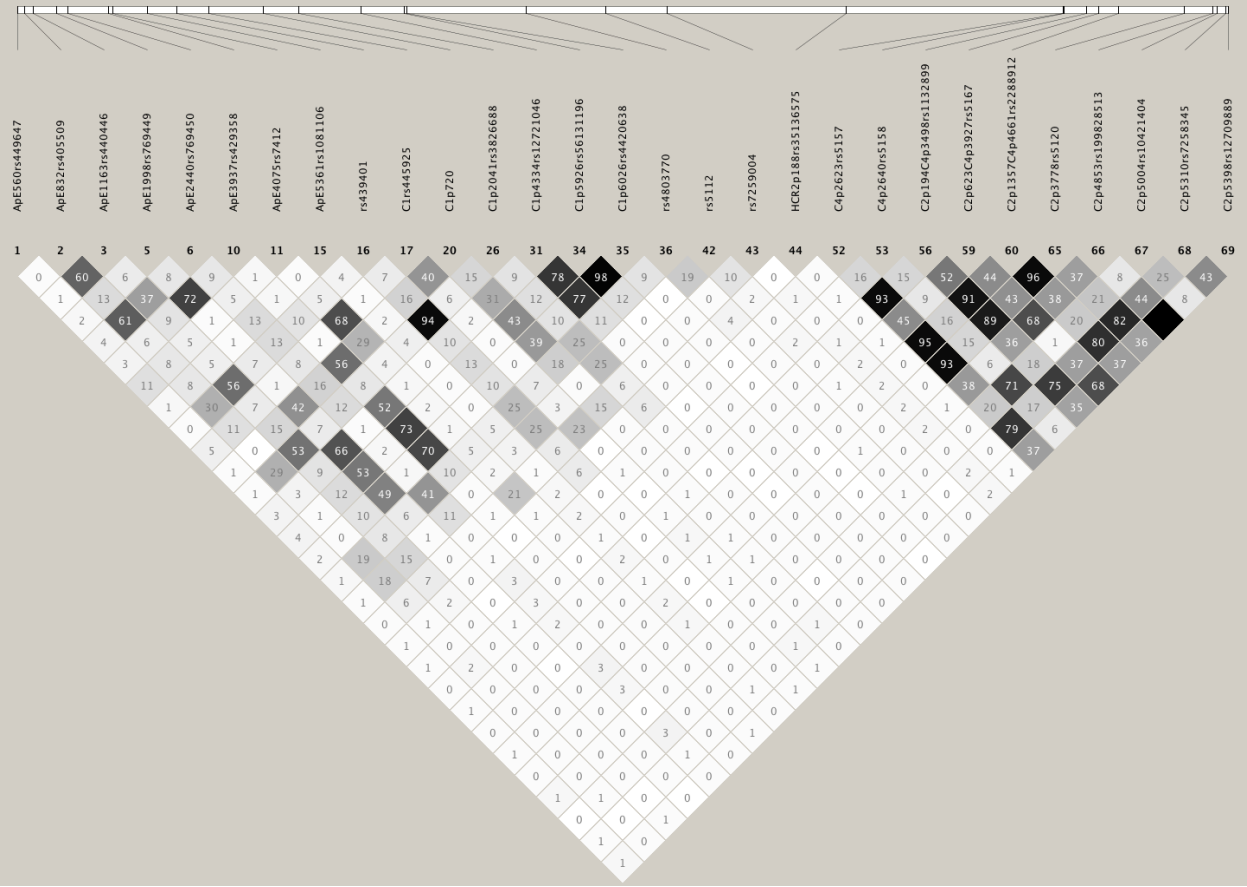

Figure 17. LD plot of the 29 genotyped common variants (MAF≥0.048, r^2=0.9) in NHWs

3.5.2 African Blacks

A total of 108 variants were successfully genotyped in 788 Blacks and were considered for the genotype-phenotype association analyses. 103 variants were mapped to the sequenced regions and the remaining 5 variants were mapped to the intergenic regions. Out of the 108 variants, 48 variants had MAF≥5% and were considered common, 31 variants had MAF 1-5% and were considered less common, and 29 variants had MAF<1% and were considered rare. The MAF, HWE, and call rate information of the 108 genotyped variants in Blacks were summarized in **Table 16**.

Table 16. Quality parameters of the 108 genotyped variants in 788 Blacks

Common Variants with (MAF≥5%)									
#	Variant name	Position	Alleles	MAF	HWE-P	%Geno	regulome db score	Function	Gene name
1	APOE73/rs1081101	45408077	C>T	0.061	0.284	99.3	4	5'flanking	APOE
2	APOE560/rs449647	45408564	A>T	0.374	0.498	96.6	5	5'flanking	APOE
3	APOE832/rs405509	45408836	G>T	0.253	0.128	99.0	1f	5'flanking	APOE
4	APOE1163/rs440446	45409167	G>C	0.100	0.862	93.6	4	intron1	APOE
5	APOE1279/rs877973	45409283	C>A	0.060	0.557	99.5	4	intron1	APOE
6	APOE2440/rs769450	45410444	G>A	0.387	0.241	90.1	5	intron 2	APOE
7	APOE3937/rs429358	45411941	T>C	0.266	0.659	98.0	5	exon 4	APOE
8	APOE4075/rs7412	45412079	G>A	0.061	1.000	99.0	5	exon 4	APOE
9	rs439401	45414451	C>T	0.109	0.043	97.4	1b	Intergenic	APOE(+6447)
10	APOC1rs445925	45415640	G>A	0.297	0.800	97.7	No Data	Intergenic	APOC1
11	APOC1p720ins4/rs71962921	45417640	insCGTT	0.274	0.233	97.8	4	5'flanking	APOC1
12	APOC1p1331/rs10408994	45418251	G>A	0.067	0.059	98.0	4	intron2	APOC1
13	APOC1p1526/rs5114	45418446	C>T	0.058	0.467	98.0	4	intron2	APOC1
14	APOC1p1684/rs12709881	45418604	G>A	0.098	0.564	99.0	4	intron2	APOC1
15	APOC1p3423/rs389261	45420343	G>A	0.331	0.980	95.0	No Data	intron3	APOC1
16	APOC1p3573/rs10424339	45420493	G>A	0.140	0.732	97.3	No Data	intron3	APOC1
17	APOC1p5006/rs112528434	45421926	G>T	0.086	0.436	89.3	No Data	intron3	APOC1
18	APOC1p5053/rs12721052	45421973	delG	0.223	0.395	98.7	No Data	intron3	APOC1
19	APOC1p5667/rs12721054	45422587	A>G	0.145	0.238	91.6	6	3'UTR	APOC1
20	APOC1p5926/rs56131196	45422846	G>A	0.175	0.806	96.9	No Data	3'flanking	APOC1
21	rs4803770	45427353	C>G	0.270	0.489	96.9	5	HCR-1	HCR1(3)
22	HCR1p575/rs157599	45427931	A>G	0.357	0.983	89.6	3a	HCR-1	HCR1
23	rs5112	45430280	C>G	0.477	0.211	91.4	4	APC1P1	APOC1P1/HCR1
24	rs7259004	45432557	G>C	0.302	0.134	97.3	6	APC1P1	HCR2
25	HCR2p188/rs35136575	45439163	C>G	0.155	0.067	97.5	2a	HCR-2	HCR2
26	APOC4p2559/rs5155	45447097	C>T	0.099	1.000	98.7	4	Intron1	APOC4
27	APOC4p2623/rs5157	45447161	C>T	0.173	0.627	97.9	4	Intron1	APOC4
28	APOC2p75C4p3380/rs12721104	45447918	G>A	0.138	1.000	98.2	5	C4-intron1	APOC4
29	APOC2p194C4p3498/rs1132899	45448036	C>T	0.239	0.604	99.0	5	C4-exon2	APOC4
30	APOC2p623C4p3927/rs5167	45448465	T>G	0.459	0.597	98.6	5	C4-exon3	APOC4
31	APOC2p853C4p4157/rs10425530	45448695	G>A	0.111	0.530	97.8	6	C4-3' UTR	APOC4
32	APOC2p1357C4p4661/rs2288912	45449199	G>C	0.257	0.882	97.9	1a	C4-3'/C2-5'	APOC2/APOC4
33	APOC2p1540C4p4844/rs75463753	45449382	G>A	0.108	0.365	92.6	4	C2-intron1	APOC2
34	APOC2p2486/rs9304645	45450328	G>A	0.368	0.094	97.5	4	Intron1	APOC2
35	APOC2p3010/rs10419086	45450852	A>G	0.124	0.539	92.2	6	Intron1	APOC2
36	APOC2p3778/rs5120	45451620	A>T	0.182	0.384	98.8	4	Intron1	APOC2
37	APOC2p3805/rs7257095	45451647	C>G	0.165	0.303	98.2	2a	Intron1	APOC2
38	APOC2p3814/rs10422603	45451656	T>G	0.301	0.706	96.3	2b	Intron1	APOC2
39	APOC2p4319/rs5123	45452161	G>A	0.059	0.074	97.0	No Data	Intron3	APOC2
40	APOC2p4587/rs5126	45452429	A>C	0.050	0.918	94.1	5	exon4	APOC2
41	APOC2p4754/rs7253690	45452596	G>A	0.061	0.101	98.8	5	exon4	APOC2

Cont. Table 16

42	APOC2p4853/rs150448996	45452694	delT	0.274	0.822	96.6	No Data	3'flanking	APOC2
43	APOC2p5004/rs10421404	45452845	C>T	0.293	0.170	98.2	No Data	3'flanking	APOC2
44	APOC2p5310/rs7258345	45453151	G>T	0.305	0.192	90.9	No Data	3'flanking	APOC2
45	APOC2p5398/rs12709889	45453239	G>A	0.259	1.000	97.7	6	3'flanking	APOC2
46	APOC2p5586/rs73558127	45453427	T>G	0.100	0.376	96.5	No Data	3'flanking	APOC2
47	APOC2p5815/rs10423208	45453656	A>G	0.316	0.818	97.8	5	3'flanking	APOC2
48	APOC2p5922/rs10422888	45453763	A>G	0.078	0.891	93.2	5	3'flanking	APOC2

Rare and less common variants (MAF<5%)

#	Variant name	Position	Alleles	MAF	HWE-P	%Geno	regulome db score	Function	Gene name
1	APOE173	45408177	A>G	0.002	1.000	99.6	3a	5'flanking	APOE
2	APOE308/rs769445	45408312	C>T	0.007	1.000	99.6	4	5'flanking	APOE
3	APOE618	45408622	G>C	0.001	1.000	99.6	4	5'flanking	APOE
4	APOE624/rs769446	45408628	T>C	0.008	1.000	91.9	3a	5'flanking	APOE
5	APOE1109/rs9282609	45409113	C>T	0.042	0.070	99.1	4	Splice site	APOE
6	APOE1231	45409235	G>A	0.012	1.000	99.5	2b	Intron1	APOE
7	APOE1539/rs184686013	45409543	A>G	0.009	0.101	99.1	4	Intron1	APOE
8	APOE2072/rs189660912	45410076	G>A	0.008	1.000	99.2	4	Intron 2	APOE
9	APOE2269/rs6135770	45410273	G>A	0.017	1.000	98.0	5	Intron 2	APOE
10	APOE3673/rs769453	45411677	C>G	0.007	1.000	99.3	5	Intron 3	APOE
11	APOE4036/rs769455	45412040	C>T	0.020	0.512	97.9	5	Exon 4	APOE
12	APOE4569	45412573	G>T	0.001	1.000	99.3	5	3'UTR	APOE
13	APOE5223	45413227	C>G	0.005	1.000	100.0	2b	3'flanking	APOE
14	APOE5231	45413235	T>G	0.027	0.197	99.2	2b	3'flanking	APOE
15	APOC1p894/rs190454394	45417814	C>T	0.002	1.000	98.8	4	5'flanking	APOC1
16	APOC1p1166/rs72654452	45418086	C>T	0.031	0.334	99.5	2b	Intron1	APOC1
17	APOC1p1642	45418562	C>T	0.011	1.000	99.3	4	Intron2	APOC1
18	APOC1p3358	45420278	A>G	0.002	1.000	94.3	No Data	Intron3	APOC1
19	HCR1p424/rs117664574	45427779	G>A	0.007	1.000	99.0	4	HCR-1	HCR1
20	HCR2p286	45439261	G>A	0.046	0.399	98.6	2a	HCR-2	HCR2
21	HCR2p523/rs118004808	45439498	C>T	0.003	1.000	99.2	2b	HCR-2	HCR2
22	APOC4p368	45444906	T>C	0.002	1.000	98.3	6	5’ flanking	APOC4
23	APOC4p637/rs113814026	45445175	G>T	0.046	1.000	98.7	No Data	5’ flanking	APOC4
24	APOC4p757/rs12721105	45445295	G>T	0.038	0.591	99.7	5	5’ flanking	APOC4
25	APOC4p1088	45445626	T>G	0.001	1.000	98.2	2b	Intron1	APOC4
26	APOC4p1130	45445668	T>C	0.001	1.000	99.1	5	Intron1	APOC4
27	APOC4p1192/rs113745034	45445730	G>A	0.012	1.000	94.9	4	Intron1	APOC4
28	APOC4p1325del3	45445863	del3	0.024	1.000	98.7	4	Intron1	APOC4
29	APOC4p1430ins	45445968	insG	0.034	1.000	87.7	5	Intron1	APOC4
30	APOC4p2099/rs111339708	45446637	G>T	0.015	1.000	99.0	No Data	Intron1	APOC4
31	APOC4p2467/rs115225947	45447005	G>A	0.014	1.000	99.1	5	Intron1	APOC4
32	APOC4p2607/rs5156	45447145	G>A	0.013	1.000	96.0	4	Intron1	APOC4
33	APOC4p2640/rs5158	45447178	C>T	0.021	1.000	98.7	2b	Intron1	APOC4
34	APOC4p2678/rs148564866	45447216	G>C	0.009	1.000	98.3	2b	Intron1	APOC4

Cont. Table 16

35	APOC4p2767/rs127721107	45447305	G>T	0.025	1.000	97.8	4	Intron1	APOC4
36	APOC4p3348	45447886	G>A	0.001	1.000	98.8	5	Intron1	APOC4
37	APOC2p228/rs5164	45448070	G>A	0.007	1.000	98.4	5	C4-exon2	APOC4
38	APOC2p288C4p3592/rs12691090	45448130	C>T	0.027	1.000	98.3	5	C4-exon2	APOC4
39	APOC2p396C4p3700	45448238	G>A	0.001	1.000	95.8	5	C4-intron2	APOC4
40	APOC2p488C4p3792/rs5165	45448330	G>A	0.015	1.000	98.0	5	C4-intron2	APOC4
41	APOC2p665C4p3969/rs138548797	45448507	A>C	0.009	1.000	98.7	No Data	C4-exon3	APOC4
42	APOC2p708C4p4012	45448550	G>A	0.001	1.000	98.4	6	C4-exon3	APOC4
43	APOC2p1042C4p4346/rs12709885	45448884	A>T	0.018	0.420	99.0	5	C4-3'/C2-5'	APOC2/APOC4
44	APOC2p1187C4p4491/rs111782345	45449029	G>A	0.018	1.000	95.3	5	C4-3'/C2-5'	APOC2/APOC4
45	APOC2p1229C4p4533/rs112698600	45449071	C>T	0.014	1.000	97.8	2b	C4-3'/C2-5'	APOC2/APOC4
46	APOC2p1275C4p4579/rs111356234	45449117	G>A	0.035	0.775	98.3	4	C4-3'/C2-5'	APOC2/APOC4
47	APOC2p2935/rs11879392	45450777	C>G	0.014	1.000	96.6	2b	Intron1	APOC2
48	APOC2p3692/rs12721060	45451534	T>G	0.017	1.000	87.3	No Data	Intron1	APOC2
49	APOC2p3892/rs5121	45451734	C>T	0.036	1.000	96.6	5	Exon2	APOC2
50	APOC2p4086/rs114780592	45451928	G>A	0.028	1.000	98.7	4	Intron2	APOC2
51	APOC2p4118/rs201709243	45451960	G>A	0.001	1.000	96.2	4	Exon3	APOC2
52	APOC2p4513/rs180809422	45452355	A>C	0.014	0.235	90.3	5	Intron3	APOC2
53	APOC2p4973/rs199828513	45452814	A>G	0.008	1.000	93.5	No Data	3'flanking	APOC2
54	APOC2p5018/rs78403558	45452859	delCTTTT	0.035	1.000	99.3	5	3'flanking	APOC2
55	APOC2p5491	45453332	C>T	0.001	1.000	98.8	6	3'flanking	APOC2
56	APOC2p5512/rs12721064	45453353	C>T	0.008	1.000	100.0	6	3'flanking	APOC2
57	APOC2p5562	45453403	G>C	0.018	1.000	96.7	No Data	3'flanking	APOC2
58	APOC2p5771	45453612	delATTTA	0.005	1.000	97.1	6	3'flanking	APOC2
59	APOC2p5965	45453806	G>A	0.001	1.000	99.1	5	3'flanking	APOC2
60	APOC2p6334	45454175	G>A	0.009	1.000	99.5	No Data	3'flanking	APOC2

Red-colored variants represent database and HapMap intergenic variants. HWE-P (Hardy Weinberg equilibrium), MAF (minor allele frequency), Position (chromosomal position corresponds to NCBI db SNPs build 138).

Tagger analysis of the genotyped common variants using MAF≥4.8%, r^2=0.9, identified 41 variants as tag-SNPs to capture information for 48 variants. **Table 17** represents tagger analysis results of the genotyped common variants in Blacks, and their LD plot is shown in **Figure 18**.

Table 17. Tagger results of the 48 common genotyped variants (MAF≥0.048, r^2=0.9) in Blacks

Bin	Test	**Alleles Captured**
1	APOC2p3814/rs10422603	APOC2p5004/rs10421404, APOC2p3814/rs10422603
2	APOC2p4319/rs5123	APOC2p4754/rs7253690, APOC2p4319/rs5123
3	APOC2p5310/rs7258345	APOC2p5815/rs10423208, APOC2p5310/rs7258345
4	APOC2p5398/rs12709889	APOC2p5398/rs12709889, APOC2p4853/rs150448996
5	APOC1p5006/rs112528434	APOC1p5006/rs112528434, APOC1p1684/rs12709881
6	rs439401	rs439401, APOE1163/rs440446
7	APOE1279/rs877973	APOC1p1526/rs5114, APOE1279/rs877973
8	APOC2p3010/rs10419086	APOC2p3010/rs10419086
9	APOC1p3423/rs389261	APOC1p3423/rs389261
10	HCR2p188/rs35136575	HCR2p188/rs35136575
11	APOC1p5667/rs12721054	APOC1p5667/rs12721054
12	APOC2p5586/rs73558127	APOC2p5586/rs73558127
13	APOC2p3805/rs7257095	APOC2p3805rs7257095
14	APOE560/rs449647	APOE560r/s449647
15	APOC2p623C4p3927/rs5167	APOC2p623C4p3927/rs5167
16	APOC1p5053/rs12721052	APOC1p5053/rs12721052
17	APOC1rs445925	APOC1rs445925
18	APOC2p4587/rs5126	APOC2p4587/rs5126
19	HCR1p575/rs157599	HCR1p575/rs157599
20	APOE4075/rs7412	APOE4075/rs7412
21	APOC2p853C4p4157/rs10425530	APOC2p853C4p4157/rs10425530
22	APOC2p1357C4p4661/rs2288912	APOC2p1357C4p4661/rs2288912
23	APOC1p1331/rs10408994	APOC1p1331/rs10408994
24	rs4803770	rs4803770
25	APOC4p2623rs5157	APOC4p2623/rs5157
26	APOE73/rs1081101	APOE73/rs1081101
27	APOC2p1540C4p4844/rs75463753	APOC2p1540C4p4844/rs75463753
28	APOE2440/rs769450	APOE2440/rs769450
29	APOC2p75C4p3380/rs12721104	APOC2p75C4p3380/rs12721104
30	APOE832/rs405509	APOE832/rs405509
31	APOC2p5922/rs10422888	APOC2p5922/rs10422888
32	APOC2p2486/rs9304645	APOC2p2486/rs9304645
33	APOC2p3778/rs5120	APOC2p3778/rs5120
34	APOC1p720ins4/rs71962921	APOC1p720ins4/rs71962921
35	APOC1p5926/rs56131196	APOC1p5926/rs56131196
36	rs7259004	rs7259004
37	APOC4p2559/rs5155	APOC4p2559/rs5155
38	rs5112	rs5112
39	APOE3937/rs429358	APOE3937/rs429358
40	APOC1p3573/rs10424339	APOC1p3573/rs10424339
41	APOC2p194C4p3498/rs1132899	APOC2p194C4p3498/rs1132899

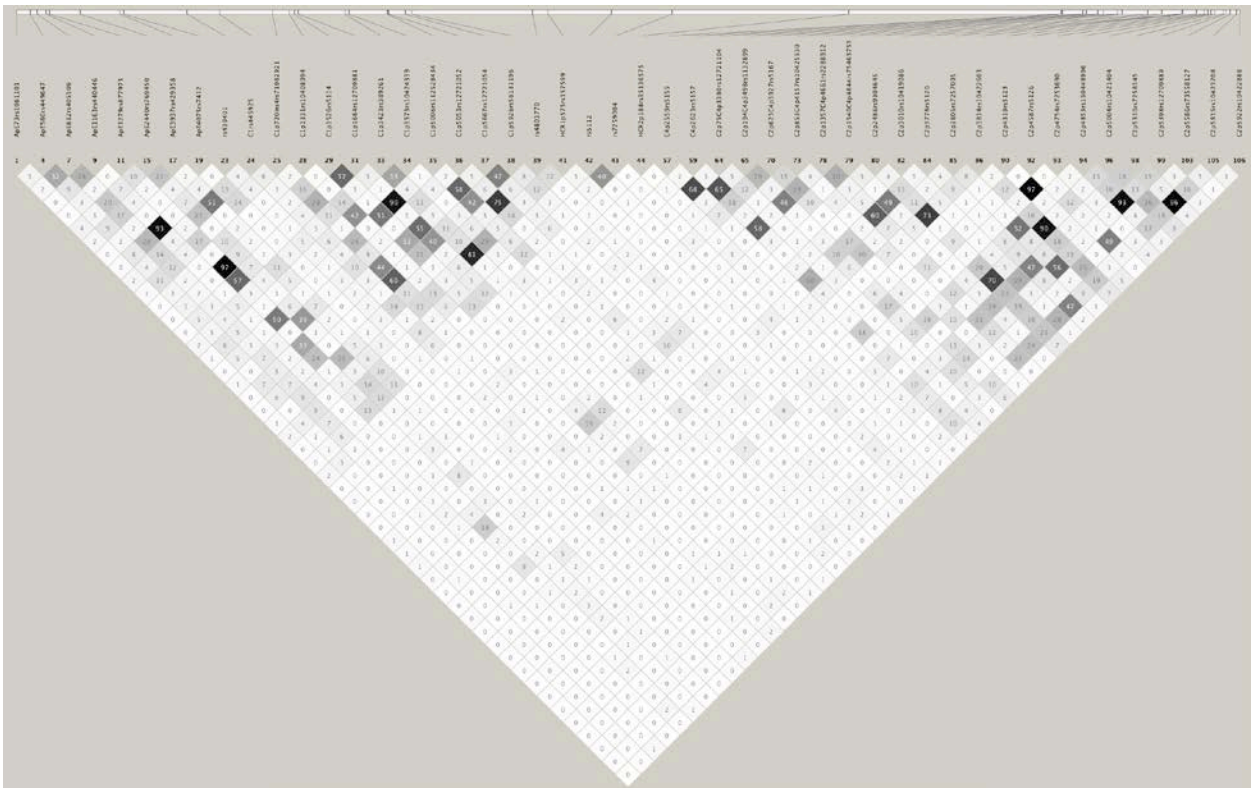

Figure 18. LD plot of the 48 common genotyped variants (MAF≥4.8%, r^2=0.09) in Blacks

3.5.3 Shared genotyped variants in NHWs and Blacks

Twenty-seven variants genotyped in both populations were considered for the genotype-phenotype association analyses. Twenty-three variants showed significant difference in their MAF in the two racial groups (P<0.05) (see **Table 18)**. The LD structure (**Figure 19** and **Figure 20**) of the 27 shared variants is different in the two population groups whereas markers tend to be much strongly correlated in NHWs than in Blacks except these two variants *APOC2*p5398/rs12709889, and *APOC2*p4853/rs199828513 were found to be in complete LD in both racial groups. As expected fewer variants were selected as tagSNPs in NHWs than in

Blacks to capture information for the total 27 variants (22 tagSNPs in NHWs vs. 25 tagSNPs in Blacks) because of their high correlation in NHWs (**Table 19**).

Table 18. Minor allele frequency of the 27 shared genotyped variants in both racial groups

#	Name	Position	Associated Allele	MAF in Blacks	MAF in NHWs	P value
1	APOE560/rs449647	45408564	T	0.369	0.162	7.12E-34
2	APOE832/rs405509	45408836	T	0.252	0.478	2.23E-35
3	APOE1163/rs440446	45409167	C	0.100	0.360	1.25E-58
4	APOE2440/rs769450	45410444	A	0.387	0.401	0.4687
5	APOE3937/rs429358	45411941	C	0.264	0.153	2.00E-12
6	APOE4075/rs7412	45412079	T	0.061	0.081	0.0364
7	rs439401	45414451	T	0.109	0.359	9.98E-55
8	APOC1rs445925	45415640	A	0.298	0.110	4.88E-33
9	APOC1p720	45417640	G	0.274	0.231	0.0108
10	APOC1p3423/rs389261	45420343	A	0.331	0.002	6.94E-107
11	APOC1p5926/rs56131196	45422846	A	0.175	0.189	0.3285
12	rs4803770	45427353	G	0.270	0.377	2.69E-09
13	HCR1p575/rs157599	45427931	G	0.360	0.002	5.35E-120
14	rs5112	45430280	C	0.520	0.464	0.0052
15	rs7259004	45432557	G	0.698	0.117	1.77E-202
16	HCR2p188/rs35136575	45439163	G	0.155	0.227	1.49E-06
17	HCR2p523	45439498	T	0.003	0.023	1.22E-06
18	APOC4p2623/rs5157	45447161	T	0.173	0.497	5.14E-74
19	APOC4p2640/rs5158	45447178	T	0.021	0.139	2.34E-32
20	APOC2p194C4p3498/rs1132899	45448036	T	0.238	0.486	2.87E-42
21	APOC2p623C4p3927/rs5167	45448465	G	0.459	0.360	1.26E-07
22	APOC2p1357C4p4661/rs2288912	45449199	C	0.258	0.497	2.28E-40
23	APOC2p3778rs5120	45451620	T	0.185	0.502	4.44E-70
24	APOC2p4853/rs199828513	45452695	W	0.274	0.279	0.7703
25	APOC2p5004/rs10421404	45452845	T	0.290	0.183	5.70E-11
26	APOC2p5310r/s7258345	45453151	T	0.307	0.534	3.38E-32
27	APOC2p5398/rs12709889	45453240	A	0.259	0.276	0.3

Red-colored p-value represents the significant ones.

Table 19. Tagger results of the 27 shared genotyped markers in NHWs and Blacks

Tagger results of the 27 shared genotyped markers in NHWs		
Bin	**Test**	**Alleles Captured**
1	APOC4p2623/rs5157	APOC2p3778/rs5120, APOC2p1357APOC4p4661/rs2288912, APOC4p2623/rs5157, APOC2p194APOC4p3498/rs1132899
2	APOC2p5398/rs12709889	APOC2p5398/rs12709889, APOC2p4853/rs199828513
3	HCR1p575/rs157599	HCR1p575/rs157599, APOC1p3423/rs389261
4	APOC2p5310/rs7258345	APOC2p5310/rs7258345
5	rs5112	rs5112
6	APOE3937/rs429358	APOE3937/rs429358
7	rs4803770	rs4803770
8	APOE4075rs7412	APOE4075rs7412
9	rs439401	rs439401
10	HR2p523	HR2p523
11	APOC4p2640/rs5158	APOC4p2640/rs5158
12	APOC1p720	APOC1p720
13	rs7259004	rs7259004
14	APOE832/rs405509	APOE832/rs405509
15	APOC2p623C4p3927/rs5167	APOC2p623C4p3927/rs5167
16	APOC1p5926/rs56131196	APOC1p5926/rs56131196
17	APOE560/rs449647	APOE560r/s449647
18	APOE1163/rs440446	APOE1163/rs440446
19	HR2p188/rs35136575	HR2p188/rs35136575
20	APOE2440/rs769450	APOE2440/rs769450
21	APOC2p5004/rs10421404	APOC2p5004/rs10421404
22	APOC1rs445925	APOC1rs445925
Tagger results of the 27 shared genotyped markers in Blacks		
Bin	**Test**	**Alleles Captured**
1	APOE1163/rs440446	APOE1163/rs440446, rs439401
2	APOC2p4853rs199828513	APOC2p5398/rs12709889, APOC2p4853/rs199828513
3	APOC2p5310/rs7258345	APOC2p5310/rs7258345
4	APOC2p194C4p3498/rs1132899	APOC2p194C4p3498/rs1132899
5	APOC1p5926/rs56131196	APOC1p5926/rs56131196
6	APOC1p720	APOC1p720
7	rs4803770	rs4803770
8	APOE4075/rs7412	APOE4075/rs7412
9	HR2p523	HR2p523
10	APOC2p5004rs10421404	APOC2p5004rs10421404
11	rs5112	rs5112
12	APOE2440/rs769450	APOE2440/rs769450
13	APOC2p623C4p3927/rs5167	APOC2p623C4p3927/rs5167
14	APOE832/rs405509	APOE832/rs405509
15	APOC1rs445925	APOC1rs445925
16	HR2p188/rs35136575	HR2p188/rs35136575
17	APOC4p2623/rs5157	APOC4p2623/rs5157
18	APOE560/rs449647	APOE560/rs449647
19	HR1p575/rs157599	HR1p575/rs157599
20	APOC1p3423/rs389261	APOC1p3423/rs389261
21	APOC4p2640/rs5158	APOC4p2640/rs5158

Cont. Table 19

22	APOE3937/rs429358	APOE3937/rs429358
23	rs7259004	rs7259004
24	APOC2p3778/rs5120	APOC2p3778/rs5120
25	APOC2p1357APOC4p4661/rs2288912	APOC2p1357APOC4p4661/rs2288912

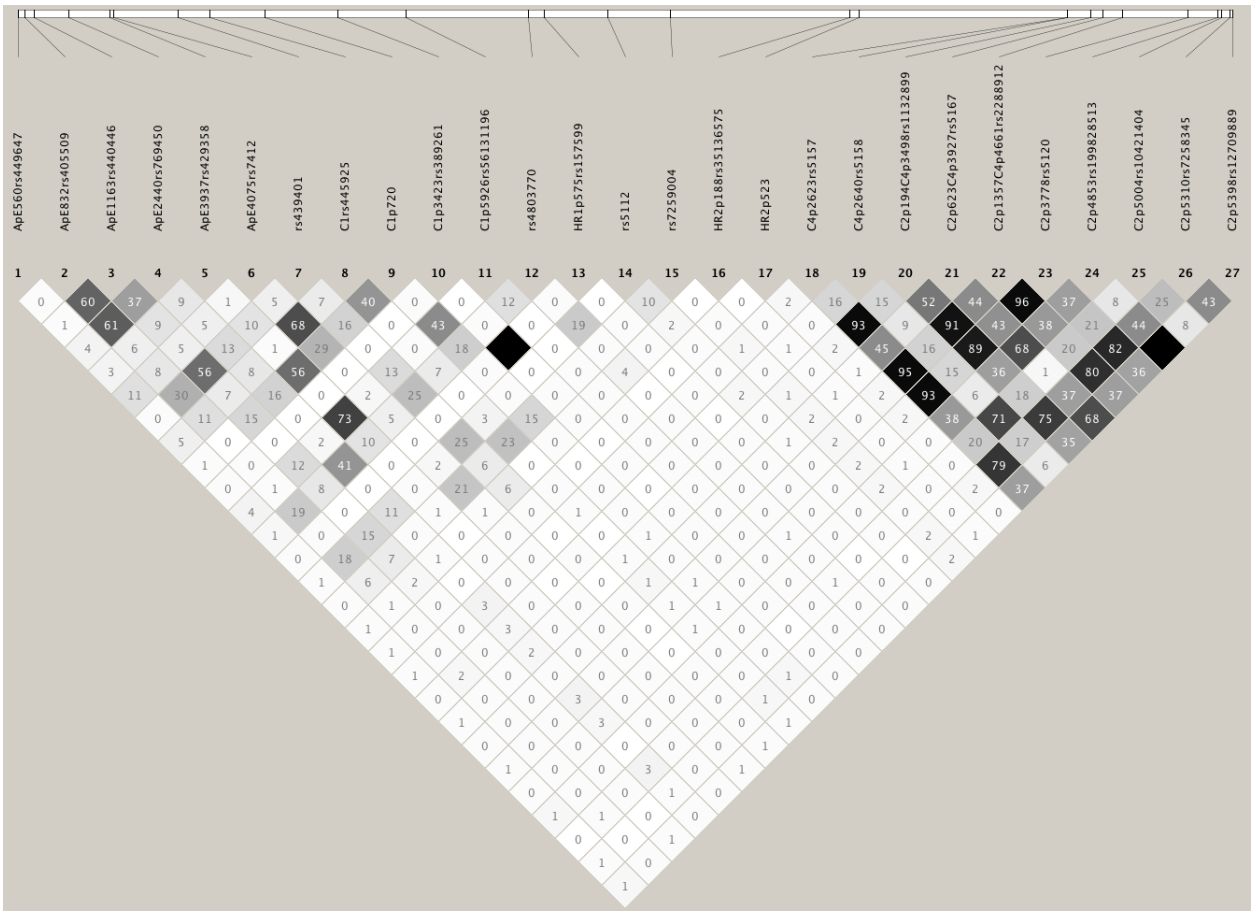

Figure 19. LD plot of the 27 genotyped shared markers in NHWs

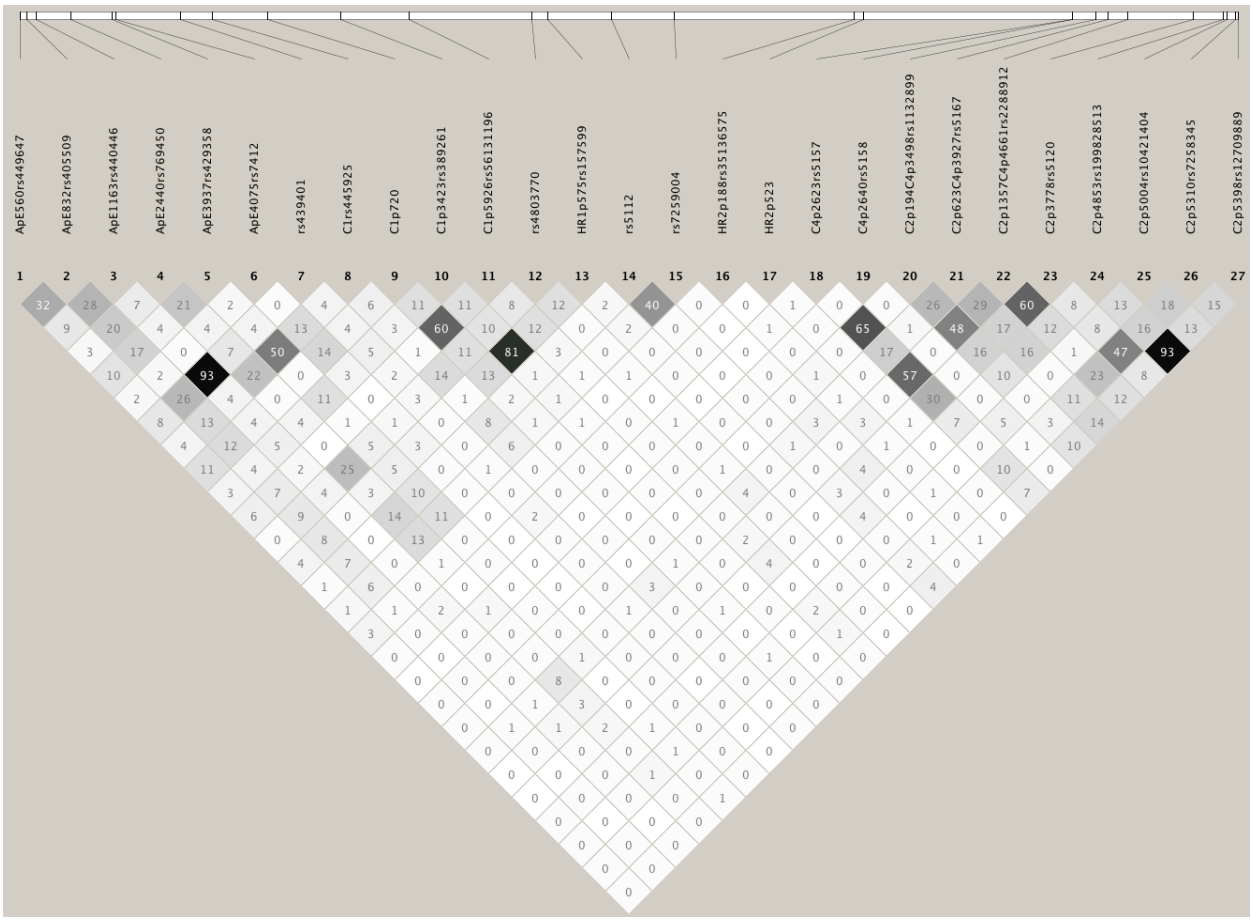

Figure 20. LD plot of the 27 genotyped shared markers in Blacks

3.6 ASSOCIATION RESULTS WITH LIPID TRAITS

3.6.1 Single-locus association analysis

Twenty variants in NHWs and twenty-four variants in Blacks with MAF>1% showed significant associations with at least one lipid trait.

3.6.1.1 NHWs

Table 20 presents the single-locus association results in NHWs, **Table 21-23** summaries the lipid traits mean values distribution among the genotype groups, and **Figure 21** showed LD plot of the 20 variants with significant associations. Twenty variants with MAF>1% showed significant associations with at least one lipid trait in NHWs. As expected, *APOE2* (*APOE*4075/rs7412) and *APOE4* (*APOE*3937/rs429358) alleles showed significant associations with LDL-C (β=-21.84; P=1.84E-07, and β=8.10; P=0.0103), TC (β=-19.46; P=9.50E-06, β=6.82; P=0.0383), and apoB (β=-5.60; P=9.70E-13, and β=2.14; P=0.0005) with E2 allele having stronger effect than E4 allele. Ten additional SNPs showed significant associations with LDL-C: *APOE*560/rs449647 (β=-7.12; P=0.0247), *APOE*2440/rs769450 (β=4.89; P=0.0378), *APOC1*rs445925 (β=-12.58; P=0.0005), *APOC1*p4334/rs12721046 (β=6.93; P=0.0306), *APOC1*p5641/rs1064725 (β=11.99; P=0.0415), *APOC1*p5926/rs56131196 (β=7.24; P=0.0142), *APOC1*p6026/rs4420638 (β=6.97; P=0.0260), rs4803770 (β=5.52; P=0.0197), rs7259004 (β=-9.78; P=0.0050), and *APOC4*p2683/rs12721109 (β=-19.14; P=0.0092). *APOC1*rs445925 was in moderate LD with E2 allele (r^2=0.68) and the other three variants, *APOC1*p4334/rs12721046 (r^2=0.52), *APOC1*p5926/rs56131196 (r^2=0.73), and *APOC1*p6026/rs4420638 (r^2=0.70) were in moderate LD with E4 allele. While *APOC1*p5926/rs56131196 was in strong LD with these two

variants; *APOC1*p4334/rs12721046 (r^2=0.78), and *APOC1*p6026/rs4420638 (r^2=0.98), the intergenic SNP rs4803770 was in moderate LD with *APOE*2440/rs769450 (r^2=0.41). Only two SNPs showed significant associations with HDL-C; *APOE*1575rs769448 (β=0.08; P=0.0197), and *HCR2*p188/rs35136575 (β=0.03; P=0.0330) and they are not in LD with each other.

In addition to the APOE2/E4 alleles, ten additional SNPs showed significant associations with TC; *APOE*560/rs449647 (β=-6.71; P=0.0428), *APOE*1998/rs769449 (β=8.31; P=0.0285), *APOE*2440/rs769450 (β=6.88; P=0.0051), *APOC1*rs445925 (β=-13.5; P=0.00032), *APOC1*p5641/rs1064725 (β=13.65; P=0.02631), *APOC1*p5926/rs56131196 (β=6.69; P=0.03046), *APOC1*p6026/rs4420638 (β=6.79; P=0.04018), rs4803770 (β=6.08; P=0.01385), rs5112 (β=-4.95; P=0.04462), and rs7259004 (β=-9.06; P=0.01342). Three variants *APOE*1998rs769449 (r^2=0.72), *APOC1*p5926/rs56131196 (r^2=0.73), and *APOC1*p6026/rs4420638 (r^2=0.70) were in moderate LD with E4 allele, while *APOC1*rs445925 was in moderate LD with E2 allele (r^2=0.68). *APOC1*p5926/rs56131196 and *APOC1*p6026/rs4420638 were in complete LD (r^2=0.98) and this SNP rs4803770 was in moderate LD with *APOE*2440/rs769450 (r^2=0.41).

Six variants showed significant associations with TG; *APOE*832/rs405509 (β=-0.07; P=0.0033), *APOE*1163/rs440446 (β=-0.08; P=0.0018), *APOE*2440/rs769450 (β=0.06; P=0.0082), rs439401 (β=-0.06; P=0.0194), *APOC1*p2041/rs3826688 (β=-0.08; P=0.0011), and *APOC4*p2683/rs12721109 (β=-0.16; P=0.0329). *APOE*832/rs405509 was in moderate LD with these two variants *APOE*1163/rs440446 (r^2=0.60), and *APOE*2440/rs769450 (r^2=0.61). rs439401 was in strong LD with *APOC1*p2041/rs3826688 (r^2=0.98) and in moderate LD with *APOE*1163/rs440446 (r^2=0.56).

Seven variants in addition to E2/E4 alleles showed significant associations with apoB; *APOE*832/rs405509 (β=1.46; P=0.0009), *APOE*1998/rs769449 (β=2.03; P=0.0030), *APOC1*rs445925 (β=-3.78; P=5.20E-08), *APOC1*p4334/rs12721046 (β=1.59; P=0.00983), *APOC1*p5926/rs56131196 (β=1.75; P=0.00229), *APOC1*p6026/rs4420638 (β=1.43; P=0.01775), and *APOC4*p2683/rs12721109 (β=-4.99; P=0.00057). The association of these two variants, *APOE*1998/rs769449 and *APOC1*rs445925, seem to be not independent because of their LD with E4/E2 alleles (r^2=0.72; r^2=0.68, respectively). Similarly the association of these three variants (*APOC1*p4334/rs12721046, *APOC1*p5926/rs56131196, and *APOC1*p6026/rs4420638) is more likely due to their moderate LD with E4 (r^2= 0.52, 0.73, 0.70). Only two SNPs showed marginal significant association with apoA1; rs7259004 (β=6.89; P=0.0460), and *HCR2*p188/rs35136575 (β=5.16; P=0.0496) and none of them was in LD with each other.

We observed thirteen variants in addition to the E2/E4 alleles have multiple associations with lipid traits implying their pleiotrophic effects. Three variants, *APOC1*rs445925, *APOC1*p5926/rs56131196, and *APOC1*p6026/rs4420638, had significant associations with 3 LDL-related traits (LDL-C, TC, and ApoB) more likely due to their moderate LD with E2/E4 alleles. Eight other variants showed significant associations with 2 LDL-related traits, *APOE*560/rs449647, *APOC1*p5641/rs1064725, rs4803770, *APOE*1998/rs769449, *APOC1*p4334/rs12721046, *APOC4*p2683/rs12721109, *APOE*2440/rs769450, and rs7259004. The last variant showed significant association with apoA1 in addition to its association with 2 LDL-related traits. *APOC4*p2683/rs12721109 and *APOE*2440/rs769450 variants showed significant association with TG in addition to their effect on 2 LDL-related traits. *APOE*832/rs405509 had significant associations with TG and apoB, while *HCR2*p188/rs35136575 had significant associations with HDL-C, and apoA1. The remaining

five variants showed evidence of association with a single lipid trait; *APOE*1575/rs769448 showed significant association only with HDL-C, while the other three variants; *APOE*1163/rs440446, rs439401, and *APOC1*p2041/rs3826688 showed significant association only with TG, and rs5112 showed significant association only with TC.

Table 20. Single-locus association results with lipid traits in NHWs

Variant				LDL-C		HDL-C[a]		TC		TG[a]		ApoB[a]		ApoA1	
Nucleotide position	Function	Regulome DB score	MAF	Beta	p_value	Beta	p_value	Beta	p_value	Beta	p_value	Beta	p_value	Beta	p_value
APOE560/rs449647	5'flanking	5	0.161	-7.12	0.0247	-0.01	0.3526	-6.71	0.0428	-0.02	0.5229	-0.95	0.129	-1.57	0.6175
APOE832/rs405509	5'flanking	1f	0.4775	0.42	0.8542	0.01	0.4031	-0.68	0.7757	-0.07	0.0033	1.46	0.0009	-1.80	0.4173
APOE1163/rs440446	intron1	4	0.3604	-2.59	0.281	0.01	0.2865	-4.26	0.0893	-0.08	0.0018	0.56	0.2319	-0.19	0.9349
APOE1575/rs769448	intron1	4	0.021	0.75	0.9232	0.08	0.0197	1.88	0.8165	-0.09	0.2323	0.94	0.5204	3.44	0.6394
APOE1998/rs769449	intron 2	4	0.1165	6.95	0.0551	-0.01	0.58	8.31	0.0285	0.01	0.6867	2.03	0.003	-4.38	0.2048
APOE2440/rs769450	intron 2	5	0.4015	4.89	0.0378	0.003	0.7725	6.88	0.0051	0.06	0.0082	0.15	0.7422	0.70	0.7656
APOE2907/rs769451	intron 2	5	0.0112	0.45	0.9668	0.05	0.339	-1.93	0.8649	-0.05	0.6157	-0.22	0.9196	3.70	0.7379
APOE3038/rs111833428	exon 3	5	0.0016	27.34	0.3354	0.10	0.4366	33.80	0.2567	0.16	0.5766	13.81	0.0342	3.29	0.9205
APOE3106/rs769452	exon 3	5	0.0008	18.03	0.6522	0.20	0.2787	21.30	0.611	-0.22	0.5865	9.15	0.1602	29.79	0.3649
APOE3937/rs429358	exon 4	5	0.1525	8.10	0.0103	-0.02	0.2233	6.82	0.0383	0.01	0.7069	2.14	0.0005	-3.66	0.2399
APOE4075/rs7412	exon 4	5	0.0806	-21.84	1.84E-07	-0.01	0.4524	-19.46	9.50E-06	0.01	0.7438	-5.60	9.70E-13	5.12	0.2081
APOE4310/rs199768005	exon 4	5	0.004	-32.56	0.0705	0.01	0.8927	-46.88	0.01279	-0.40	0.026	1.05	0.822	-35.74	0.1245
APOE4528	3' UTR	5	0.0008	-12.30	0.7585	0.24	0.1926	36.03	0.38978	0.92	0.0232	***	***	***	***
APOE4737/rs117656888	3'flanking	5	0.0081	13.58	0.2867	0.12	0.0487	23.15	0.08353	0.09	0.5084	1.60	0.5203	-5.55	0.6576
APOE5361/rs1081106	3'flanking	3a	0.0852	4.00	0.3272	0.03	0.0915	4.62	0.27914	-0.01	0.8928	0.12	0.8813	3.30	0.4318
rs439401	intergenic region	1b	0.3596	-1.76	0.4521	0.01	0.5449	-2.82	0.24856	-0.06	0.0194	0.39	0.3975	0.91	0.6915
rs445925	intergenic region	No Data	0.1094	-12.58	0.0005	-0.02	0.2723	-13.53	0.00032	0.01	0.8251	-3.78	5.20E-08	3.53	0.3231
APOC1p698/rs72654449	5'flanking	4	0.004	-14.29	0.4275	-0.02	0.7892	-23.70	0.20878	-0.17	0.3425	-2.77	0.55052	-4.70	0.8413
APOC1p703/rs3207187	5'flanking	4	0.0008	12.09	0.7629	***	***	52.40	0.21236	-0.07	0.8607	-0.88	0.89283	102.96	0.0016
APOC1p720/rs72654451	5'flanking	4	0.2299	-3.67	0.1768	-0.02	0.086	-4.42	0.12017	0.01	0.7351	-0.82	0.11683	-0.46	0.8612
APOC1p1170	intron1	2b	0.0008	-41.75	0.2956	0.40	0.0333	-29.40	0.48393	-0.61	0.1281	7.14	0.27763	18.30	0.5723
APOC1p1294	intron2	4	0.0008	-6.76	0.866	0.27	0.1533	13.45	0.74854	-0.10	0.8036	3.07	0.63865	27.03	0.4118
APOC1p1317/rs12721048	intron2	4	0.0016	13.48	0.6321	0.32	0.0162	34.50	0.24424	-0.01	0.9701	11.18	0.01598	66.89	0.0042
APOC1p1422	intron2	4	0.0016	-51.98	0.0657	0.18	0.183	-53.33	0.07215	-0.49	0.0838	1.88	0.77425	-26.52	0.4203
APOC1p1566/rs12691088	intron2	2b	0.0058	3.19	0.835	-0.07	0.3064	-2.77	0.86244	-0.08	0.6183	-4.95	0.12948	-27.45	0.0915

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APOC1p2041/rs3826688	intron2	5	0.3424	-2.38	0.3246	0.01	0.3985	-3.60	0.15405	-0.08	0.0011	0.30	0.51703	0.24	0.9176
APOC1p2629	exon3	4	0.0008	-47.60	0.2349	0.30	0.1117	-24.89	0.55247	-0.02	0.9634	-5.12	0.43402	2.54	0.9383
APOC1p2817	intron3	2b	0.0033	-5.57	0.7794	0.13	0.2246	8.17	0.69433	0.04	0.8334	-4.46	0.23676	21.20	0.27
APOC1p3423/rs389261	intron3	No Data	0.0025	-18.83	0.4163	-0.18	0.0994	-32.02	0.18592	-0.02	0.9169	-3.50	0.35153	-21.68	0.2583
APOC1p3494	intron3	No Data	0.0016	73.63	0.0092	0.26	0.0478	103.78	0.00044	0.40	0.1643	5.38	0.41256	-1.39	0.9662
APOC1p4334/rs12721046	intron3	6	0.1522	6.93	0.0306	-0.0001	0.9967	5.95	0.07734	0.02	0.4787	1.59	0.00983	-2.11	0.4956
APOC1p5641/rs1064725	3'UTR	No Data	0.0388	11.99	0.0415	0.03	0.3253	13.65	0.02631	-0.05	0.4064	2.00	0.09267	-4.32	0.4728
APOC1p5773	3'flanking	No Data	0.0008	-11.49	0.7742	0.24	0.1956	37.56	0.36991	0.93	0.0211	***	***	***	***
APOC1p5926/rs56131196	3'flanking	No Data	0.1885	7.24	0.0142	-0.01	0.6146	6.69	0.03046	0.01	0.7677	1.75	0.00229	-2.59	0.3695
APOC1p6026/rs4420638	3'flanking	No Data	0.1556	6.97	0.026	-0.01	0.57	6.79	0.04018	0.03	0.3924	1.43	0.01775	-1.10	0.716
rs4803770	HCR1	5	0.3779	5.52	0.0197	0.003	0.7653	6.08	0.01385	0.04	0.0801	0.56	0.21851	0.02	0.9937
HCR1p292/rs4803771	HCR1	4	0.0245	3.86	0.596	-0.02	0.5402	1.40	0.85412	0.02	0.8188	0.68	0.64404	-5.81	0.4273
HCR1p362	HCR1	2a	0.0025	-14.29	0.5362	0.001	0.9915	-3.80	0.87495	0.30	0.203	2.07	0.75319	-3.48	0.9159
HCR1p423	HCR1	4	0.0258	-6.26	0.3686	0.06	0.091	-7.84	0.28132	-0.12	0.08	2.10	0.14804	11.09	0.1293
HCR1p575/rs157599	HCR1	3a	0.0024	-19.28	0.4063	-0.18	0.0996	-32.24	0.18436	-0.02	0.926	-3.48	0.35815	-21.80	0.2531
HCR1p727/rs149345	HCR1	3a	0.0024	-19.80	0.3919	-0.18	0.1015	-33.23	0.16946	-0.03	0.9053	-3.47	0.35832	-21.70	0.2544
rs5112	APOC1P1	4	0.4633	-4.61	0.0515	-0.01	0.6533	-4.95	0.04462	-0.02	0.3217	-0.15	0.75492	-0.67	0.7769
rs7259004	APOC1P1	6	0.1176	-9.78	0.005	0.01	0.7115	-9.06	0.01342	0.05	0.2103	-1.33	0.05153	6.89	0.046
HCR2p188/rs35136575	HCR2	2a	0.2274	-3.15	0.2324	0.03	0.033	-2.25	0.41394	-0.03	0.283	-0.48	0.36635	5.16	0.0496
HCR2p365	HCR2	2b	0.0041	2.62	0.8844	-0.02	0.8182	-6.50	0.72951	-0.20	0.266	3.05	0.41812	10.58	0.581
HCR2p523	HCR2	2b	0.0226	3.50	0.6577	-0.03	0.3751	8.10	0.3266	0.02	0.7664	1.04	0.47773	3.82	0.6061
APOC4p636	5’ flanking	No Data	0.0008	54.33	0.1769	-0.36	0.0564	63.55	0.13031	0.73	0.0732	***	***	***	***
APOC4p968/rs76214972	5’ UTR	4	0.0362	-1.85	0.7658	-0.03	0.3434	-5.60	0.38784	0.02	0.8085	1.25	0.29092	2.03	0.733
APOC4p1150/rs148247675	Intron1	5	0.0017	73.90	0.009	0.26	0.0474	103.80	0.00043	0.39	0.1698	5.53	0.3975	-1.61	0.9608
APOC4p1229	Intron1	2b	0.0016	18.29	0.5205	-0.36	0.0073	16.99	0.57007	0.68	0.0186	***	***	***	***
APOC4p2557	Intron1	4	0.0008	-35.35	0.3781	-0.27	0.1454	-57.38	0.17273	0.12	0.7681	-5.26	0.42411	-14.77	0.6541
APOC4p2623/rs5157	Intron1	4	0.4976	-1.55	0.4962	-0.01	0.4816	-0.35	0.88515	0.02	0.3751	-0.30	0.49795	0.34	0.8797
APOC4p2640/rs5158	Intron1	2b	0.1381	-1.55	0.6408	0.02	0.1402	-1.79	0.60759	-0.04	0.2219	0.35	0.59389	-1.45	0.662
APOC4p2683/rs12721109	Intron1	2b	0.0237	-19.14	0.0092	0.03	0.3859	-12.75	0.09785	-0.16	0.0329	-4.99	0.00057	-9.31	0.1964
APOC4p2703/rs12721108	Intron1	2a	0.0081	1.93	0.8798	-0.04	0.5344	-9.51	0.47603	-0.15	0.2384	-1.23	0.59732	-9.00	0.4435
APOC2p194-C4p3498/rs1132899	C4-exon2	5	0.4863	-1.91	0.4071	-0.01	0.4295	-0.62	0.79728	0.02	0.3465	-0.12	0.79089	1.35	0.5467

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APOC2p242-C4p3546/rs12691089	C4-exon2	5	0.0032	2.18	0.9136	-0.01	0.9111	-5.18	0.80551	-0.16	0.4444	-1.80	0.69724	0.65	0.9778
APOC2p543-C4p3847/rs186448850	C4-intron2	5	0.0016	18.71	0.5103	-0.36	0.0074	17.51	0.55783	0.68	0.0171	***	***	***	***
APOC2p623-C4p3927/rs5167	C4-exon3	5	0.3596	4.19	0.0824	-0.001	0.9252	2.94	0.24431	-0.004	0.8759	0.11	0.81626	-1.01	0.6722
APOC2p1357-C4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	0.4968	0.74	0.745	0.01	0.5896	-0.65	0.78596	-0.02	0.3813	0.19	0.66177	0.03	0.988
APOC2p1591-C4p4895	C2-intron1	4	0.0008	54.17	0.1764	-0.36	0.0511	62.97	0.13292	0.73	0.0712	***	***	***	***
APOC2p1851/rs12709886	intron1	6	0.0372	-1.31	0.8311	-0.02	0.4118	-4.49	0.48475	0.03	0.5845	1.35	0.2357	5.83	0.3078
APOC2p2870	intron1	4	0.004	53.09	0.003	0.03	0.7577	58.43	0.00179	0.12	0.5116	6.33	0.05291	-36.20	0.0279
APOC2p3348/rs10420434	intron1	No Data	0.0371	-6.86	0.264	0.05	0.1052	-2.44	0.70432	-0.09	0.1736	-1.24	0.3101	6.94	0.2529
APOC2p3778/rs5120	intron1	4	0.4976	1.24	0.5845	0.01	0.5135	-1.32	0.57843	-0.02	0.2809	0.14	0.74796	0.29	0.8954
APOC2p4853/rs199828513	3'flamking	No Data	0.2783	4.36	0.0943	-0.01	0.3208	2.44	0.37077	0.01	0.6741	0.21	0.6757	-2.81	0.2692
APOC2p5004/rs10421404	3'flanking	No Data	0.1823	-2.35	0.418	0.02	0.2558	-3.09	0.30928	-0.03	0.3591	0.26	0.63942	1.64	0.5604
APOC2p5310/rs7258345	3'flanking	No Data	0.4649	1.99	0.3817	-0.002	0.8455	-0.13	0.95612	-0.01	0.8191	0.36	0.41406	-1.16	0.6041
APOC2p5398/rs12709889	3'flanking	6	0.276	3.95	0.1322	-0.01	0.274	1.98	0.47012	0.01	0.5974	0.06	0.91243	-3.11	0.233
APOC2p5644	3'flanking	6	0.0092	20.49	0.0948	0.01	0.8947	14.86	0.24546	-0.10	0.4103	1.74	0.42698	7.67	0.4929

Yellow-highlighted values represent significant p-values; (*) unavailable results because of missing phenotype data for subjects carry the rare allele, Nucleotide position is according to the reference sequence (Accession # AF261279.1); Ch. Position: chromosomal position is according to NCBI build 138; MAF: minor allele frequency; LDL-C: low-density lipoprotein cholesterol; HDL-C: high-density lipoprotein cholesterol; TC: total cholesterol; TG: triglyceride; ApoB: apolipoprotein B; ApoA1: apolipoprotein A1; [a] Cox-Box transformed variables; Age, Gender, Smoking, and BMI are significant covariates that were included in the final model.

Table 21. Genotype-specific means (± SD) of LDL-C and HDL-C for genotyped SNPs in NHWs

						LDL-C				HDL-C[a]			
Variant name	**Function**	**RegulomeDB score**	**MAF**	**Genotype**	**GT Count**	**AdjMean**	**GT_SD**	**Beta**	**p_value**	**AdjMean**	**GT_SD**	**Beta**	**p_value**
APOE560/rs449647	5'flanking	5	0.161	AA/AT/TT	433/176/12	139.19/132.29/124.15	38.8/45.3/36.3	-7.12	0.0247	50.95/49.6/50.65	14.4/13.4/11.0	-0.01	0.3526
APOE832/rs405509	5'flanking	1f	0.4775	GG/GT/TT	170/310/142	135.68/138.13/136.32	40.3/42.7/37.3	0.42	0.8542	50.07/50.56/51.17	13.9/14.0/14.2	0.01	0.4031
APOE1163/rs440446	intron1	4	0.3604	CC/GC/GG	76/297/250	130.59/137.86/137.91	37.8/40.7/41.7	-2.59	0.281	51.8/50.73/50.04	13.8/14.3/13.7	0.01	0.2865
APOE1575/rs769448	intron1	4	0.021	CC/CT/TT	595/24/1	136.96/137.36/142.42	41.3/29.6/NA	0.75	0.9232	50.27/55.4/70.05	13.8/17.1/NA	0.08	0.0197
APOE1998/rs769449	intron 2	4	0.1165	AA/AG/GG	6/132/480	160.24/141.21/135.47	19.9/41.4/40.7	6.95	0.0551	48.13/50.11/50.79	9.6/14.0/14.1	-0.01	0.58
APOE2440/rs769450	intron 2	5	0.4015	AA/GA/GG	95/307/217	144.97/136.5/133.97	40.1/40.9/40.9	4.89	0.0378	50.42/50.88/50.12	15.4/13.5/14.2	0.003	0.7725
APOE2907/rs769451	intron 2	5	0.0112	GT/TT	14/609	137.43/136.98	36.6/40.9	0.45	0.9668	52.84/50.53	11.4/14.1	0.05	0.339
APOE3038/rs111833428	exon 3	5	0.0016	AG/GG	2/616	164.05/136.78	57.3/40.9	27.34	0.3354	55.59/50.51	4.2/14.1	0.10	0.4366
APOE3106/rs769452	exon 3	5	0.0008	TC/TT	1/620	154.92/136.93	NA/40.9	18.03	0.6522	61.96/50.57	NA/14.1	0.20	0.2787
APOE3937/rs429358	exon 4	5	0.1525	CC/CT/TT	14/159/440	153.24/142.39/134.84	23.3/39.4/41.2	8.10	0.0103	47.93/49.89/51.01	12.7/14.1/14.1	-0.02	0.2233
APOE4075/rs7412	exon 4	5	0.0806	CC/TC/TT	523/94/3	140.26/120.22/73.75	39.2/44.6/37.0	-21.84	1.84E-07	50.76/49.16/54.02	14.3/12.6/16.1	-0.01	0.4524
APOE4310/rs199768005	exon 4	5	0.004	TA/TT	5/617	105/137.26	35.7/40.8	-32.56	0.0705	50.32/50.54	10.5/14.0	0.01	0.8927
APOE4528	3' UTR	5	0.0008	CC/CT	622/1	137.01/124.75	40.8/NA	-12.30	0.7585	50.56/64.69	14.0/NA	0.24	0.1926
APOE4737/rs117656888	3'flanking	5	0.0081	CC/GC	610/10	136.68/150.24	40.7/52.3	13.58	0.2867	50.4/58.73	13.9/20.1	0.12	0.0487
APOE5361/rs1081106	3'flanking	3a	0.0852	CC/TC/TT	4/98/520	163.88/138.72/136.47	28.8/37.4/41.5	4.00	0.3272	54.27/52.26/50.19	17.2/14.3/13.9	0.03	0.0915
rs439401	intergenic region	1b	0.3596	CC/CT/TT	255/270/84	136.61/139.86/129.57	39.4/42.1/39.8	-1.76	0.4521	50.14/50.35/51.41	13.6/14.6/13.6	0.01	0.5449
APOC1rs445925	intergenic region	No Data	0.1094	AA/GA/GG	7/121/489	100.87/129/139.75	55.8/41.5/39.6	-12.58	0.0005	46.15/49.94/50.91	15.2/13.2/14.2	-0.02	0.2723
APOC1p698/rs72654449	5'flanking	4	0.004	CA/CC	5/613	122.75/136.92	21.6/40.9	-14.29	0.4275	48.45/50.65	12.8/14.1	-0.02	0.7892
APOC1p703/rs3207187	5'flanking	4	0.0008	CC/CT	619/1	136.94/148.98	40.9/NA	12.09	0.7629	***	***	***	***
APOC1p720/rs72654451	5'flanking	4	0.2299	II/WI/WW	31/224/367	140.13/132.63/139.44	45.0/41.0/40.3	-3.67	0.1768	47.92/49.79/51.31	12.8/13.4/14.5	-0.02	0.086
APOC1p1170	intron1	2b	0.0008	GA/GG	1/609	94.93/136.57	NA/40.7	-41.75	0.2956	77.93/50.64	NA/14.1	0.40	0.0333
APOC1p1294	intron2	4	0.0008	AA/AC	618/1	136.83/130.1	40.8/NA	-6.76	0.866	50.57/71.84	14.0/NA	0.27	0.1533
APOC1p1317/rs12721048	intron2	4	0.0016	GA/GG	2/607	150.98/137.55	38.8/40.6	13.48	0.6321	74.31/50.58	11.3/14.0	0.32	0.0162
APOC1p1422	intron2	4	0.0016	GA/GG	2/621	85.21/137.16	14.7/40.8	-51.98	0.0657	61.07/50.55	7.1/14.0	0.18	0.183
APOC1p1566/rs12691088	intron2	2b	0.0058	GA/GG	7/598	139.78/136.62	31.2/41.0	3.19	0.835	48.07/50.63	21.0/14.0	-0.07	0.3064
APOC1p2041/rs3826688	intron2	5	0.3424	AA/GA/GG	73/269/264	127.94/139.99/137.23	39.9/42.4/39.8	-2.38	0.3246	52.15/50.6/50.26	14.5/14.4/13.7	0.01	0.3985
APOC1p2629	exon3	4	0.0008	GA/GG	1/618	89.64/137.14	NA/40.8	-47.60	0.2349	74.09/50.6	NA/14.0	0.30	0.1117
APOC1p2817	intron3	2b	0.0033	CC/CT	603/4	136.39/130.83	40.5/22.8	-5.57	0.7794	50.49/57.95	14.0/13.0	0.13	0.2246
APOC1p3423/rs389261	intron3	No Data	0.0025	GA/GG	3/605	118.03/136.72	3.2/40.8	-18.83	0.4163	41.42/50.59	5/14.0	-0.18	0.0994

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APOC1p3494	intron3	No Data	0.0016	CC/CT	619/2	136.81/210.37	40.5/98.3	73.63	0.0092	50.54/72.29	13.9/38.2	0.26	0.0478
APOC1p4334/rs12721046	intron3	6	0.1522	AA/GA/GG	13/160/438	156.43/140.12/134.82	30.1/41.8/40.3	6.93	0.0306	45.6/51.2/50.56	8.1/14.5/14.1	-0.0001	0.9967
APOC1p5641/rs1064725	3'UTR	No Data	0.0388	GG/GT/TT	1/46/571	182.23/147.16/136.24	NA/49.0/40.1	11.99	0.0415	53.95/51.58/50.49	NA/12.4/14.2	0.03	0.3253
APOC1p5773	3'flanking	No Data	0.0008	GA/GG	1/604	125.4/136.86	NA/40.9	-11.49	0.7742	64.58/50.52	NA/14.1	0.24	0.1956
APOC1p5926/rs56131196	3'flanking	No Data	0.1885	AA/GA/GG	19/195/404	154.08/140.17/134.32	29.1/42.7/40.0	7.24	0.0142	47.37/50.67/50.75	11.2/14.1/14.2	-0.01	0.6146
APOC1p6026/rs4420638	3'flanking	No Data	0.1556	AA/GA/GG	405/129/22	134.61/137.65/157.81	40.1/42.6/35.1	6.97	0.026	50.73/51.06/47.64	14.1/15.4/11.2	-0.01	0.57
rs4803770	HCR1	5	0.3779	CC/GC/GG	229/281/84	132.08/139.47/141.86	43.1/39.1/35.6	5.52	0.0197	49.8/51.14/49.72	13.5/13.7/14.6	0.003	0.7653
HCR1p292/rs4803771	HCR1	4	0.0245	CC/CG/GG	583/28/1	136.96/140.3/151.37	41.2/38.5/NA	3.86	0.596	50.51/50.04/33.57	14.1/13.4/NA	-0.02	0.5402
HCR1p362	HCR1	2a	0.0025	CA/CC	3/605	122.75/136.98	35.9/40.9	-14.29	0.5362	54.67/50.49	32.5/14.0	0.001	0.9915
HCR1p423	HCR1	4	0.0258	CC/CG/GG	589/30/1	137.58/131.7/119.83	40.9/32.7/NA	-6.26	0.3686	50.48/53.78/54.15	14.0/13.5/NA	0.06	0.091
HCR1p575/rs157599	HCR1	3a	0.0024	AA/AG	618/3	137.14/118.01	40.9/3.2	-19.28	0.4063	50.65/41.6	14.0/5.0	-0.18	0.0996
HCR1p727/rs149345	HCR1	3a	0.0024	TG/TT	3/611	117.41/137.05	3.2/40.8	-19.80	0.3919	41.69/50.72	5.0/14.1	-0.18	0.1015
rs5112	APOC1P1	4	0.4633	CC/GC/GG	123/284/165	128.41/138.56/138.35	39.4/42.5/38.1	-4.61	0.0515	50.33/50.31/50.79	14.1/14.2/14.3	-0.01	0.6533
rs7259004	APOC1P1	6	0.1176	CC/CG/GG	476/128/8	139.62/127.55/136.46	41.0/34.0/48.6	-9.78	0.005	50.51/50.11/56.11	14.2/13.9/12.8	0.01	0.7115
HCR2p188/rs35136575	HCR2	2a	0.2274	CC/GC/GG	369/203/37	138.79/134.82/134.1	41.5/39.4/37.3	-3.15	0.2324	49.76/51.64/51.86	14.2/13.9/12.8	0.03	0.033
HCR2p365	HCR2	2b	0.0041	CA/CC	5/606	139.15/136.56	47.3/40.7	2.62	0.8844	49.01/50.56	12.6/14.0	-0.02	0.8182
HCR2p523	HCR2	2b	0.0226	CC/CT	571/27	136.48/139.97	40.6/47.5	3.50	0.6577	50.56/47.97	14.2/11.1	-0.03	0.3751
APOC4p636	5’ flanking	No Data	0.0008	CC/CT	601/1	137.18/191.27	40.9/NA	54.33	0.1769	50.49/31.26	14.1/NA	-0.36	0.0564
APOC4p968/rs76214972	5’ UTR	4	0.0362	AA/AG	576/45	137.18/135.34	40.8/42.0	-1.85	0.7658	50.73/49.07	14.1/13.8	-0.03	0.3434
APOC4p1150/rs148247675	Intron1	5	0.0017	AA/GA	601/2	136.38/210.21	40.5/98.3	73.90	0.009	50.43/72.29	13.8/38.2	0.26	0.0474
APOC4p1229	Intron1	2b	0.0016	GC/GG	2/619	155.09/136.99	49.6/40.8	18.29	0.5205	34.08/50.66	5.7/14.0	-0.36	0.0073
APOC4p2557	Intron1	4	0.0008	CA/CC	1/619	101.86/137	NA/40.8	-35.35	0.3781	34.71/50.63	NA/14.1	-0.27	0.1454
APOC4p2623/rs5157	Intron1	4	0.4976	CC/CT/TT	155/315/152	138/137.55/134.89	40.3/40.2/42.9	-1.55	0.4962	51.28/50.4/50.19	14.4/14.1/13.5	-0.01	0.4816
APOC4p2640/rs5158	Intron1	2b	0.1381	CC/CT/TT	459/149/11	137.39/135.98/133.59	40.1/43.6/35.3	-1.55	0.6408	50.38/50.84/59.86	13.9/14.4/15.2	0.02	0.1402
APOC4p2683/rs12721109	Intron1	2b	0.0237	AA/AG/GG	1/27/584	120.81/117.3/137.95	NA/48.3/40.4	-19.14	0.0092	68.58/51.11/50.6	NA/12.2/14.1	0.03	0.3859
APOC4p2703/rs12721108	Intron1	2a	0.0081	GG/GT	609/10	136.91/138.84	41.0/27.6	1.93	0.8798	50.69/47.23	14.1/8.4	-0.04	0.5344
APOC2p194-C4p3498/rs1132899	C4-exon2	5	0.4863	CC/CT/TT	160/317/143	139.55/136.4/135.81	40.7/39.8/43.2	-1.91	0.4071	51.44/50.19/50.27	14.5/14.1/13.5	-0.01	0.4295
APOC2p242-C4p3546/rs12691089	C4-exon2	5	0.0032	AG/GG	4/617	139.21/137.04	25.8/40.9	2.18	0.9136	50.34/50.61	13.8/14.1	-0.01	0.9111
APOC2p543-C4p3847/rs186448850	C4-intron2	5	0.0016	CT/TT	2/609	155.44/136.92	49.6/40.9	18.71	0.5103	33.96/50.54	5.7/14.0	-0.36	0.0074
APOC2p623-C4p3927/rs5167	C4-exon3	5	0.3596	GG/TG/TT	74/300/249	141.08/138.79/133.61	36.0/40.9/42.0	4.19	0.0824	51.38/50.12/50.9	14.9/13.7/14.3	-0.001	0.9252
APOC2p1357-C4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	0.4968	CC/CG/GG	155/316/151	136.3/136.98/137.79	42.8/40.0/40.7	0.74	0.745	50.37/50.37/51.28	13.3/14.3/14.3	0.01	0.5896
APOC2p1591-C4p4895	C2-intron1	4	0.0008	GA/GG	1/620	190.9/136.96	NA/40.8	54.17	0.1764	31.06/50.64	NA/14.0	-0.36	0.0511

Cont. Table 21

APOC2p1851/rs12709886	intron1	6	0.0372	GA/GG	46/572	135.89/137.2	42.0/40.7	-1.31	0.8311	49.18/50.69	13.4/14.1	-0.02	0.4118
APOC2p2870	intron1	4	0.004	GG/GT	616/5	136.62/189.62	40.4/62.6	53.09	0.003	50.58/53.91	14.0/25.2	0.03	0.7577
APOC2p3348/rs10420434	intron1	No Data	0.0371	GA/GG	46/574	130.8/137.63	41.0/40.8	-6.86	0.264	53.83/50.33	16.3/13.8	0.05	0.1052
APOC2p3778/rs5120	intron1	4	0.4976	AA/AT/TT	154/305/157	137.73/137.42/135.27	40.2/39.6/43.9	1.24	0.5845	51.27/50.52/50.26	14.4/14.3/13.5	0.01	0.5135
APOC2p4853/rs199828513	3'flamking	No Data	0.2783	DD/WD/WW	316/260/42	134.46/139.37/142.11	41.1/41.3/36.1	4.36	0.0943	51.01/49.98/50.19	14.1/13.7/15.7	-0.01	0.3208
APOC2p5004/rs10421404	3'flanking	No Data	0.1823	CC/CT/TT	416/177/24	138.15/133.69/139.56	40.6/42.0/34.1	-2.35	0.418	50.38/50.53/54.51	14.1/14.1/13.7	0.02	0.2558
APOC2p5310/rs7258345	3'flanking	No Data	0.4649	GG/TG/TT	133/303/176	138.69/138.01/134.9	41.0/38.7/43.4	1.99	0.3817	50.87/50.35/51.03	14.3/13.9/14.2	-0.002	0.8455
APOC2p5398/rs12709889	3'flanking	6	0.276	AA/GA/GG	41/252/312	141.78/138.36/134.24	36.6/40.9/41.1	3.95	0.1322	50.64/49.73/51.18	15.9/13.4/14.3	-0.01	0.274
APOC2p5644	3'flanking	6	0.0092	AG/GG	11/585	156.45/136.18	41.7/40.8	20.49	0.0948	50.04/50.43	10.7./14.2	0.01	0.8947

[a] Cox-Box transformed variables.
MAF: minor allele frequency.
LDL-C: low-density lipoprotein cholesterol; HDL-C: high-density lipoprotein cholesterol.
Age, Gender, Smoking, and BMI are significant covariates that were included in the final model.
AdjMean: adjusted means; GT-SD: standard deviation in genotype group.

Table 22. Genotype-specific means (± SD) of TC and TG for genotyped SNPs in NHWs

						TC				TG[a]			
Variant name	**Function**	**RegulomeDB score**	**MAF**	**Genotype**	**GT Count**	**AdjMean**	**GT_SD**	**Beta**	**p_value**	**AdjMean**	**GT_SD**	**Beta**	**p_value**
APOE560/rs449647	5'flanking	5	0.161	AA/AT/TT	433/176/12	218.99/212.89/202.5	42.5/45.1/46.4	-6.71	0.0428	139.61/134.35/133.8	68.2/59.3/67.0	-0.02	0.5229
APOE832/rs405509	5'flanking	1f	0.4775	GG/GT/TT	170/310/142	216.51/218.33/214.93	42.7/46.0/39.1	-0.68	0.7757	148.79/135.95/129.7	71.4/63.4/62.4	-0.07	0.0033
APOE1163/rs440446	intron1	4	0.3604	CC/GC/GG	76/297/250	209.86/216.67/219.53	38.1/43.8/44.7	-4.26	0.0893	123.14/135.63/145.12	56.1/65.4/67.8	-0.08	0.0018
APOE1575/rs769448	intron1	4	0.021	CC/CT/TT	595/24/1	216.84/218.67/220.93	43.8/37.5/NA	1.88	0.8165	138.4/130.89/34.9	66.3/48.8/NA	-0.09	0.2323
APOE1998/rs769449	intron 2	4	0.1165	AA/AG/GG	6/132/480	242.18/222.31/215.21	25.3/44.7/43.2	8.31	0.0285	179.59/135.92/138	80.3/63.7/66.0	0.01	0.6867
APOE2440/rs769450	intron 2	5	0.4015	AA/GA/GG	95/307/217	226.44/217.25/211.92	42.8/44.6/41.8	6.88	0.0051	148.93/137.7/132.05	67.2/64.5/65.2	0.06	0.0082
APOE2907/rs769451	intron 2	5	0.0112	GT/TT	14/609	215.12/217.03	41.9/43.6	-1.93	0.8649	124.87/138.24	48.8/66.1	-0.05	0.6157
APOE3038/rs111833428	exon 3	5	0.0016	AG/GG	2/616	250.2/216.77	63.6/43.6	33.80	0.2567	146.64/138.14	10.6/66.0	0.16	0.5766
APOE3106/rs769452	exon 3	5	0.0008	TC/TT	1/620	238.11/216.93	NA/43.6	21.30	0.611	101.15/137.96	NA/65.7	-0.22	0.5865
APOE3937/rs429358	exon 4	5	0.1525	CC/CT/TT	14/159/440	229.3/221.27/214.71	26.6/42.9/43.3	6.82	0.0383	142.88/138.64/137.37	74.6/64.4/65.4	0.01	0.7069
APOE4075/rs7412	exon 4	5	0.0806	CC/TC/TT	523/94/3	219.92/201.81/164.37	42.4/46.8/29.1	-19.46	9.50E-06	137.8/138.76/179.42	65.0/70.1/93.6	0.01	0.7438
APOE4310/rs199768005	exon 4	5	0.004	TA/TT	5/617	171.03/217.35	42.6/43.5	-46.88	0.01279	78.12/138.52	20.5/65.9	-0.40	0.026
APOE4528	3' UTR	5	0.0008	CC/CT	622/1	216.93/252.76	43.6/NA	36.03	0.38978	137.65/311.89	65.5/NA	0.92	0.0232
APOE4737/rs117656888	3'flanking	5	0.0081	CC/GC	610/10	216.53/239.47	42.8/79.1	23.15	0.08353	137.88/153.84	65.6/79.0	0.09	0.5084
APOE5361/rs1081106	3'flanking	3a	0.0852	CC/TC/TT	4/98/520	255.84/218.31/216.42	31.7/42.3/43.8	4.62	0.27914	186.18/134.11/138.33	76.3/65.6/65.7	-0.01	0.8928
rs439401	intergenic region	1b	0.3596	CC/CT/TT	255/270/84	217.84/218.43/209.8	43.5/45.4/37.5	-2.82	0.24856	143.91/135.33/129.53	66.6/65.0/63.0	-0.06	0.0194
APOC1rs445925	intergenic region	No Data	0.1094	AA/GA/GG	7/121/489	178.72/207.77/219.45	53.0/42.1/42.6	-13.53	0.00032	150.57/139.2/137.03	62.1/73.1/63.7	0.01	0.8251
APOC1p698/rs72654449	5'flanking	4	0.004	CA/CC	5/613	193.51/217	24.7/43.7	-23.70	0.20878	109.41/137.85	29.6/65.9	-0.17	0.3425
APOC1p703/rs3207187	5'flanking	4	0.0008	CC/CT	619/1	216.89/268.82	43.5/NA	52.40	0.21236	138.15/118.38	65.9/NA	-0.07	0.8607
APOC1p720/rs72654451	5'flanking	4	0.2299	II/WI/WW	31/224/367	216.21/213.01/219.56	44.3/44.1/43.1	-4.42	0.12017	142.81/138.71/137.05	61.0/70.8/63.1	0.01	0.7351
APOC1p1170	intron1	2b	0.0008	GA/GG	1/609	187.55/216.79	NA/43.5	-29.40	0.48393	70.3/138.55	NA/66.1	-0.61	0.1281
APOC1p1294	intron2	4	0.0008	AA/AC	618/1	216.82/230.18	43.5/NA	13.45	0.74854	137.94/119.94	65.9/NA	-0.10	0.8036
APOC1p1317/rs12721048	intron2	4	0.0016	GA/GG	2/607	251.51/217.24	11.3/43.3	34.50	0.24424	138.26/137.77	81.3/65.1	-0.01	0.9701
APOC1p1422	intron2	4	0.0016	GA/GG	2/621	164.28/217.16	31.1/43.5	-53.33	0.07215	85.16/138.1	46.7/65.7	-0.49	0.0838
APOC1p1566/rs12691088	intron2	2b	0.0058	GA/GG	7/598	214.02/216.77	36.5/43.7	-2.77	0.86244	130.06/138.08	78.5/65.9	-0.08	0.6183
APOC1p2041/rs3826688	intron2	5	0.3424	AA/GA/GG	73/269/264	208.35/218.41/218.56	37.2/45.6/43.6	-3.60	0.15405	122.52/133.62/144.45	59.9/63.3/66.8	-0.08	0.0011
APOC1p2629	exon3	4	0.0008	GA/GG	1/618	192.39/217.2	NA/43.6	-24.89	0.55247	124.61/138.12	NA/65.7	-0.02	0.9634
APOC1p2817	intron3	2b	0.0033	CC/CT	603/4	216.34/224.48	43.1/28.0	8.17	0.69433	138.22/132.67	66.3/26.9	0.04	0.8334
APOC1p3423/rs389261	intron3	No Data	0.0025	GA/GG	3/605	185.1/216.81	21.2/43.4	-32.02	0.18592	132.55/138.06	72.0/66.0	-0.02	0.9169

Cont. Table 22

APOC1p3494	intron3	No Data	0.0016	CC/CT	619/2	216.76/320.11	42.8/153.4	103.78	0.00044	137.8/197.85	65.7/84.9	0.40	0.1643
APOC1p4334/rs12721046	intron3	6	0.1522	AA/GA/GG	13/160/438	233.5/219.8/215.22	33.9/44.1/43.4	5.95	0.07734	161.1/137.57/137.8	71.8/63.8/66.4	0.02	0.4787
APOC1p5641/rs1064725	3'UTR	No Data	0.0388	GG/GT/TT	1/46/571	259.34/228.98/216.15	NA/45.2/43.4	13.65	0.02631	108.18/134.02/138.5	NA/68.9/65.6	-0.05	0.4064
APOC1p5773	3'flanking	No Data	0.0008	GA/GG	1/604	254.09/216.74	NA/43.8	37.56	0.36991	313.01/137.37	NA/65.4	0.93	0.0211
APOC1p5926/rs56131196	3'flanking	No Data	0.1885	AA/GA/GG	19/195/404	229.72/220.53/214.39	31.3/44.8/43.1	6.69	0.03046	144.93/137.9/137.39	69.4/66.6/65.4	0.01	0.7677
APOC1p6026/rs4420638	3'flanking	No Data	0.1556	AA/GA/GG	405/129/22	214.64/218.18/235.77	43.2/44.6/38.8	6.79	0.04018	137.4/139.11/153.86	65.2/63.6/77.5	0.03	0.3924
rs4803770	HCR1	5	0.3779	CC/GC/GG	229/281/84	210.83/219.75/221.05	41.2/43.7/43.5	6.08	0.01385	134.33/140.66/144.51	66.7/67.0/63.2	0.04	0.0801
HCR1p292/rs4803771	HCR1	4	0.0245	CC/CG/GG	583/28/1	217.05/216.36/248.27	44.1/37.6/NA	1.40	0.85412	138.16/130.59/300.06	65.5/62.2/NA	0.02	0.8188
HCR1p362	HCR1	2a	0.0025	CA/CC	3/605	213.1/216.88	19.7/43.7	-3.80	0.87495	186.45/137.65	81.3/65.5	0.30	0.203
HCR1p423	HCR1	4	0.0258	CC/CG/GG	589/30/1	217.22/209.32/203.05	43.1/40.8/NA	-7.84	0.28132	139.12/115.81/142.97	66.3/51.5/NA	-0.12	0.08
HCR1p575/rs157599	HCR1	3a	0.0024	AA/AG	618/3	217.25/185.31	43.6/21.2	-32.24	0.18436	138.02/132.76	65.8/72.0	-0.02	0.926
HCR1p727/rs149345	HCR1	3a	0.0024	TG/TT	3/611	184.31/217.22	21.2/43.4	-33.23	0.16946	131.91/137.89	72.0/65.9	-0.03	0.9053
rs5112	APOC1P1	4	0.4633	CC/GC/GG	123/284/165	208.18/218.08/218.71	38.1/44.7/44.1	-4.95	0.04462	134.65/136.13/139.61	68.2/64.2/64.0	-0.02	0.3217
rs7259004	APOC1P1	6	0.1176	CC/CG/GG	476/128/8	218.82/207.45/218.26	43.5/36.3/54.2	-9.06	0.01342	135.49/147.31/121.5	63.6/74.3/42.6	0.05	0.2103
HCR2p188/rs35136575	HCR2	2a	0.2274	CC/GC/GG	369/203/37	217.48/215.6/212.29	45.0/39.3/44.9	-2.25	0.41394	138.5/136.9/132.18	63.1/69.0/61.4	-0.03	0.283
HCR2p365	HCR2	2b	0.0041	CA/CC	5/606	210.22/216.65	51.3/43.3	-6.50	0.72951	110.77/138.24	42.7/66.1	-0.20	0.266
HCR2p523	HCR2	2b	0.0226	CC/CT	571/27	216.31/224.33	43.4/44.7	8.10	0.3266	138.42/139.96	66.2/60.6	0.02	0.7664
APOC4p636	5′ flanking	No Data	0.0008	CC/CT	601/1	217.16/280.36	43.5/NA	63.55	0.13031	137.96/275.05	65.6/NA	0.73	0.0732
APOC4p968/rs76214972	5′ UTR	4	0.0362	AA/AG	576/45	217.5/211.93	43.7/42.1	-5.60	0.38784	138/137.87	66.3/59.4	0.02	0.8085
APOC4p1150/rs148247675	Intron1	5	0.0017	AA/GA	601/2	216.26/319.6	42.6/153.4	103.80	0.00043	137.73/196.79	65.5/84.9	0.39	0.1698
APOC4p1229	Intron1	2b	0.0016	GC/GG	2/619	233.67/217.04	60.1/43.5	16.99	0.57007	245.77/137.64	24.0/65.6	0.68	0.0186
APOC4p2557	Intron1	4	0.0008	CA/CC	1/619	160.39/217.07	NA/43.5	-57.38	0.17273	135.71/137.99	NA/65.9	0.12	0.7681
APOC4p2623/rs5157	Intron1	4	0.4976	CC/CT/TT	155/315/152	216.43/217.92/215.73	42.9/43.6/44.4	-0.35	0.88515	135.81/136.86/142.57	65.7/62.7/71.8	0.02	0.3751
APOC4p2640/rs5158	Intron1	2b	0.1381	CC/CT/TT	459/149/11	217.61/215.36/216.86	42.0/49.0/33.7	-1.79	0.60759	139.65/133.48/121.82	67.4/61.5/58.6	-0.04	0.2219
APOC4p2683/rs12721109	Intron1	2b	0.0237	AA/AG/GG	1/27/584	204.3/204.19/217.79	NA/60.0/42.7	-12.75	0.09785	69.01/121.05/139.06	NA/67.2/65.9	-0.16	0.0329
APOC4p2703/rs12721108	Intron1	2a	0.0081	GG/GT	609/10	217.09/207.6	43.8/33.1	-9.51	0.47603	137.98/111.71	65.7/43.4	-0.15	0.2384
APOC2p194-C4p3498/rs1132899	C4-exon2	5	0.4863	CC/CT/TT	160/317/143	218.31/216.28/217.16	43.3/43.4/44.3	-0.62	0.79728	136.29/135.87/143.8	65.2/61.7/72.3	0.02	0.3465
APOC2p242-C4p3546/rs12691089	C4-exon2	5	0.0032	AG/GG	4/617	211.98/217.12	26.7/43.6	-5.18	0.80551	115.55/138.14	63.9/65.8	-0.16	0.4444
APOC2p543-C4p3847/rs186448850	C4-intron2	5	0.0016	CT/TT	2/609	234/216.86	60.1/43.7	17.51	0.55783	246.13/137.59	24.0/65.3	0.68	0.0171
APOC2p623-C4p3927/rs5167	C4-exon3	5	0.3596	GG/TG/TT	74/300/249	220.48/217.95/214.8	40.4/42.5/45.8	2.94	0.24431	139.36/136.28/139.49	68.8/61.7/69.4	-0.004	0.8759

Cont. Table 22

APOC2p1357-C4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	0.4968	CC/CG/GG	155/316/151	217.56/217.08/216.26	44.4/43.7/42.6	-0.65	0.78596	143.66/135.77/136.19	73.4/61.6/66.0	-0.02	0.3813
APOC2p1591-C4p4895	C2-intron1	4	0.0008	GA/GG	1/620	279.62/216.99	NA/43.5	62.97	0.13292	275.28/137.77	NA/65.6	0.73	0.0712
APOC2p1851/rs12709886	intron1	6	0.0372	GA/GG	46/572	213.01/217.48	42.4/43.7	-4.49	0.48475	140.23/137.95	59.2/66.5	0.03	0.5845
APOC2p2870	intron1	4	0.004	GG/GT	616/5	216.62/274.94	42.7/96.4	58.43	0.00179	137.83/157.24	65.7/79.6	0.12	0.5116
APOC2p3348/rs10420434	intron1	No Data	0.0371	GA/GG	46/574	214.96/217.38	37.0/44.1	-2.44	0.70432	130.78/138.84	74.3/65.0	-0.09	0.1736
APOC2p3778/rs5120	intron1	4	0.4976	AA/AT/TT	154/305/157	215.87/216.86/218.48	42.5/42.7/46.2	-1.32	0.57843	134.51/136.63/143.81	63.7/62.5/73.2	-0.02	0.2809
APOC2p4853/rs199828513	3'flamking	No Data	0.2783	DD/WD/WW	316/260/42	215.57/218.43/219.64	44.6/43.0/40.1	2.44	0.37077	138.01/138.21/139.6	68.6/62.4/67.6	0.01	0.6741
APOC2p5004/rs10421404	3'flanking	No Data	0.1823	CC/CT/TT	416/177/24	218.5/212.98/219.46	41.9/47.7/37.0	-3.09	0.30928	139.84/134.54/131.31	68.0/61.5/63.5	-0.03	0.3591
APOC2p5310/rs7258345	3'flanking	No Data	0.4649	GG/TG/TT	133/303/176	217.14/216.27/217.27	43.5/42.7/43.7	-0.13	0.95612	137.94/134.99/141.53	64.4/61.1/72.8	-0.01	0.8191
APOC2p5398/rs12709889	3'flanking	6	0.276	AA/GA/GG	41/252/312	219.86/217.27/215.5	40.6/42.5/44.4	1.98	0.47012	139.76/138.57/137.76	67.7/62.7/68.7	0.01	0.5974
APOC2p5644	3'flanking	6	0.0092	AG/GG	11/585	230.97/216.28	42.0/43.5	14.86	0.24546	123.92/138.57	53.6/66.2	-0.10	0.4103

[a] Cox-Box transformed variables.
MAF: minor allele frequency.
TC: total cholesterol; TG: triglyceride.
Age, Gender, Smoking, and BMI are significant covariates that were included in the final model.
AdjMean: adjusted means; GT-SD: standard deviation in genotype group.

Table 23. Genotype-specific means (± SD) of ApoB and ApoA1 for genotyped SNPs in NHWs

						ApoB[a]				ApoA1			
Variant name	**Function**	**RegulomeDB score**	**MAF**	**Genotype**	**GT Count**	**AdjMean**	**GT_SD**	**Beta**	**p_value**	**AdjMean**	**GT_SD**	**Beta**	**p_value**
APOE560/rs449647	5'flanking	5	0.161	AA/AT/TT	433/176/12	88.92/84.42/90.53	23.4/24.7/13.2	-0.95	0.129	150.06/149.21/141.94	34.5/29.0/24.3	-1.57	0.6175
APOE832/rs405509	5'flanking	1f	0.4775	GG/GT/TT	170/310/142	81.67/89.51/91.58	26.1/22.6/22.9	1.46	0.0009	151.84/149.07/148.29	34.4/32.5/34.0	-1.80	0.4173
APOE1163/rs440446	intron1	4	0.3604	CC/GC/GG	76/297/250	88.2/89.54/85.95	23.0/23.5/24.8	0.56	0.2319	153.72/147.42/151.01	30.9/32.7/34.6	-0.19	0.9349
APOE1575/rs769448	intron1	4	0.021	CC/CT/TT	595/24/1	87.88/90.73/93.77	24.3/17.4/NA	0.94	0.5204	149.53/144.71/224.9	33.2/37.3/NA	3.44	0.6394
APOE1998/rs769449	intron 2	4	0.1165	AA/AG/GG	6/132/480	93.32/93.83/85.99	23.2/22.4/24.1	2.03	0.003	159.38/145.16/151.06	32.5/35.0/32.9	-4.38	0.2048
APOE2440/rs769450	intron 2	5	0.4015	AA/GA/GG	95/307/217	89.59/87.42/87.95	24.1/23.9/24.1	0.15	0.7422	152.48/148.5/149.87	36.4/31.6/34.5	0.70	0.7656
APOE2907/rs769451	intron 2	5	0.0112	GT/TT	14/609	87.57/87.92	32.9/23.8	-0.22	0.9196	153.23/149.54	21.6/33.6	3.70	0.7379
APOE3038/rs111833428	exon 3	5	0.0016	AG/GG	2/616	140.55/87.71	NA/23.8	13.81	0.0342	152.88/149.59	NA/33.4	3.29	0.9205
APOE3106/rs769452	exon 3	5	0.0008	TC/TT	1/620	121.87/87.93	NA/23.9	9.15	0.1602	179.31/149.54	NA/33.4	29.79	0.3649
APOE3937/rs429358	exon 4	5	0.1525	CC/CT/TT	14/159/440	90.86/94.72/85.3	17.2/22.9/24.1	2.14	0.0005	138.97/147.69/150.56	34.4/36.3/32.3	-3.66	0.2399
APOE4075/rs7412	exon 4	5	0.0806	CC/TC/TT	523/94/3	90.92/73.55/32.32	23.0/21.1/17.1	-5.60	9.70E-13	148.66/154.66/149.98	33.4/33.6/14.5	5.12	0.2081
APOE4310/rs199768005	exon 4	5	0.004	TA/TT	5/617	92.47/87.91	45.3/23.9	1.05	0.822	114.13/149.7	11.9/33.3	-35.74	0.1245
APOE4528	3' UTR	5	0.0008	CC/CT	622/1	***	***	***	***	***	***	***	***
APOE4737/rs117656888	3'flanking	5	0.0081	CC/GC	610/10	87.82/93.42	24.0/22.9	1.60	0.5203	149.66/144.12	33.3/44.1	-5.55	0.6576
APOE5361/rs1081106	3'flanking	3a	0.0852	CC/TC/TT	4/98/520	107.81/86.35/88.01	28.0/23.3/24.0	0.12	0.8813	152.9/152.7/149.1	10.8/35.9/33.1	3.30	0.4318
rs439401	intergenic region	1b	0.3596	CC/CT/TT	255/270/84	85.66/91.09/85.24	24.8/23.5/22.6	0.39	0.3975	149.41/147.97/152.86	32.7/35.3/28.7	0.91	0.6915
APOC1rs445925	intergenic region	No Data	0.1094	AA/GA/GG	7/121/489	50.38/79.28/90.44	27.9/23.8/22.9	-3.78	5.20E-08	152.11/152.68/148.68	15.1/36.1/32.8	3.53	0.3231
APOC1p698/rs72654449	5'flanking	4	0.004	CA/CC	5/613	77.26/88	16.2/24.0	-2.77	0.55052	145.12/149.76	3.7/33.5	-4.70	0.8413
APOC1p703/rs3207187	5'flanking	4	0.0008	CC/CT	619/1	87.93/83.81	24.0/NA	-0.88	0.89283	149.23/251.77	33.0/NA	102.96	0.0016
APOC1p720/rs72654451	5'flanking	4	0.2299	II/WI/WW	31/224/367	82.72/86.9/89.18	27.6/24.6/23.1	-0.82	0.11683	156.43/147.39/150.62	39.6/33.3/32.7	-0.46	0.8612
APOC1p1170	intron1	2b	0.0008	GA/GG	1/609	113.69/87.76	NA/24.1	7.14	0.27763	168.25/149.95	NA/33.0	18.30	0.5723
APOC1p1294	intron2	4	0.0008	AA/AC	618/1	87.88/98.11	24.0/NA	3.07	0.63865	149.49/176.37	33.4/NA	27.03	0.4118
APOC1p1317/rs12721048	intron2	4	0.0016	GA/GG	2/607	130.48/87.94	17.4/23.9	11.18	0.01598	216.08/149.57	43.8/33.2	66.89	0.0042
APOC1p1422	intron2	4	0.0016	GA/GG	2/621	93.79/87.9	NA/24.0	1.88	0.77425	123.27/149.68	NA/33.4	-26.52	0.4203
APOC1p1566/rs12691088	intron2	2b	0.0058	GA/GG	7/598	69.72/88.14	9.3/23.9	-4.95	0.12948	123.04/150.35	24.9/33.0	-27.45	0.0915
APOC1p2041/rs3826688	intron2	5	0.3424	AA/GA/GG	73/269/264	83.5/91.49/85.59	21.0/23.6/24.8	0.30	0.51703	151.51/148.58/149.85	27.1/34.5/33.7	0.24	0.9176
APOC1p2629	exon3	4	0.0008	GA/GG	1/618	69.33/88.11	NA/24.0	-5.12	0.43402	152.46/149.93	NA/33.3	2.54	0.9383
APOC1p2817	intron3	2b	0.0033	CC/CT	603/4	87.84/71.24	23.8/6.9	-4.46	0.23676	149.33/170.37	33.6/34.2	21.20	0.27
APOC1p3423/rs389261	intron3	No Data	0.0025	GA/GG	3/605	74.76/87.94	10.7/23.8	-3.50	0.35153	128.16/149.72	12.2/33.6	-21.68	0.2583

Cont. Table 23

APOC1p3494	intron3	No Data	0.0016	CC/CT	619/2	87.88/107.03	24.0/NA	5.38	0.41256	149.65/148.26	33.4/NA	-1.39	0.9662
APOC1p4334/rs12721046	intron3	6	0.1522	AA/GA/GG	13/160/438	102.6/90.83/86.13	25.1/22.7/24.2	1.59	0.00983	143.94/148.57/150.28	27.8/34.4/33.2	-2.11	0.4956
APOC1p5641/rs1064725	3'UTR	No Data	0.0388	GG/GT/TT	1/46/571	53.28/98.46/87.22	NA/25.9/23.6	2.00	0.09267	151.6/145.08/150.14	NA/28.1/33.8	-4.32	0.4728
APOC1p5773	3'flanking	No Data	0.0008	GA/GG	1/604	***	***	***	***	***	***	***	***
APOC1p5926/rs56131196	3'flanking	No Data	0.1885	AA/GA/GG	19/195/404	97.38/91.68/85.37	22.9/23.0/24.2	1.75	0.00229	138.59/149.26/150.3	29.6/35.8/32.2	-2.59	0.3695
APOC1p6026/rs4420638	3'flanking	No Data	0.1556	AA/GA/GG	405/129/22	85.38/89.53/97.75	24.2/23.2/21.6	1.43	0.01775	150.61/151.88/142.57	32.2/36.8/30.4	-1.10	0.716
rs4803770	HCR1	5	0.3779	CC/GC/GG	229/281/84	85.8/89.24/88.61	23.5/24.5/20.4	0.56	0.21851	148.59/150.64/147.18	34.5/32.1/35.1	0.02	0.9937
HCR1p292/rs4803771	HCR1	4	0.0245	CC/CG/GG	583/28/1	87.78/89.74/101.01	23.7/30.3/NA	0.68	0.64404	149.65/145.25/126.7	33.4/33.6/NA	-5.81	0.4273
HCR1p362	HCR1	2a	0.0025	CA/CC	3/605	94.53/87.84	NA/24.1	2.07	0.75319	146/149.46	NA/33.5	-3.48	0.9159
HCR1p423	HCR1	4	0.0258	CC/CG/GG	589/30/1	87.52/98.35/78.55	23.6/30.1/NA	2.10	0.14804	149.16/160.49/169.19	33.2/38.2/NA	11.09	0.1293
HCR1p575/rs157599	HCR1	3a	0.0024	AA/AG	618/3	88.02/74.88	24.0/10.7	-3.48	0.35815	149.8/128.13	33.4/12.2	-21.80	0.2531
HCR1p727/rs149345	HCR1	3a	0.0024	TG/TT	3/611	74.72/87.81	10.7/23.8	-3.47	0.35832	128.14/149.71	12.2/33.4	-21.70	0.2544
rs5112	APOC1P1	4	0.4633	CC/GC/GG	123/284/165	86.97/88.52/88.35	21.1/25.6/23.3	-0.15	0.75492	147.66/150.29/149.24	32.7/33.8/35.7	-0.67	0.7769
rs7259004	APOC1P1	6	0.1176	CC/CG/GG	476/128/8	89.05/82.56/94.13	23.3/24.3/35.9	-1.33	0.05153	147.93/153/173.55	32.3/37.7/22.4	6.89	0.046
HCR2p188/rs35136575	HCR2	2a	0.2274	CC/GC/GG	369/203/37	88.13/88.97/79.55	23.5/25.5/20.6	-0.48	0.36635	146.45/154.06/151.77	32.8/34.8/29.8	5.16	0.0496
HCR2p365	HCR2	2b	0.0041	CA/CC	5/606	99.1/87.77	32.0/23.9	3.05	0.41812	159.91/149.39	31.6/33.5	10.58	0.581
HCR2p523	HCR2	2b	0.0226	CC/CT	571/27	87.49/91.33	23.8/26.3	1.04	0.47773	149.23/153.04	33.7/31.3	3.82	0.6061
APOC4p636	5′ flanking	No Data	0.0008	CC/CT	601/1	***	***	***	***	***	***	***	***
APOC4p968/rs76214972	5′ UTR	4	0.0362	AA/AG	576/45	87.57/92.24	23.8/26.3	1.25	0.29092	149.5/151.52	33.9/26.9	2.03	0.733
APOC4p1150/rs148247675	Intron1	5	0.0017	AA/GA	601/2	87.74/107.42	23.9/NA	5.53	0.3975	149.68/148.08	33.3/NA	-1.61	0.9608
APOC4p1229	Intron1	2b	0.0016	GC/GG	2/619	***	***	***	***	***	***	***	***
APOC4p2557	Intron1	4	0.0008	CA/CC	1/619	68.6/87.95	NA/24.0	-5.26	0.42411	134.92/149.59	NA/33.4	-14.77	0.6541
APOC4p2623/rs5157	Intron1	4	0.4976	CC/CT/TT	155/315/152	89.47/87.43/87.27	23.5/24.9/22.5	-0.30	0.49795	151.15/147.68/151.88	32.5/32.5/35.8	0.34	0.8797
APOC4p2640/rs5158	Intron1	2b	0.1381	CC/CT/TT	459/149/11	87.34/90.18/81.09	23.6/25.2/24.6	0.35	0.59389	150.47/147/160.11	33.8/32.3/27.4	-1.45	0.662
APOC4p2683/rs12721109	Intron1	2b	0.0237	AA/AG/GG	1/27/584	53.83/71.26/88.65	NA/23.5/23.8	-4.99	0.00057	202.37/133.19/150.53	NA/30.4/33.6	-9.31	0.1964
APOC4p2703/rs12721108	Intron1	2a	0.0081	GG/GT	609/10	88.02/83.12	24.0/16.8	-1.23	0.59732	149.85/140.86	33.6/20.4	-9.00	0.4435
APOC2p194-C4p3498/rs1132899	C4-exon2	5	0.4863	CC/CT/TT	160/317/143	89.22/87.06/88.46	23.1/25.1/22.5	-0.12	0.79089	150.64/147.15/153.66	32.2/32.5/36.5	1.35	0.5467
APOC2p242-C4p3546/rs12691089	C4-exon2	5	0.0032	AG/GG	4/617	80.57/87.96	0.6/24.0	-1.80	0.69724	150.3/149.65	3.8/33.4	0.65	0.9778
APOC2p543-C4p3847/rs186448850	C4-intron2	5	0.0016	CT/TT	2/609	***	***	***	***	***	***	***	***
APOC2p623-C4p3927/rs5167	C4-exon3	5	0.3596	GG/TG/TT	74/300/249	88.12/88.12/87.59	19.2/25.5/23.3	0.11	0.81626	150.17/148.48/150.92	32.6/32.5/34.7	-1.01	0.6722

Cont. Table 23

APOC2p1357-C4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	0.4968	CC/CG/GG	155/316/151	87.57/87.5/89.09	22.2/24.9/23.9	0.19	0.66177	152.58/146.48/152.73	35.5/32.5/32.4	0.03	0.988
APOC2p1591-C4p4895	C2-intron1	4	0.0008	GA/GG	1/620	***	***	***	***	***	***	***	***
APOC2p1851/rs12709886	intron1	6	0.0372	GA/GG	46/572	92.79/87.56	28.6/23.5	1.35	0.2357	154.75/148.94	29.9/33.6	5.83	0.3078
APOC2p2870	intron1	4	0.004	GG/GT	616/5	87.71/110.92	23.9/16.9	6.33	0.05291	149.98/113.84	33.2/43.7	-36.20	0.0279
APOC2p3348/rs10420434	intron1	No Data	0.0371	GA/GG	46/574	84/88.23	27.1/23.8	-1.24	0.3101	156.21/149.31	35.7/32.8	6.94	0.2529
APOC2p3778/rs5120	intron1	4	0.4976	AA/AT/TT	154/305/157	88.77/87.16/87.61	24.1/24.7/22.2	0.14	0.74796	153.3/146.82/152.67	32.1/32.4/35.5	0.29	0.8954
APOC2p4853/rs199828513	3'flamking	No Data	0.2783	DD/WD/WW	316/260/42	87.77/87.53/91.29	23.6/25.2/19.6	0.21	0.6757	151.65/146.49/150.53	35.5/30.1/33.1	-2.81	0.2692
APOC2p5004/rs10421404	3'flanking	No Data	0.1823	CC/CT/TT	416/177/24	87.5/87.88/91.32	23.3/24.6/26.0	0.26	0.63942	149.13/148.48/158.91	32.7/34.8/28.8	1.64	0.5604
APOC2p5310/rs7258345	3'flanking	No Data	0.4649	GG/TG/TT	133/303/176	89.54/87.89/86.85	22.7/25.4/22.5	0.36	0.41406	151.44/146.73/153.03	30.8/32.7/35.6	-1.16	0.6041
APOC2p5398/rs12709889	3'flanking	6	0.276	AA/GA/GG	41/252/312	90.49/87.02/87.9	19.5/25.1/23.2	0.06	0.91243	150.8/146.25/151.97	33.6/30.5/35.8	-3.11	0.233
APOC2p5644	3'flanking	6	0.0092	AG/GG	11/585	94.14/87.4	30.6/23.7	1.74	0.42698	156.78/149.16	27.7/33.8	7.67	0.4929

[a] Cox-Box transformed variables.
MAF: minor allele frequency.
ApoB: Apolipoprotein B;ApoA1: apolipoprotein A1.
Age, Gender, Smoking, and BMI are significant covariates that were included in the final model.
AdjMean: adjusted means; GT-SD: standard deviation in genotype group.

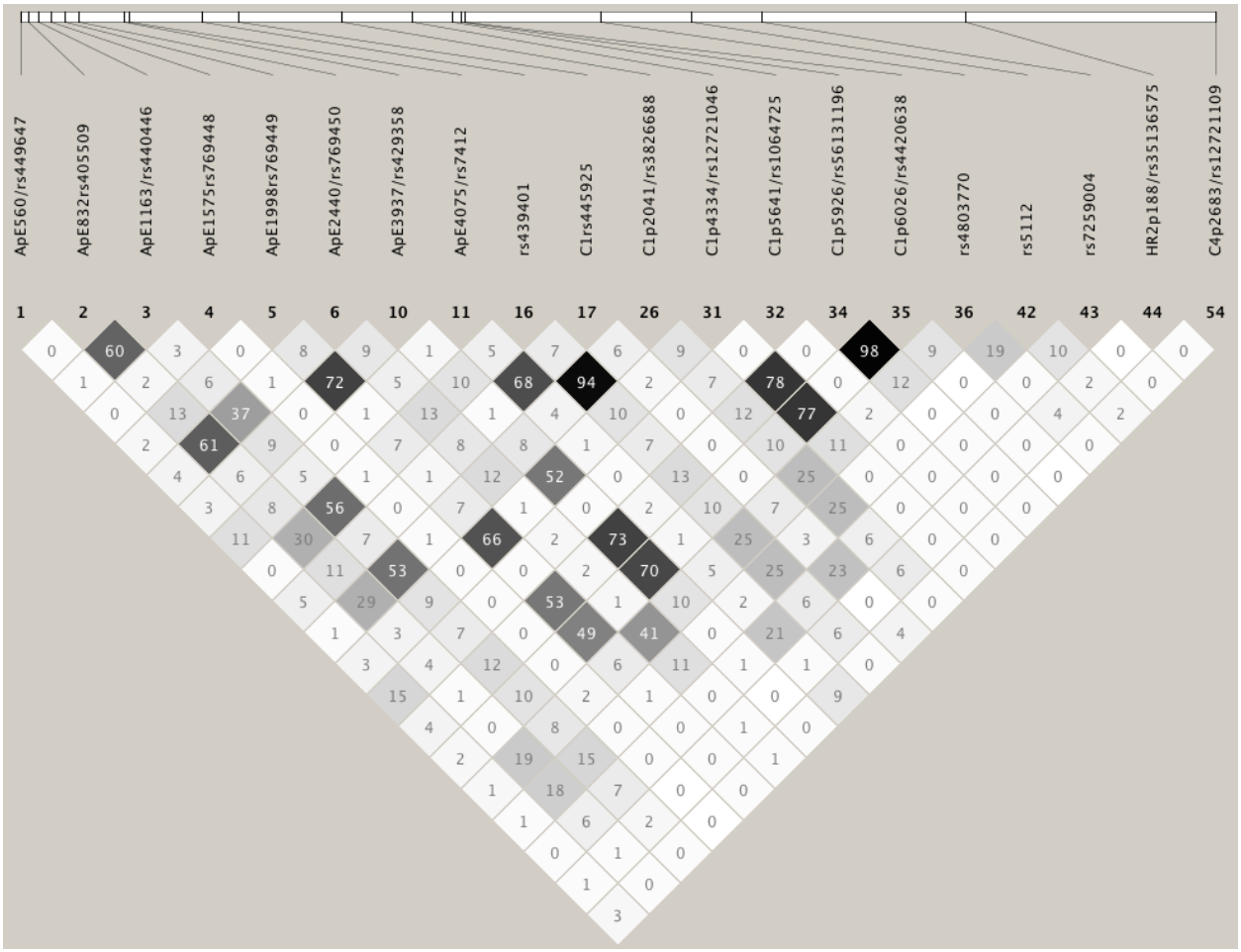

Figure 21. LD plot of the 20 common variants (MAF≥1%) with significant associations in NHWs

3.6.1.2 African Blacks

Single-locus association results with lipid traits in Blacks are shown in **Table 24,** the distribution of lipid traits adjusted means among the genotype groups are presented in **Table 25-27**, and **Figure 22** represents the LD structure of the 24 variants with significant associations in Blacks. Twenty-four variants (0.0135≤MAF≤0.366) showed evidence of associations with at least one lipid trait (5.35E-07 ≤ P ≤ 0.048). More associations were observed with LDL-C followed by

TC, TG, and apoB. The established association of *APOE2/E4* alleles with LDL-C is replicated in African Blacks. E2 allele was observed to be associated with lower LDL-C (β=-2.05, P=5.35E-07), TC (β=-0.82, P=0.0001), apoB (β=-2.35, P=0.0356), and higher apoA1 (β=3.85, P=0.00008), while E4 allele was observed to be associated only with higher LDL-C (β=0.46, P=0.0317).

Eleven variants, in addition to the *APOE2/E4* alleles, showed significant associations with LDL-C; *APOE*560/rs449647 (β=0.58, P=0.0031), *APOE*832/rs405509 (β=0.60, P=0.0044), *APOE*2269/rs6135770 (β=-2.05, P=0.0064), *APOE*4036/rs769455 (β=-2.23, P=0.0009), *APOC1*p720/rs71962921 (β=-0.57, P=0.0084), *APOC1*p5667/rs127210054 (β=-0.77, P=0.0063), *APOC2*p1357C4p4661/rs2288912 (β=0.51, P=0.020), *APOC2*p1540C4p4844/rs75463753 (β=0.8, P=0.0114), *APOC2*p2486/rs9304645 (β=-0.54, P=0.0084), *APOC2*p5815/rs10423208 (β=0.42, P=0.0474), and *APOC2*p5922/rs10422888 (β=0.98, P=0.0079). None of the variants that showed evidence of association with LDL-C were correlated with either *E2/E4* allele. However, most of them were correlated with each other. *APOE*560/rs449647 and *APOE*832/rs405509 were in moderate LD (r^2=0.32), while *APOE*2269/rs6135770 and *APOE*4036/rs769455 were in complete LD. *APOC1*p720/rs71962921 and *APOC1*p5667/rs127210054 were in moderate LD (r^2=0.44), and similarly *APOC2*p1357C4p4661/rs2288912 and *APOC2*p1540C4p4844/rs75463753 were in moderate LD (r^2=0.32). More interestingly, none of the LDL-associated variants was in LD with *E2/E4* alleles and their effects on LDL-C seem to be independent of *E2/E4*.

Only two variants showed significant associations with HDL-C: rs439401 (β-0.60, P=0.044), and *APOC1*p3573/rs10424339 (β=0.55, P=0.045). In addition to the *E2* allele, seven variants showed significant associations with TC, *APOE*560/rs449647 (β=0.2, P=0.017),

*APOE*4036/rs769455 (β=-0.9, P=0.0129), *APOC1*p5667/rs127210054 (β=-0.3, P=0.047), *APOC2*p1357C4p4661/rs2288912 (β=0.3, P=0.0153), *APOC2*p1540C4p4844/rs75463753 (β=0.4, P=0.011), *APOC2*p3778/rs5120 (β=0.3, P=0.012), and *APOC2*p5922/rs10422888 (β=0.5, P=0.0129). *APOC2*p3778/rs5120 was in moderate LD with multiple variants; *APOC2*p1357C4p4661/rs2288912 (r^2=0.60), *APOC2*p1540C4p4844/rs75463753 (r^2=0.49) and their effect seem to be not independent. However, none of the TC-associated variants was in LD with *E2/E4* allele and their effects seem to be independents.

Seven variants were associated with TG; *APOE*73/rs1081101 (β=0.04, P=0.0093), *APOE*4036/rs769455 (β=0.06, P=0.037), *APOC1*p5667/rs127210054 (β=-0.03, P=0.007), *APOC1*p5926/rs56131196 (β=-0.02, P=0.0442), *APOC4*p757/rs12721105 (β=0.06, P=0.0005), *APOC4*p2640/rs5158 (β=-0.05, P=0.035), and *APOC2*p2935/rs11879392 (β=-0.07, P=0.028). Moderate LDs were observed between *APOE*73/rs1081101 and *APOE*4036/rs769455 (r^2=0.29), and between *APOC1*p5926/rs56131196 and *APOC1*p5667/rs127210054 (r^2=0.47). On the other hand, *APOC4*p2640/rs5158 and *APOC2*p2935/rs11879392 were in strong LD (r^2=0.84).

In addition to *APOE2*, 4 variants showed significant associations with apoB: *APOE*1163/rs440446 (β=2.3, P=0.0109), *APOC4*p2623/rs5157 (β=1.4, P=0.044), *APOC2*p1042C4p4346/rs12709885 (β=-4.4, P=0.024), and *APOC2*p1357C4p4661/rs2288912 (β=1.4, P=0.023). While *APOC4*p2623/rs5157 was in moderate LD with *APOC2*p1357C4p4661/rs2288912 (r^2=0.58), these two variants (*APOE*1163/rs440446, and *APOC2*p1042C4p4346/rs12709885) seem to have independent effect on apoB. In addition to the *APOE2* allele, two more variants showed significant associations with apoA1: *APOC1*p720/rs71962921 (β=1.0, P=0.048), and *APOC2*p1042C4p4346/rs12709885 (β=5.9, P=0.0007) and they were not in LD with each other.

Seven variants, in addition to the *APOE2* allele, showed significant associations with multiple lipid traits in Blacks while the remaining sixteen variants showed single associations. Only one variant: *APOC2*p1357C4p4661/rs2288912 showed significant associations with the 3 LDL-related traits (LDL-C, TC, and apoB). Six variants showed significant associations with 2 LDL-related traits (LDL-C, and TC): *APOE*560/rs449647, *APOE*4036/rs769455, *APOC1*p5667/rs12721054, *APOC2*p1540C4p4844/rs75463753, *APOC2*p3778/rs5120, and *APOC2*p5922/rs10422888. Two of the variants that had associations with 2 LDL-related traits (LDL-C, and TC) were associated also with TG: *APOE*4036/rs769455, and *APOC1*p5667/rs12721054.

The remaining sixteen variants showed evidence of association with single lipid trait, including *APOE4* allele. In addition to the *APOE4* allele, four other variants showed single association with LDL-C: *APOE*832/rs405509, *APOE*2269/rs6135770, *APOC1*p720/rs71962921, *APOC2*p2486/rs9304645, and *APOC2*p5815/rs10423208. Two variants showed single association with HDL-C: rs439401, and *APOC1*p3573/rs10424339. Five variants showed single association with TG: *APOE*73/rs1081101, *APOC1*p5926/rs56131196, *APOC4*p757/rs12721105, *APOC4*p2640/rs5158, and *APOC2*p2935/rs118793392. Three variants showed single association with ApoB: *APOE*1163/rs440446, *APOC4*p2623/rs5157, and *APOC2*p1042C4p4346/rs12709885.

Table 24. Single-locus association results with lipid traits in African Blacks

				LDL-C[a]		HDL-C[a]		TC[a]		TG[a]		ApoB[a]		ApoA1[a]	
Variant name	function	regulome db score	MAF	Beta	p_value	Beta	p_value	Beta	p_value	Beta	p_value	Beta	p_value	Beta	p_value
APOE73/rs1081101	5'flanking	4	0.0611	-0.62	0.111	0.30	0.42732	-0.20	0.3283	0.038	0.0093	0.65	0.54877	-0.003	0.99719
APOE173	5'flanking	3a	0.002	-1.14	0.5979	-2.10	0.32058	0.41	0.7151	0.037	0.7028	3.20	0.59226	6.86	0.19127
APOE308/rs769445	5'flanking	4	0.0072	-0.37	0.7576	-1.06	0.34278	-0.06	0.9218	0.056	0.2065	1.87	0.55135	3.21	0.2461
APOE560/rs449647	5'flanking	5	0.3663	0.58	0.0031	-0.18	0.35635	0.25	0.0177	-0.001	0.8482	0.92	0.09509	-0.49	0.31886
APOE618	5'flanking	4	0.0006	-2.85	0.4432	-12.25	0.00079	-3.62	0.0634	0.025	0.856	4.15	0.68762	-18.42	0.04342
APOE624/rs769446	5'flanking	3a	0.0077	-2.86	0.0214	0.65	0.56874	-1.25	0.044	0.005	0.9096	-4.19	0.20373	3.55	0.20204
APOE832/rs405509	5'flanking	1f	0.2561	0.60	0.0044	-0.19	0.36119	0.22	0.0529	0.003	0.7457	0.66	0.26113	-0.67	0.19928
APOE1109/rs9282609	Splice site	4	0.0415	0.05	0.9183	0.61	0.17876	0.12	0.6321	0.023	0.1814	1.38	0.27683	0.24	0.83418
APOE1163/rs440446	intron1	4	0.1004	0.44	0.1791	-0.54	0.09464	0.12	0.4748	0.023	0.0537	2.30	0.01093	-0.44	0.58046
APOE1231	intron1	2b	0.0125	-0.71	0.4139	-0.27	0.755	-0.46	0.3315	-0.030	0.3441	-1.71	0.47484	-1.12	0.59594
APOE1279/rs877973	intron1	4	0.0597	-0.15	0.7208	0.51	0.19812	0.04	0.8544	-0.029	0.0513	-0.45	0.68467	1.06	0.27597
APOE1539/rs184686013	intron1	4	0.0086	-1.03	0.2862	1.35	0.15682	-0.33	0.5172	0.002	0.9546	0.23	0.93296	4.24	0.0738
APOE2072/rs189660912	intron 2	4	0.0079	-0.50	0.6433	-0.40	0.70658	-0.40	0.4796	0.009	0.8229	0.70	0.81486	-1.35	0.61188
APOE2269/rs6135770	intron 2	5	0.0169	-2.05	0.0064	0.77	0.29121	-0.69	0.0771	0.040	0.1489	-2.56	0.22005	1.09	0.55027
APOE2440/rs769450	intron 2	5	0.387	0.20	0.3409	-0.02	0.93935	0.11	0.3081	-0.003	0.7396	-0.50	0.37248	-0.17	0.73856
APOE3673/rs769453	intron 3	5	0.0066	-0.37	0.7649	-1.10	0.34567	-0.07	0.9054	0.037	0.4242	2.02	0.5386	3.93	0.17574
APOE3937/rs429358	exon 4	5	0.2656	0.46	0.0317	-0.14	0.50743	0.17	0.1323	-0.008	0.3075	0.05	0.9371	-1.00	0.05924
APOE4036/rs769455	exon 4	5	0.02	-2.23	0.0009	-0.46	0.48274	-0.87	0.0129	0.056	0.0372	-3.45	0.06644	-0.71	0.66412
APOE4075/rs7412	exon 4	5	0.0605	-2.05	5.35E-07	0.75	0.06615	-0.82	0.0001	-0.018	0.2376	-2.35	0.03564	3.85	0.00008
APOE4569	3'UTR	5	0.0007	8.87	0.0173	5.29	0.14968	5.12	0.0089	0.073	0.5976	14.25	0.1684	15.53	0.08835
APOE5223	3'flanking	2b	0.0051	-2.25	0.0874	0.39	0.763	-0.94	0.1738	0.006	0.9078	-2.54	0.51655	1.29	0.70886
APOE5231	3'flanking	2b	0.027	-0.10	0.8587	-0.18	0.76449	-0.03	0.9208	-0.023	0.2836	-0.82	0.60359	-0.03	0.98493
rs439401	intragenic region	1b	0.1092	0.39	0.1933	-0.60	0.04448	0.07	0.6621	0.011	0.3401	1.42	0.0862	-0.50	0.50161
APOC1rs445925	intragenic region	No Data	0.299	-0.01	0.9509	0.10	0.64004	-0.01	0.8983	-0.007	0.3748	-0.31	0.59161	0.36	0.48026
APOC1p720ins4/rs71962921	5'flanking region	4	0.2737	-0.57	0.0084	0.27	0.20872	-0.20	0.0741	-0.013	0.1137	-1.10	0.06438	1.03	0.04836
APOC1p894/rs190454394	5'flanking region	4	0.002	3.70	0.0852	0.74	0.72955	1.71	0.1317	0.021	0.7907	8.19	0.17048	0.40	0.93927
APOC1p1166/rs72654452	intron1	2b	0.0308	0.49	0.3678	-0.61	0.25404	0.31	0.2783	0.028	0.163	0.98	0.51091	-1.09	0.40589

Cont. Table 24

APOC1p1331/rs10408994	intron2	4	0.0666	0.62	0.1238	0.35	0.38621	0.34	0.1116	0.016	0.2862	-0.83	0.46727	-0.66	0.50656
APOC1p1526/rs5114	intron2	4	0.0579	-0.05	0.9053	0.55	0.1745	0.12	0.5876	-0.025	0.1117	-0.22	0.84865	1.38	0.165
APOC1p1642	intron2	4	0.0103	-1.05	0.2648	-0.59	0.53986	-0.64	0.2132	-0.019	0.5831	-1.86	0.47702	-1.90	0.4104
APOC1p1684/rs12709881	intron2	4	0.0973	-0.51	0.1179	0.40	0.20729	-0.16	0.364	-0.017	0.1541	-1.48	0.09465	0.73	0.34454
APOC1p3358	intron3	No Data	0.0021	-0.25	0.9068	3.44	0.10895	0.34	0.7632	0.003	0.9727	-3.96	0.50955	-2.34	0.6601
APOC1p3423/rs389261	intron3	No Data	0.331	0.19	0.3556	0.24	0.26136	0.12	0.2958	-0.002	0.8116	-0.04	0.94719	-0.36	0.48713
APOC1p3573/rs10424339	intron3	No Data	0.1396	-0.02	0.9374	0.55	0.0455	0.07	0.6371	0.001	0.9096	-0.71	0.36467	0.40	0.55931
APOC1p5006/rs112528434	intron3	No Data	0.085	-0.38	0.2887	0.32	0.3879	-0.10	0.6053	-0.018	0.1732	-1.22	0.2099	0.67	0.44123
APOC1p5053/rs12721052	intron3	No Data	0.22	0.30	0.1905	-0.31	0.16174	0.13	0.2728	0.004	0.6524	0.66	0.29256	-0.42	0.4506
APOC1p5667/rs12721054	3'UTR	6	0.1446	-0.77	0.0063	0.23	0.42209	-0.30	0.0474	-0.028	0.007	-1.01	0.18808	1.01	0.14096
APOC1p5926/rs56131196	3'flanking region	No Data	0.1745	-0.22	0.3925	0.31	0.22541	-0.05	0.7296	-0.019	0.0442	-0.70	0.33774	0.87	0.17334
rs4803770	HCR-1	5	0.2695	0.38	0.081	-0.27	0.21475	0.18	0.1102	0.005	0.5732	0.90	0.13554	-0.53	0.32036
HCR1p424/rs117664574	HCR-1	4	0.0073	-0.58	0.6076	2.06	0.06453	0.12	0.8344	0.025	0.5525	2.07	0.5106	5.74	0.04801
HCR1p575/rs157599	HCR-1	3a	0.3595	0.17	0.4067	0.19	0.36879	0.08	0.469	-0.004	0.6132	0.27	0.64249	-0.63	0.22016
rs5112	APC1P1	4	0.4797	0.10	0.6073	0.25	0.18503	0.16	0.1091	0.010	0.1818	0.54	0.31703	0.80	0.0924
rs7259004	APC1P1	6	0.302	-0.02	0.9061	0.29	0.15235	0.09	0.3976	0.006	0.4328	0.37	0.51449	0.83	0.10102
HCR2p188/rs35136575	HCR-2	2a	0.1546	-0.16	0.5327	0.30	0.23716	0.01	0.9184	0.005	0.604	-0.61	0.4015	0.85	0.18117
HCR2p286	HCR-2	2a	0.0457	0.79	0.0785	-0.70	0.11626	0.31	0.1847	0.026	0.1292	1.37	0.27692	-0.59	0.59403
HCR2p523/rs118004808	HCR-2	2b	0.0026	2.74	0.1418	0.02	0.99167	1.17	0.2362	0.034	0.6289	6.71	0.19588	-0.21	0.96328
APOC4p368	5’ flanking region	6	0.0019	1.04	0.6283	0.33	0.87548	0.71	0.529	0.088	0.2641	-1.39	0.81479	-0.69	0.8967
APOC4p637/rs113814026	5’ flanking region	No Data	0.0452	-0.23	0.6127	0.10	0.82864	-0.13	0.5832	-0.013	0.4457	1.34	0.29549	0.14	0.90262
APOC4p757/rs12721105	5’ flanking region	5	0.0376	0.14	0.778	-0.19	0.69377	0.13	0.6192	0.063	0.0005	0.45	0.7436	-1.40	0.23935
APOC4p1088	intron1	2b	0.0013	-2.69	0.3048	-4.26	0.10128	-1.51	0.2767	0.182	0.0633	-2.07	0.7775	-4.80	0.45794
APOC4p1130	intron1	5	0.0007	-0.71	0.8491	9.46	0.00979	1.50	0.4435	0.097	0.48	-21.03	0.04207	14.38	0.11483
APOC4p1192/rs113745034	intron1	4	0.0124	-0.63	0.4823	0.35	0.69302	-0.31	0.5056	-0.008	0.8015	2.83	0.26681	3.44	0.12841
APOC4p1325del3	intron1	4	0.0245	0.70	0.2711	0.30	0.63292	0.28	0.4099	-0.040	0.0909	1.71	0.33255	-0.31	0.84012
APOC4p1430ins	intron1	5	0.0341	0.32	0.5609	0.69	0.22691	0.35	0.229	-0.009	0.6459	1.43	0.35841	2.68	0.05543
APOC4p2099/rs111339708	intron1	No Data	0.0141	-0.83	0.3026	0.35	0.6678	-0.42	0.3367	-0.033	0.2745	1.19	0.59549	3.04	0.13403
APOC4p2467/rs115225947	intron1	5	0.0141	0.68	0.4056	0.03	0.96646	0.30	0.4923	-0.027	0.3794	-0.42	0.85407	-2.52	0.2125
APOC4p2559/rs5155	intron1	4	0.0986	-0.27	0.4028	-0.20	0.53148	-0.22	0.209	-0.008	0.4908	-0.98	0.27438	-1.47	0.06609
APOC4p2607/rs5156	intron1	4	0.0129	-1.04	0.235	0.43	0.62963	-0.49	0.2981	-0.029	0.3791	1.60	0.50775	3.60	0.10172
APOC4p2623/rs5157	intron1	4	0.1723	0.28	0.2703	-0.14	0.59553	0.13	0.3287	0.001	0.9481	1.43	0.04428	0.78	0.21466
APOC4p2640/rs5158	intron1	2b	0.0213	0.55	0.414	-0.29	0.66191	0.01	0.9712	-0.052	0.0353	1.44	0.44596	-1.12	0.4997

Cont. Table 24

APOC4p2678/rs148564866	intron1	2b	0.0086	-0.61	0.555	0.07	0.94518	-0.31	0.584	0.041	0.288	0.87	0.76308	2.67	0.29564
APOC4p2767/rs127721107	intron1	4	0.0254	0.35	0.5788	0.56	0.37292	0.16	0.6279	-0.007	0.7599	3.15	0.07284	2.17	0.1601
APOC4p3348	intron1	5	0.0007	-2.86	0.4403	11.56	0.00153	0.74	0.7067	-0.230	0.0947	-9.98	0.33555	14.52	0.11008
APOC2p75-C4p3380/rs12721104	C4-intron1	5	0.1368	0.02	0.9358	-0.11	0.69346	-0.01	0.9244	0.015	0.1633	-0.07	0.92847	-1.25	0.06839
APOC2p194-C4p3498/rs1132899	C4-exon2	5	0.2368	0.21	0.3615	-0.14	0.53341	0.11	0.3546	-0.001	0.8783	0.95	0.13191	0.88	0.11098
APOC2p228/rs5164	C4-exon2	5	0.0066	-0.78	0.5126	-0.72	0.54187	-0.43	0.4953	0.036	0.4138	2.49	0.4501	3.31	0.25501
APOC2p288-C4p3592/rs12691090	C4-exon2	5	0.0272	-0.02	0.9753	0.75	0.21469	0.02	0.9419	-0.008	0.7262	1.96	0.24561	2.00	0.17721
APOC2p396-C4p3700	C4-intron2	5	0.0007	-4.47	0.2324	5.90	0.11176	-1.40	0.4802	-0.139	0.3161	-9.04	0.38386	11.51	0.21156
APOC2p488-C4p3792/rs5165	C4-intron2	5	0.0146	0.13	0.8735	-0.04	0.96019	-0.07	0.8663	-0.025	0.4059	-0.83	0.71058	-1.54	0.43321
APOC2p623-C4p3927/rs5167	C4-exon3	5	0.4594	-0.37	0.0527	0.05	0.77107	-0.16	0.1057	0.007	0.3421	-0.54	0.31017	0.19	0.6794
APOC2p665-C4p3969/rs138548797	C4-exon3	No Data	0.0086	0.18	0.8649	-0.06	0.94985	0.00	0.9938	0.017	0.6686	4.09	0.15807	-2.07	0.41707
APOC2p708-C4p4012	C4-exon3	6	0.0007	-1.33	0.7212	-7.15	0.05187	-1.34	0.4936	0.287	0.0381	6.46	0.53306	-9.42	0.30174
APOC2p853-C4p4157/rs10425530	C4-3' UTR	6	0.11	-0.20	0.5315	0.24	0.43314	-0.06	0.7051	-0.004	0.7518	-0.53	0.5399	1.17	0.12757
APOC2p1042-C4p4346/rs12709885	C4-3'FR/C2-5'FR	5	0.0178	-1.25	0.0855	1.10	0.13505	-0.55	0.1548	-0.035	0.1866	-4.39	0.02431	5.95	0.00071
APOC2p1187-C4p4491/rs111782345	C4-3'FR/C2-5'FR	5	0.0178	0.21	0.7773	0.58	0.44007	0.17	0.6739	-0.013	0.6376	3.17	0.13276	3.23	0.08379
APOC2p1229-C4p4533/rs112698600	C4-3'FR/C2-5'FR	2b	0.014	-0.17	0.8398	0.83	0.31821	0.04	0.9328	-0.007	0.8154	2.78	0.23927	3.20	0.12314
APOC2p1275-C4p4579/rs111356234	C4-3'FR/C2-5'FR	4	0.0352	-0.95	0.0752	-0.18	0.7323	-0.48	0.0954	0.006	0.7493	-0.23	0.87888	0.35	0.79182
APOC2p1357-C4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	0.2581	0.51	0.0202	0.05	0.80869	0.28	0.0153	-0.007	0.3614	1.37	0.02344	0.80	0.13323
APOC2p1540-C4p4844/rs75463753	C2-intron1	4	0.1079	0.80	0.0114	0.09	0.77127	0.42	0.0111	-0.008	0.5	1.08	0.21814	0.48	0.5384
APOC2p2486/rs9304645	intron1	4	0.3655	-0.54	0.0084	0.09	0.65299	-0.20	0.0737	0.011	0.1406	-0.21	0.7176	0.75	0.13555
APOC2p2935/rs11879392	intron1	2b	0.0135	0.87	0.317	0.57	0.49871	0.27	0.5399	-0.069	0.0285	0.44	0.85516	0.18	0.93035
APOC2p3010/rs10419086	intron1	6	0.1253	0.03	0.9215	0.15	0.62186	-0.05	0.7439	-0.017	0.1272	-0.91	0.2581	-1.32	0.06568
APOC2p3692/rs12721060	intron1	No Data	0.0172	-0.19	0.8123	0.76	0.3536	-0.04	0.9297	-0.015	0.6229	2.28	0.31473	3.01	0.14108
APOC2p3778/rs5120	intron1	4	0.1845	0.60	0.0158	0.08	0.74123	0.33	0.0129	-0.0001	0.9937	1.11	0.10763	0.79	0.19964
APOC2p3805/rs7257095	intron1	2a	0.1649	0.35	0.1883	-0.16	0.53621	0.13	0.3551	-0.003	0.7465	0.72	0.33716	-0.55	0.40568
APOC2p3814/rs10422603	intron1	2b	0.3008	-0.30	0.1716	0.25	0.23836	-0.08	0.4714	0.012	0.1454	-0.10	0.87424	0.97	0.06515
APOC2p3892/rs5121	exon2	5	0.0358	-0.21	0.6957	-0.03	0.95269	-0.11	0.6979	0.004	0.8416	-0.03	0.98356	0.20	0.87741
APOC2p4086/rs114780592	intron2	4	0.0278	-0.04	0.9509	0.49	0.40801	-0.02	0.9506	-0.004	0.8486	3.05	0.0669	1.53	0.29745
APOC2p4118/rs201709243	exon3	4	0.0007	-6.14	0.1016	***	***	0.52	0.7926	***	***	-2.87	0.7826	***	***
APOC2p4319/rs5123	intron3	No Data	0.0592	0.19	0.6268	-0.14	0.71873	0.15	0.4796	-0.008	0.6025	-0.25	0.82293	0.49	0.61561
APOC2p4513/rs180809422	intron3	5	0.0135	0.46	0.5715	0.82	0.32552	0.34	0.438	-0.021	0.5011	2.64	0.26202	3.47	0.09379
APOC2p4587/rs5126	exon4	5	0.0499	-0.14	0.757	0.12	0.80049	-0.07	0.771	-0.011	0.5193	1.71	0.18011	0.68	0.54818

Cont. Table 24

APOC2p4754/rs7253690	exon4	5	0.0606	0.26	0.5088	-0.01	0.9801	0.25	0.2212	-0.004	0.787	0.19	0.85817	1.17	0.22087
APOC2p4853/rs150448996	3'flamking region	No Data	0.2736	0.10	0.6544	-0.18	0.40916	-0.02	0.8445	0.001	0.9083	-0.05	0.93724	-0.86	0.10718
APOC2p4973/rs199828513	3'flamking region	No Data	0.0082	-1.49	0.1714	-0.60	0.58323	-0.79	0.1664	0.010	0.8053	3.46	0.24889	0.16	0.95293
APOC2p5004/rs10421404	3'flanking region	No Data	0.2908	-0.34	0.1149	0.16	0.46461	-0.11	0.3371	0.011	0.1599	-0.04	0.94186	0.61	0.24821
APOC2p5018/rs78403558	3'flanking region	5	0.0352	0.77	0.1368	0.00	0.9939	0.30	0.2761	-0.024	0.2111	1.27	0.37773	0.36	0.77793
APOC2p5310/rs7258345	3'flanking region	No Data	0.3067	0.37	0.1018	0.11	0.61363	0.17	0.1497	-0.010	0.216	0.29	0.63627	-0.42	0.44209
APOC2p5398/rs12709889	3'flanking region	6	0.2587	0.19	0.3893	-0.12	0.59063	0.02	0.8441	-0.001	0.9294	0.16	0.79862	-0.63	0.24337
APOC2p5491	3'flanking region	6	0.0007	7.19	0.053	6.53	0.0762	4.21	0.0315	-0.040	0.775	-8.06	0.43745	-5.71	0.53224
APOC2p5512/rs12721064	3'flanking region	6	0.0083	-1.02	0.3246	0.05	0.96332	-0.10	0.8634	0.087	0.0297	-2.23	0.43911	0.10	0.96886
APOC2p5562	3'flanking region	No Data	0.0175	-0.41	0.6012	-0.67	0.37221	-0.21	0.5949	-0.015	0.6109	-0.92	0.67145	0.65	0.73492
APOC2p5586/rs73558127	3'flanking region	No Data	0.1001	-0.58	0.0713	0.47	0.13813	-0.23	0.1778	-0.008	0.485	0.13	0.88663	1.00	0.20571
APOC2p5771	3'flanking region	6	0.0047	***	***	-0.58	0.67563	***	***	0.031	0.5541	***	***	-1.10	0.74972
APOC2p5815/rs10423208	3'flanking region	5	0.3164	0.42	0.0474	0.03	0.8759	0.18	0.117	-0.010	0.203	0.34	0.55855	-0.43	0.41044
APOC2p5922/rs10422888	3'flanking region	5	0.0784	0.98	0.0079	-0.01	0.98595	0.48	0.0129	0.015	0.2582	1.47	0.14838	0.05	0.95405
APOC2p5965	3'flanking region	5	0.0013	2.76	0.295	2.75	0.29064	1.58	0.2542	-0.006	0.9512	-10.45	0.15456	-2.79	0.66578
APOC2p6334	3'flanking region	No Data	0.0096	1.76	0.0678	0.60	0.52729	0.94	0.0628	0.014	0.6886	3.15	0.2415	-2.30	0.33277

yellow highlighted values represent significant p-value; MAF: minor allele frequency; LDL-C: low-density lipoprotein cholesterol; ApoB: apolipoprotein B; TG: triglyceride; HDL-C: high-density lipoprotein cholesterol; [a] Cox-Box transformed variables; Age, gender, smoking, BMI, waist, Jobmin, staff level were included in the final model as covariat

Table 25. Genotype-specific means (± SD) of LDL-C and HDL-C genotyped SNPs in African Blacks

						LDL-C[a]				HDL-C[a]			
Variant name	**Function**	**regulome db score**	**MAF**	**Genotype**	**GT Count**	**AdjMean**	**GT_SD**	**Beta**	**p_value**	**AdjMean**	**GT_SD**	**Beta**	**p_value**
APOE73/rs1081101	5'flanking	4	0.0611	CC/CT/TT	660/82/5	109.82/104.38/99.53	34.8/33.9/34.1	-0.62	0.111	47.72/49.03/48.5	12.6/13.7/5.6	0.30	0.42732
APOE173	5'flanking	3a	0.002	AA/GA	746/3	109.16/99.49	34.7/40.5	-1.14	0.5979	47.84/40.69	12.7/11.2	-2.10	0.32058
APOE308/rs769445	5'flanking	4	0.0072	CC/TC	739/10	109.16/106.69	34.6/42.5	-0.37	0.7576	47.86/44.21	12.7/11.0	-1.06	0.34278
APOE560/rs449647	5'flanking	5	0.3663	AA/AT/TT	300/334/105	105.33/110.93/115.09	33.1/36.0/33.4	0.58	0.0031	48.06/47.85/46.63	12.5/13.0/12.7	-0.18	0.35635
APOE618	5'flanking	4	0.0006	GC/GG	1/763	83.39/109.35	NA/34.5	-2.85	0.4432	13.45/47.78	NA/12.6	-12.25	0.00079
APOE624/rs769446	5'flanking	3a	0.0077	TC/TT	9/690	85.79/109.43	33.9/34.4	-2.86	0.0214	49.89/47.71	15.1/12.9	0.65	0.56874
APOE832/rs405509	5'flanking	1f	0.2561	GG/GT/TT	428/267/61	105.85/114.09/111.31	34.0/36.1/30.7	0.60	0.0044	47.91/48.13/45.19	12.9/12.7/11.3	-0.19	0.36119
APOE1109/rs9282609	Splice site	4	0.0415	CC/TC/TT	686/55/4	109.01/109/110.06	34.7/33.6/31.7	0.05	0.9183	47.63/50.15/49.36	12.6/13.7/6.6	0.61	0.17876
APOE1163/rs440446	intron1	4	0.1004	CC/CG/GG	8/126/569	106.24/113.53/108.52	22.4/36.0/34.7	0.44	0.1791	45.27/46.49/48.41	14.2/12.5/12.8	-0.54	0.09464
APOE1231	intron1	2b	0.0125	GA/GG	19/729	102.61/109.3	30.1/34.8	-0.71	0.4139	46.84/47.87	11.5/12.7	-0.27	0.755
APOE1279/rs877973	intron1	4	0.0597	AA/CA/CC	3/81/664	75.36/111.5/109.08	40.0/39.9/34.0	-0.15	0.7208	49.78/49.36/47.61	11.2/12.3/12.7	0.51	0.19812
APOE1539/rs184686013	intron1	4	0.0086	AA/AG/GG	733/11/1	109.19/102.23/77.29	34.6/30.1/NA	-1.03	0.2862	47.68/54.07/46.37	12.7/13.5/NA	1.35	0.15682
APOE2072/rs189660912	intron 2	4	0.0079	GA/GG	12/734	103.59/109.27	21.4/34.9	-0.50	0.6433	46.66/47.85	15.0/12.7	-0.40	0.70658
APOE2269/rs6135770	intron 2	5	0.0169	GA/GG	25/723	92.91/110.08	30.6/34.6	-2.05	0.0064	50.39/47.78	12.6/12.7	0.77	0.29121
APOE2440/rs769450	intron 2	5	0.387	AA/AG/GG	107/308/261	112.51/109.87/108.31	37.6/35.0/33.7	0.20	0.3409	46.94/48.89/47.64	13.4/13.3/12.3	-0.02	0.93935
APOE3673/rs769453	intron 3	5	0.0066	CC/GC	738/9	109.07/106.76	34.4/44.5	-0.37	0.7649	47.85/44.06	12.7/11.5	-1.10	0.34567
APOE3937/rs429358	exon 4	5	0.2656	CC/CT/TT	58/285/406	109.67/113.33/106.49	31.8/35.5/34.3	0.46	0.0317	46.45/47.78/48	12.5/12.0/13.3	-0.14	0.50743
APOE4036/rs769455	exon 4	5	0.02	CC/TC/TT	708/27/1	109.86/91.6/71.5	34.4/28.0/NA	-2.23	0.0009	47.95/48.87/15.7	12.7/12.5/NA	-0.46	0.48274
APOE4075/rs7412	exon 4	5	0.0605	AA/GA/GG	2/84/670	50.48/95.05/111.16	6.8/30.7/34.7	-2.05	5.35E-07	50.84/49.96/47.54	12.7/11.5/12.8	0.75	0.06615
APOE4569	3'UTR	5	0.0007	GG/GT	746/1	109.02/201.25	34.6/NA	8.87	0.0173	47.84/66.63	12.7/NA	5.29	0.14968
APOE5223	3'flanking	2b	0.0051	CC/CG	758/8	109.45/90.42	34.5/28.8	-2.25	0.0874	47.74/48.97	12.7/12.1	0.39	0.763
APOE5231	3'flanking	2b	0.027	GG/GT/TT	2/36/708	93.74/109.69/109.12	32.2/36.0/34.7	-0.10	0.8587	51.97/46.78/47.88	NA/11.1/12.8	-0.18	0.76449
rs439401	intragenic region	1b	0.1092	CC/CT/TT	587/130/15	108.47/112.63/109.57	34.9/34.5/23.2	0.39	0.1933	48.34/46.18/44.72	12.8/12.4/12.1	-0.60	0.04448
APOC1rs445925	intragenic region	No Data	0.299	AA/GA/GG	68/310/367	108.26/109.76/109.34	35.4/33.8/34.7	-0.01	0.9509	47.56/48.18/47.55	12.3/12.0/13.2	0.10	0.64004
APOC1p720ins4/rs71962921	5'flanking	4	0.2737	II/WI/WW	60/279/396	100.36/107.87/111.26	36.7/34.7/34.4	-0.57	0.0084	48.48/48.36/47.27	11.6/12.3/13.2	0.27	0.20872
APOC1p894/rs190454394	5'flanking	4	0.002	CC/CT	740/3	108.86/142.2	34.6/39.3	3.70	0.0852	47.81/50.62	12.7/21.6	0.74	0.72955
APOC1p1166/rs72654452	intron1	2b	0.0308	CC/CT/TT	715/42/2	108.8/116.01/91.06	34.2/38.4/11.9	0.49	0.3678	47.84/46.05/44.23	12.5/15.1/12.2	-0.61	0.25404
APOC1p1331/rs10408994	intron2	4	0.0666	AG/GG	98/639	113.82/108.81	32.4/34.9	0.62	0.1238	48.89/47.56	14.7/12.4	0.35	0.38621
APOC1p1526/rs5114	intron2	4	0.0579	CC/CT/TT	657/77/3	108.95/112.62/75.24	33.9/40.4/40.0	-0.05	0.9053	47.54/49.45/49.82	12.8/12.5/11.2	0.55	0.1745

Cont. Table 25

APOC1p1642	intron2	4	0.0103	CC/CT	742/16	109.44/100.1	34.6/31.8	-1.05	0.2648	47.86/45.82	12.7/11.7	-0.59	0.53986
APOC1p1684/rs12709881	intron2	4	0.0973	AA/GA/GG	8/130/617	85.21/108.63/109.75	39.5/37.5/33.9	-0.51	0.1179	47.84/49.16/47.6	8.5/12.3/12.7	0.40	0.20729
APOC1p3358	intron3	No Data	0.0021	AA/GA	706/3	109.04/105.39	35.0/16.6	-0.25	0.9068	47.78/59.16	12.8/10.3	3.44	0.10895
APOC1p3423/rs389261	intron3	No Data	0.331	AA/GA/GG	79/317/318	110.34/110.1/108.09	31.8/34.3/36.0	0.19	0.3556	48.12/48.58/47.01	12.8/14.0/11.5	0.24	0.26136
APOC1p3573/rs10424339	intron3	No Data	0.1396	AA/GA/GG	16/174/541	102.24/109.75/109.18	27.8/31.9/35.7	-0.02	0.9374	45.5/50.39/47.19	13.9/13.8/12.2	0.55	0.0455
APOC1p5006/rs112528434	intron3	No Data	0.085	GG/GT/TT	573/101/7	110.62/110.94/87.02	34.3/38.4/39.6	-0.38	0.2887	47.76/48.84/49.39	12.9/13.4/7.8	0.32	0.3879
APOC1p5053/rs12721052	intron3	No Data	0.22	DD/WD/WW	42/247/465	117.3/109.24/108.24	37.7/35.8/33.3	0.30	0.1905	46.26/47.2/48.25	12.4/13.0/12.4	-0.31	0.16174
APOC1p5667/rs12721054	3'UTR	6	0.1446	AA/GA/GG	507/163/18	111.06/107.84/87.84	34.4/37.1/28.9	-0.77	0.0063	47.56/48.09/49.87	13.0/12.9/10.7	0.23	0.42209
APOC1p5926/rs56131196	3'flanking	No Data	0.1745	AA/AG/GG	21/214/494	107.45/108.09/109.77	44.0/34.7/34.2	-0.22	0.3925	49.89/48.35/47.53	9.9/12.3/13.1	0.31	0.22541
rs4803770	HCR-1	5	0.2695	CC/GC/GG	393/278/57	108.62/108.21/121.09	33.9/34.9/36.8	0.38	0.081	48.61/47.03/47.95	12.4/13.3/11.2	-0.27	0.21475
HCR1p424/rs117664574	HCR-1	4	0.0073	AG/GG	11/733	104.69/109.12	38.8/34.6	-0.58	0.6076	54.72/47.7	13.2/12.7	2.06	0.06453
HCR1p575/rs157599	HCR-1	3a	0.3595	AA/AG/GG	282/309/92	108.34/108.93/111.46	35.5/33.9/32.7	0.17	0.4067	47.6/48.7/48.8	11.6/14.1/12.6	0.19	0.36879
rs5112	APC1P1	4	0.4797	CC/GC/GG	201/331/166	110.1/109.54/111.98	34.7/35.0/33.7	0.10	0.6073	46.88/48.82/48.57	11.9/12.2313.8	0.25	0.18503
rs7259004	APC1P1	6	0.302	CC/CG/GG	74/289/368	111.32/108/109.83	33.5/35.4/34.3	-0.02	0.9061	48.65/48.54/47.07	13.3/13.2/12.2	0.29	0.15235
HCR2p188/rs35136575	HCR-2	2a	0.1546	CC/GC/GG	530/178/25	109.72/107.36/109.53	34.7/34.6/37.3	-0.16	0.5327	47.26/49.37/46.84	12.3/13.8/13.7	0.30	0.23716
HCR2p286	HCR-2	2a	0.0457	AA/AG/GG	3/62/676	104.96/117.78/108.53	19.3/39.8/34.1	0.79	0.0785	40.61/45.9/47.95	12.9/12.6/12.8	-0.70	0.11626
HCR2p523/rs118004808	HCR-2	2b	0.0026	CC/TC	742/4	109.04/133.43	34.6/32.2	2.74	0.1418	47.78/47.96	12.7/18.0	0.02	0.99167
APOC4p368	5’ flanking	6	0.0019	TC/TT	3/749	116.63/109.09	25.2/34.7	1.04	0.6283	50.1/47.75	29.7/12.7	0.33	0.87548
APOC4p637/rs113814026	5’ flanking	No Data	0.0452	GG/GT/TT	685/68/1	109.16/110.12/33.76	34.2/35.9/NA	-0.23	0.6127	47.73/48.19/41.63	12.7/12.1/NA	0.10	0.82864
APOC4p757/rs12721105	5’ flanking	5	0.0376	GG/GT/TT	708/53/2	109.13/109.85/115.39	34.6/34.7/0.8	0.14	0.778	47.83/46.7/54.95	12.5/13.3/37.2	-0.19	0.69377
APOC4p1088	intron1	2b	0.0013	GT/TT	2/736	87.39/109.34	41.9/34.6	-2.69	0.3048	34.51/47.87	19.7/12.7	-4.26	0.10128
APOC4p1130	intron1	5	0.0007	CT/TT	1/744	100.46/109.12	NA/34.7	-0.71	0.8491	82.19/47.76	NA/12.7	9.46	0.00979
APOC4p1192/rs113745034	intron1	4	0.0124	GA/GG	18/695	104.03/109.18	39.1/34.7	-0.63	0.4823	48.92/47.83	12.4/12.9	0.35	0.69302
APOC4p1325del3	intron1	4	0.0245	WD/WW	36/706	114.84/108.99	34.4/34.6	0.70	0.2711	49.06/47.81	16.2/12.5	0.30	0.63292
APOC4p1430ins	intron1	5	0.0341	II/WI/WW	1/45/622	104.28/110.81/108.33	NA/29.3/34.8	0.32	0.5609	28.01/51.13/47.62	NA/11.9/13.2	0.69	0.22691
APOC4p2099/rs111339708	intron1	No Data	0.0141	GG/GT	735/22	109.41/102.23	34.6/36.2	-0.83	0.3026	47.75/48.85	12.7/12.7	0.35	0.6678
APOC4p2467/rs115225947	intron1	5	0.0141	GA/GG	21/736	115.18/108.98	38.8/34.4	0.68	0.4056	48.04/47.79	14.5/12.7	0.03	0.96646
APOC4p2559/rs5155	intron1	4	0.0986	CC/CT/TT	616/132/7	109.2/108.23/93.93	34.2/35.1/23.7	-0.27	0.4028	47.79/47.95/37.85	12.7/12.4/12.5	-0.20	0.53148
APOC4p2607/rs5156	intron1	4	0.0129	AG/GG	19/702	100.55/109.48	37.2/34.9	-1.04	0.235	49.11/47.76	12.5/12.8	0.43	0.62963
APOC4p2623/rs5157	intron1	4	0.1723	CC/CT/TT	506/220/20	107.96/111.8/106.4	34.5/35.4/31.9	0.28	0.2703	47.74/48.15/42.77	12.9/12.5/8.5	-0.14	0.59553
APOC4p2640/rs5158	intron1	2b	0.0213	CC/CT	723/31	108.83/113.04	34.6/31.4	0.55	0.414	47.8/46.98	12.5/15.3	-0.29	0.66191
APOC4p2678/rs148564866	intron1	2b	0.0086	GC/GG	13/726	103.53/109.31	32.1/34.7	-0.61	0.555	47.93/47.81	12.0/12.8	0.07	0.94518

Cont. Table 25

APOC4p2767/rs127721107	intron1	4	0.0254	GG/GT	697/38	109.12/112.5	34.6/36.8	0.35	0.5788	47.63/49.33	12.8/11.6	0.56	0.37292
APOC4p3348	intron1	5	0.0007	AG/GG	1/742	84.76/109.22	NA/34.6	-2.86	0.4403	90.23/47.79	NA/12.6	11.56	0.00153
APOC2p75-C4p3380/rs12721104	C4-intron1	5	0.1368	AA/GA/GG	14/174/562	106.69/109.64/108.85	29.7/36.1/34.2	0.02	0.9358	42.19/48.31/47.79	16.0/12.8/12.6	-0.11	0.69346
APOC2p194-C4p3498/rs1132899	C4-exon2	5	0.2368	CC/CT/TT	434/282/40	107.42/112.24/104.09	33.9/35.5/32.8	0.21	0.3615	47.94/47.82/46.02	12.9/12.4/12.2	-0.14	0.53341
APOC2p228/rs5164	C4-exon2	5	0.0066	AG/GA/GG	9/1/730	101.28/110.29/109.33	31.4/NA/34.7	-0.78	0.5126	48.31/21.33/47.81	11.9/NA/12.7	-0.72	0.54187
APOC2p288-C4p3592/rs12691090	C4-exon2	5	0.0272	CC/CT	698/41	109.21/109.85	34.5/38.0	-0.02	0.9753	47.64/49.98	12.8/11.9	0.75	0.21469
APOC2p396-C4p3700	C4-intron2	5	0.0007	GA/GG	1/719	68.26/109.69	NA/34.8	-4.47	0.2324	68.22/47.77	NA/12.8	5.90	0.11176
APOC2p488-C4p3792/rs5165	C4-intron2	5	0.0146	GA/GG	22/715	109.02/109.11	24.8/34.9	0.13	0.8735	47.63/47.84	12.3/12.8	-0.04	0.96019
APOC2p623-C4p3927/rs5167	C4-exon3	5	0.4594	GG/GT/TT	164/367/223	106.02/108.97/112.39	33.8/34.6/34.8	-0.37	0.0527	47.74/47.89/47.38	13.0/12.5/12.9	0.05	0.77107
APOC2p665-C4p3969/rs138548797	C4-exon3	No Data	0.0086	AA/CA	729/13	108.93/110.64	34.5/39.0	0.18	0.8649	47.81/47.51	12.8/11.9	-0.06	0.94985
APOC2p708-C4p4012	C4-exon3	6	0.0007	GA/GG	1/739	96.57/109.29	NA/34.7	-1.33	0.7212	24.53/47.82	NA/12.7	-7.15	0.05187
APOC2p853-C4p4157/rs10425530	C4-3' UTR	6	0.11	AA/GA/GG	7/153/587	95/109.14/109.57	17.7/35.7/34.4	-0.20	0.5315	46.9/48.65/47.54	14.3/12.8/12.7	0.24	0.43314
APOC2p1042-C4p4346/rs12709885	C4-3'FR/C2-5'FR	5	0.0178	AA/TA/TT	720/23/1	109.64/95.95/116.41	34.8/26.9/NA	-1.25	0.0855	47.7/51.29/53.52	12.7/11.9/NA	1.10	0.13505
APOC2p1187-C4p4491/rs111782345	C4-3'FR/C2-5'FR	5	0.0178	AG/GG	26/691	110.91/108.93	37.5/34.6	0.21	0.7773	49.54/47.8	10.1/12.9	0.58	0.44007
APOC2p1229-C4p4533/rs112698600	C4-3'FR/C2-5'FR	2b	0.014	CC/CT	714/21	109.09/107.88	34.6/38.8	-0.17	0.8398	47.74/50.43	12.7/12.0	0.83	0.31821
APOC2p1275-C4p4579/rs111356234	C4-3'FR/C2-5'FR	4	0.0352	GA/GG	52/687	101.79/109.92	30.9/34.8	-0.95	0.0752	47.4/47.82	14.6/12.6	-0.18	0.7323
APOC2p1357-C4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	0.2581	CC/GC/GG	50/288/411	113.84/112.38/106.7	35.0/35.9/33.4	0.51	0.0202	46.71/48.36/47.62	11.4/12.6/13.0	0.05	0.80869
APOC2p1540-C4p4844/rs75463753	C2-intron1	4	0.1079	AA/GA/GG	11/128/558	118.79/114.78/107.23	41.9/34.5/34.6	0.80	0.0114	47.48/47.99/47.65	14.1/11.8/13.2	0.09	0.77127
APOC2p2486/rs9304645	intron1	4	0.3655	AA/GA/GG	89/364/292	104.84/107.27/112.78	36.7/33.5/34.4	-0.54	0.0084	47.83/47.89/47.32	14.5/12.4/12.5	0.09	0.65299
APOC2p2935/rs11879392	intron1	2b	0.0135	CC/GC	707/19	108.91/116.82	34.6/39.3	0.87	0.317	47.79/49.99	12.6/17.5	0.57	0.49871
APOC2p3010/rs10419086	intron1	6	0.1253	AA/AG/GG	539/150/14	109.73/109.62/109.09	35.5/33.3/22.0	0.03	0.9215	47.78/48.88/46.09	12.7/13.8/11.1	0.15	0.62186
APOC2p3692/rs12721060	intron1	No Data	0.0172	GT/TT	23/633	107.76/109.43	37.3/34.9	-0.19	0.8123	50.36/47.98	11.5/13.0	0.76	0.3536
APOC2p3778/rs5120	intron1	4	0.1845	AA/AT/TT	500/232/23	107.58/111.87/120.21	34.8/34.2/30.3	0.60	0.0158	47.62/48.02/47.5	13.0/11.9/14.4	0.08	0.74123
APOC2p3805/rs7257095	intron1	2a	0.1649	CC/CG/GG	509/213/16	108.23/110.64/117.89	34.0/36.1/35.4	0.35	0.1883	47.93/47.64/45.13	13.0/12.1/12.5	-0.16	0.53621
APOC2p3814/rs10422603	intron1	2b	0.3008	GG/GT/TT	63/309/352	107.1/108.14/110.88	39.3/34.3/34.3	-0.30	0.1716	48.94/48.34/47.37	14.7/12.4/12.7	0.25	0.23836
APOC2p3892/rs5121	exon2	5	0.0358	CC/TC/TT	675/50/1	109.5/105.9/125.78	35.3/28.2/NA	-0.21	0.6957	47.88/47.21/57.02	12.9/10.9/NA	-0.03	0.95269
APOC2p4086/rs114780592	intron2	4	0.0278	GA/GG	42/700	109.37/109.04	37.5/34.5	-0.04	0.9509	49.23/47.69	12.5/12.7	0.49	0.40801
APOC2p4118/rs201709243	exon3	4	0.0007	GA/GG	1/722	62.68/109.3	NA/34.8	-6.14	0.1016	***	***	***	***
APOC2p4319/rs5123	intron3	No Data	0.0592	AA/GA/GG	6/74/649	112.84/110.41/109.17	21.9/34.0/34.9	0.19	0.6268	48.08/47.3/47.88	8.9/13.2/12.7	-0.14	0.71873

Cont. Table 25

APOC2p4513/rs180809422	intron3	5	0.0135	AA/AC/CC	666/17/1	108.77/115.46/90.54	34.4/35.7/NA	0.46	0.5715	47.73/50.5/52.34	12.9/12.7/NA	0.82	0.32552
APOC2p4587/rs5126	exon4	5	0.0499	AA/CA/CC	636/70/1	109.47/111.18/34.61	34.6/36.8/NA	-0.14	0.757	47.83/48.33/42.04	12.8/12.0/NA	0.12	0.80049
APOC2p4754/rs7253690	exon4	5	0.0606	AA/GA/GG	6/79/670	113.2/110.92/109.17	21.9/32.8/34.8	0.26	0.5088	47.92/47.81/47.77	8.9/13.4/12.7	-0.01	0.9801
APOC2p4853/rs150448996	3'flamking	No Data	0.2736	DD/WD/WW	386/284/57	108.19/111.6/106.19	33.5/36.4/34.6	0.10	0.6544	48.34/47.18/47.93	13.1/12.1/13.7	-0.18	0.40916
APOC2p4973/rs199828513	3'flamking	No Data	0.0082	WI/WW	12/704	96.67/109.4	35.9/34.3	-1.49	0.1714	45.89/47.98	11.4/12.9	-0.60	0.58323
APOC2p5004/rs10421404	3'flanking	No Data	0.2908	CC/CT/TT	370/326/56	111.01/107.73/106.6	34.1/34.1/38.2	-0.34	0.1149	47.43/47.85/48.84	12.6/12.4/15.5	0.16	0.46461
APOC2p5018/rs78403558	3'flanking	5	0.0352	DD/WD/WW	1/51/708	125.58/115.27/108.7	NA/36.5/34.4	0.77	0.1368	63.14/47.35/47.77	NA/15.3/12.5	0.00	0.9939
APOC2p5310/rs7258345	3'flanking	No Data	0.3067	GG/GT/TT	326/313/57	107.52/108.38/115.79	35.7/33.8/27.7	0.37	0.1018	47.88/48.51/48.08	13.3/12.6/12.4	0.11	0.61363
APOC2p5398/rs12709889	3'flanking	6	0.2587	AA/GA/GG	50/279/405	106.53/111.31/107.46	32.2/36.2/33.6	0.19	0.3893	47.86/47.3/48.09	13.7/12.0/13.2	-0.12	0.59063
APOC2p5491	3'flanking	6	0.0007	CC/TC	742/1	108.89/184.16	34.4/NA	7.19	0.053	47.76/70.37	12.7/NA	6.53	0.0762
APOC2p5512/rs12721064	3'flanking	6	0.0083	CC/CT	753/13	109.45/100.18	34.5/31.2	-1.02	0.3246	47.75/47.73	12.7/10.4	0.05	0.96332
APOC2p5562	3'flanking	No Data	0.0175	CG/GG	24/704	105.94/109.08	36.0/34.7	-0.41	0.6012	45.55/47.83	11.8/12.8	-0.67	0.37221
APOC2p5586/rs73558127	3'flanking	No Data	0.1001	GG/GT/TT	9/127/589	93.17/107.05/110.17	40.0/36.9/34.3	-0.58	0.0713	47.55/49.36/47.38	13.2/11.9/12.9	0.47	0.13813
APOC2p5771	3'flanking	6	***	***	***	***	***	***	***	45.84/47.8	13.9/12.6	-0.58	0.67563
APOC2p5815/rs10423208	3'flanking	5	0.3164	AA/GA/GG	340/323/72	108.02/108.74/117.45	35.9/34.6/28.4	0.42	0.0474	47.59/48.15/47.14	13.0/12.6/12.3	0.03	0.8759
APOC2p5922/rs10422888	3'flanking	5	0.0784	AA/AG/GG	597/99/5	107.54/119.18/97.09	34.2/35.4/41.2	0.98	0.0079	47.93/47.55/52.87	12.6/12.9/30.7	-0.01	0.98595
APOC2p5965	3'flanking	5	0.0013	GA/GG	2/743	138.11/109.1	75.9/34.5	2.76	0.295	57.22/47.78	19.5/12.7	2.75	0.29064
APOC2p6334	3'flanking	No Data	0.0096	GA/GG	15/746	123.57/109.11	26.5/34.6	1.76	0.0678	49.99/47.73	16.1/12.5	0.60	0.52729

LDL-C: low-density lipoprotein cholesterol; HDL-C: high-density lipoprotein cholesterol.

[a] Cox-Box transformed variables.

Age, Gender, Smoking, BMI, Waist, Jobmin, Staff level were included in the final model as covariates.

GTcount: genotype count; AdjMean: adjusted means; GT-SD: genotype standard deviation.

Table 26. Genotype-specific means (± SD) of TC and TG genotyped SNPs in African Blacks

						TC[a]				TG[a]			
Variant name	**Function**	**regulome db score**	**MAF**	**Genotype**	**GT Count**	**AdjMean**	**GT_SD**	**Beta**	**p_value**	**AdjMean**	**GT_SD**	**Beta**	**p_value**
APOE73/rs1081101	5'flanking	4	0.0611	CC/CT/TT	660/82/5	172.52/168.95/165.88	38.8/39.9/34.5	-0.20	0.3283	69.19/76.65/92.6	29.8/34.0/55.5	0.038	0.0093
APOE173	5'flanking	3a	0.002	AA/GA	746/3	171.99/177.58	39.0/13.7	0.41	0.7151	70.13/73.71	30.6/30.4	0.037	0.7028
APOE308/rs769445	5'flanking	4	0.0072	CC/TC	739/10	172.04/170.26	39.0/36.3	-0.06	0.9218	70.03/77.84	30.7/23.3	0.056	0.2065
APOE560/rs449647	5'flanking	5	0.3663	AA/AT/TT	300/334/105	168.65/173.25/177.78	37.3/40.2/37.3	0.25	0.0177	70.73/69.69/70.08	31.6/28.9/31.7	-0.001	0.8482
APOE618	5'flanking	4	0.0006	GC/GG	1/763	110.73/172.23	NA/38.7	-3.62	0.0634	68.05/70.26	NA/30.5	0.025	0.856
APOE624/rs769446	5'flanking	3a	0.0077	TC/TT	9/690	149.63/172.21	36.3/38.7	-1.25	0.044	69.92/70.44	27.6/30.6	0.005	0.9096
APOE832/rs405509	5'flanking	1f	0.2561	GG/GT/TT	428/267/61	169.18/176.96/170.86	38.8/39.5/34.5	0.22	0.0529	69.98/71.39/68.15	31.2/30.0/30.0	0.003	0.7457
APOE1109/rs9282609	Splice site	4	0.0415	CC/TC/TT	686/55/4	171.7/173.68/176.55	38.8/39.8/31.0	0.12	0.6321	69.83/73.46/88.67	30.5/28.6/66.8	0.023	0.1814
APOE1163/rs440446	intron1	4	0.1004	CC/CG/GG	8/126/569	170.43/175.07/172.02	34.5/39.6/39.0	0.12	0.4748	92.59/72.71/69.62	59.4/28.8/30.5	0.023	0.0537
APOE1231	intron1	2b	0.0125	GA/GG	19/729	163.93/172.25	38.1/38.9	-0.46	0.3315	67.34/70.14	38.4/30.4	-0.030	0.3441
APOE1279/rs877973	intron1	4	0.0597	AA/CA/CC	3/81/664	162.54/174.33/171.91	25.5/43.6/38.4	0.04	0.8544	60.01/64.63/70.92	23.2/26.1/31.1	-0.029	0.0513
APOE1539/rs184686013	intron1	4	0.0086	AA/AG/GG	733/11/1	171.95/169.31/139.83	38.8/39.8/NA	-0.33	0.5172	70.28/66.57/80.4	30.7/27.1/NA	0.002	0.9546
APOE2072/rs189660912	intron 2	4	0.0079	GA/GG	12/734	164.23/172.16	31.3/39.0	-0.40	0.4796	68.98/70.12	25.0/30.7	0.009	0.8229
APOE2269/rs6135770	intron 2	5	0.0169	GA/GG	25/723	160.71/172.86	35.5/38.8	-0.69	0.0771	79.21/69.84	37.5/30.0	0.040	0.1489
APOE2440/rs769450	intron 2	5	0.387	AA/AG/GG	107/308/261	175.27/173.72/170.84	42.5/39.9/37.2	0.11	0.3081	69.13/70.46/70.84	29.1/30.7/31.3	-0.003	0.7396
APOE3673/rs769453	intron 3	5	0.0066	CC/GC	738/9	171.92/169.91	38.9/37.3	-0.07	0.9054	70.23/74.25	30.7/23.4	0.037	0.4242
APOE3937/rs429358	exon 4	5	0.2656	CC/CT/TT	58/285/406	171.28/175.76/169.72	35.1/39.9/38.7	0.17	0.1323	67.14/69.52/70.98	27.5/30.9/30.7	-0.008	0.3075
APOE4036/rs769455	exon 4	5	0.02	CC/TC/TT	708/27/1	172.65/158.44/126.63	38.7/34.7/NA	-0.87	0.0129	69.45/83.67	29.8/42.8	0.056	0.0372
APOE4075/rs7412	exon 4	5	0.0605	AA/GA/GG	2/84/670	132.98/159.61/173.83	26.7/35.6/39.0	-0.82	0.0001	49.67/68.01/70.51	16.9/29.1/30.8	-0.018	0.2376
APOE4569	3'UTR	5	0.0007	GG/GT	746/1	171.93/285.01	38.7/NA	5.12	0.0089	70.08/77.54	30.6/NA	0.073	0.5976
APOE5223	3'flanking	2b	0.0051	CC/CG	758/8	172.3/153.66	38.8/21.6	-0.94	0.1738	70.38/70.64	30.7/29.6	0.006	0.9078
APOE5231	3'flanking	2b	0.027	GG/GT/TT	2/36/708	177.07/171.06/172.08	NA/40.3/38.9	-0.03	0.9208	68.24/66.1/70.39	17.7/32.2/30.6	-0.023	0.2836
rs439401	intragenic	1b	0.1092	CC/CT/TT	587/130/15	171.84/173.4/170.9	39.4/38.1/29.0	0.07	0.6621	69.35/71.64/77.45	30.2/29.1/48.4	0.011	0.3401
APOC1rs445925	intragenic	No Data	0.299	AA/GA/GG	68/310/367	171.23/172.47/172.52	39.6/36.7/39.6	-0.01	0.8983	69.27/69.27/71.63	30.9/28.9/31.9	-0.007	0.3748
APOC1p720ins4/rs71962921	5'flanking	4	0.2737	II/WI/WW	60/279/396	164.47/171.23/173.59	38.6/39.4/38.8	-0.20	0.0741	66.67/68.98/71.51	27.9/29.7/31.4	-0.013	0.1137
APOC1p894/rs190454394	5'flanking	4	0.002	CC/CT	740/3	171.74/205.36	38.8/53.9	1.71	0.1317	70.01/68.41	30.5/15.2	0.021	0.7907
APOC1p1166/rs72654452	intron1	2b	0.0308	CC/CT/TT	715/42/2	171.47/181.29/148.14	38.3/43.5/17.7	0.31	0.2783	69.6/78.54/69.87	30.0/39.4/31.8	0.028	0.163
APOC1p1331/rs10408994	intron2	4	0.0666	AG/GG	98/639	177.72/171.39	38.9/39.1	0.34	0.1116	73.13/69.81	32.7/30.4	0.016	0.2862
APOC1p1526/rs5114	intron2	4	0.0579	CC/CT/TT	657/77/3	171.74/176.03/162.64	38.4/44.1/25.5	0.12	0.5876	70.84/65.76/59.97	31.1/26.7/23.2	-0.025	0.1117

Cont. Table 26

APOC1p1642	intron2	4	0.0103	CC/CT	742/16	172.35/161.09	38.7/40.2	-0.64	0.2132	70.09/69.91	30.2/40.5	-0.019	0.5831
APOC1p1684/rs12709881	intron2	4	0.0973	AA/GA/GG	8/130/617	156.49/171.71/172.5	39.8/41.6/38.2	-0.16	0.364	70.29/66.84/70.55	42.3/28.2/30.4	-0.017	0.1541
APOC1p3358	intron3	No Data	0.0021	AA/GA	706/3	171.94/176.29	39.2/26.1	0.34	0.7632	70.07/64.64	30.7/4.6	0.003	0.9727
APOC1p3423/rs389261	intron3	No Data	0.331	AA/GA/GG	79/317/318	173.68/173.27/170.57	35.1/39.4/39.9	0.12	0.2958	70.17/69.28/71.2	29.1/29.3/32.2	-0.002	0.8116
APOC1p3573/rs10424339	intron3	No Data	0.1396	AA/GA/GG	16/174/541	164.72/174.52/171.68	36.4/36.2/39.9	0.07	0.6371	83.79/67.92/70.5	31.9/30.3/30.7	0.001	0.9096
APOC1p5006/rs112528434	intron3	No Data	0.085	GG/GT/TT	573/101/7	173.47/174.06/156.23	38.6/43.1/39.0	-0.10	0.6053	70.4/66.8/75.44	30.7/29.8/48.7	-0.018	0.1732
APOC1p5053/rs12721052	intron3	No Data	0.22	DD/WD/WW	42/247/465	178.43/172.75/171	44.3/40.3/37.1	0.13	0.2728	69.77/71.12/69.87	29.5/31.2/30.3	0.004	0.6524
APOC1p5667/rs12721054	3'UTR	6	0.1446	AA/GA/GG	507/163/18	173.87/170.98/153.32	38.8/41.5/31.7	-0.30	0.0474	72.28/66.04/65.85	31.3/27.9/31.8	-0.028	0.007
APOC1p5926/rs56131196	3'flanking	No Data	0.1745	AA/AG/GG	21/214/494	170.86/171.58/172.33	41.2/39.1/38.7	-0.05	0.7296	60.05/68.66/71.08	25.6/30.4/30.9	-0.019	0.0442
rs4803770	HCR-1	5	0.2695	CC/GC/GG	393/278/57	171.64/170.95/185.27	38.0/39.2/42.8	0.18	0.1102	69.84/69.66/74.13	30.4/29.8/36.3	0.005	0.5732
HCR1p424/rs117664574	HCR-1	4	0.0073	AG/GG	11/733	174.18/171.92	39.3/38.9	0.12	0.8344	72.62/70.09	24.5/30.7	0.025	0.5525
HCR1p575/rs157599	HCR-1	3a	0.3595	AA/AG/GG	282/309/92	171.82/172.01/175.29	38.9/39.5/34.8	0.08	0.469	71.87/68.48/70.03	33.0/28.6/29.2	-0.004	0.6132
rs5112	APC1P1	4	0.4797	CC/GC/GG	201/331/166	171.13/173.37/177.09	39.3/38.4/37.2	0.16	0.1091	68.98/70.65/72.02	31.9/29.7/32.1	0.010	0.1818
rs7259004	APC1P1	6	0.302	CC/CG/GG	74/289/368	176.55/171.72/171.5	37.8/39.2/39.1	0.09	0.3976	70.51/70.37/69.79	29.6/30.0/31.5	0.006	0.4328
HCR2p188/rs35136575	HCR-2	2a	0.1546	CC/GC/GG	530/178/25	171.86/171.73/172.93	39.1/38.8/40.7	0.01	0.9184	69.43/71.86/64.97	30.2/31.6/26.4	0.005	0.604
HCR2p286	HCR-2	2a	0.0457	AA/AG/GG	3/62/676	153.32/180.43/171.37	28.6/41.5/38.7	0.31	0.1847	45.01/77.9/69.6	8.3/34.1/30.2	0.026	0.1292
HCR2p523/rs118004808	HCR-2	2b	0.0026	CC/TC	742/4	171.93/194.43	38.8/44.3	1.17	0.2362	70.19/71.25	30.6/13.4	0.034	0.6289
APOC4p368	5' flanking	6	0.0019	TC/TT	3/749	184.54/171.95	37.8/38.9	0.71	0.529	88.72/70.33	37.2/30.6	0.088	0.2641
APOC4p637/rs113814026	5' flanking	No Data	0.0452	GG/GT/TT	685/68/1	172.06/172.49/85.95	38.6/38.1/NA	-0.13	0.5832	70.59/69.02/44.6	30.7/30.9/NA	-0.013	0.4457
APOC4p757/rs12721105	5' flanking	5	0.0376	GG/GT/TT	708/53/2	171.91/173.9/184.62	38.6/40.0/43.8	0.13	0.6192	69.34/84.01/72.01	30.0/36.9/29.0	0.063	0.0005
APOC4p1088	intron1	2b	0.0013	GT/TT	2/736	146.52/172.31	48.8/38.9	-1.51	0.2767	113.92/70.15	63.6/30.5	0.182	0.0633
APOC4p1130	intron1	5	0.0007	CT/TT	1/744	198.57/171.99	NA/38.9	1.50	0.4435	83.99/70.21	NA/30.6	0.097	0.48
APOC4p1192/rs113745034	intron1	4	0.0124	GA/GG	18/695	166.8/172.17	44.7/38.9	-0.31	0.5056	70.29/70.26	39.1/30.5	-0.008	0.8015
APOC4p1325del3	intron1	4	0.0245	WD/WW	36/706	176.47/171.96	35.7/39.0	0.28	0.4099	61.96/70.6	22.0/30.9	-0.040	0.0909
APOC4p1430ins	intron1	5	0.0341	II/WI/WW	1/45/622	144.75/178.76/170.96	NA/35.8/39.2	0.35	0.229	63.94/67.93/70.05	NA/28.8/30.6	-0.009	0.6459
APOC4p2099/rs111339708	intron1	No Data	0.0141	GG/GT	735/22	172.27/164.72	38.7/42.9	-0.42	0.3367	70.28/66.38	30.0/38.0	-0.033	0.2745
APOC4p2467/rs115225947	intron1	5	0.0141	GA/GG	21/736	177.8/171.89	42.9/38.7	0.30	0.4923	62.56/70.49	20.4/30.8	-0.027	0.3794
APOC4p2559/rs5155	intron1	4	0.0986	CC/CT/TT	616/132/7	172.28/170.33/144.83	38.3/39.3/30.3	-0.22	0.209	70.33/69.56/74.26	29.8/32.4/41.2	-0.008	0.4908
APOC4p2607/rs5156	intron1	4	0.0129	AG/GG	19/702	163.6/172.41	43.8/39.0	-0.49	0.2981	68.08/70.39	40.6/30.6	-0.029	0.3791
APOC4p2623/rs5157	intron1	4	0.1723	CC/CT/TT	506/220/20	170.66/175.33/164.71	39.3/38.4/35.3	0.13	0.3287	70.08/69.51/75.22	30.0/29.4/41.4	0.001	0.9481
APOC4p2640/rs5158	intron1	2b	0.0213	CC/CT	723/31	171.84/171.36	38.8/33.7	0.01	0.9712	70.51/59.46	30.5/19.6	-0.052	0.0353
APOC4p2678/rs148564866	intron1	2b	0.0086	GC/GG	13/726	165.62/172.23	32.1/39.1	-0.31	0.584	77.27/70	31.2/30.4	0.041	0.288

Cont. Table 26

APOC4p2767/rs127721107	intron1	4	0.0254	GG/GT	697/38	171.99/175.77	38.7/44.1	0.16	0.6279	70.58/68.95	30.7/29.5	-0.007	0.7599
APOC4p3348	intron1	5	0.0007	AG/GG	1/742	183.75/172.05	NA/39.0	0.74	0.7067	35.82/70.21	NA/30.6	-0.230	0.0947
APOC2p75-C4p3380/rs12721104	C4-intron1	5	0.1368	AA/GA/GG	14/174/562	165.15/172.76/171.78	39.0/40.5/38.2	-0.01	0.9244	81.44/72.36/69.17	46.0/32.2/29.2	0.015	0.1633
APOC2p194-C4p3498/rs1132899	C4-exon2	5	0.2368	CC/CT/TT	434/282/40	170.08/175.69/164.97	39.0/38.7/34.4	0.11	0.3546	70.04/70.4/68.5	30.1/30.0/33.0	-0.001	0.8783
APOC2p228/rs5164	C4-exon2	5	0.0066	AG/GA/GG	9/1/730	164.83/154.22/172.26	34.6/NA/39.1	-0.43	0.4953	78.63/113.47/70.16	42.0/NA/30.4	0.036	0.4138
APOC2p288-C4p3592/rs12691090	C4-exon2	5	0.0272	CC/CT	698/41	172.07/173.5	38.7/45.2	0.02	0.9419	70.45/68.6	30.7/28.8	-0.008	0.7262
APOC2p396-C4p3700	C4-intron2	5	0.0007	GA/GG	1/719	144.11/172.63	NA/39.2	-1.40	0.4802	40.57/70.3	NA/30.6	-0.139	0.3161
APOC2p488-C4p3792/rs5165	C4-intron2	5	0.0146	GA/GG	22/715	169.39/172.03	26.1/39.4	-0.07	0.8663	63.29/70.23	20.8/30.9	-0.025	0.4059
APOC2p623-C4p3927/rs5167	C4-exon3	5	0.4594	GG/GT/TT	164/367/223	168.86/171.92/174.54	38.9/39.2/37.7	-0.16	0.1057	70.36/70.44/68.91	28.6/30.5/31.1	0.007	0.3421
APOC2p665-C4p3969/rs138548797	C4-exon3	No Data	0.0086	AA/CA	729/13	171.82/172.47	38.8/45.3	0.00	0.9938	70/73.28	30.5/41.2	0.017	0.6686
APOC2p708-C4p4012	C4-exon3	6	0.0007	GA/GG	1/739	145.97/172.21	NA/38.9	-1.34	0.4936	136.39/70.13	NA/30.6	0.287	0.0381
APOC2p853-C4p4157/rs10425530	C4-3' UTR	6	0.11	AA/GA/GG	7/153/587	154.39/172.94/172.12	19.7/41.6/38.2	-0.06	0.7051	68.14/70.48/70.05	43.0/31.0/29.9	-0.004	0.7518
APOC2p1042-C4p4346/rs12709885	C4-3'FR/C2-5'FR	5	0.0178	AA/TA/TT	720/23/1	172.53/159.97/173.87	39.1/31.2/NA	-0.55	0.1548	70.31/66.75/39.45	30.5/32.9/NA	-0.035	0.1866
APOC2p1187-C4p4491/rs111782345	C4-3'FR/C2-5'FR	5	0.0178	AG/GG	26/691	175.33/171.82	43.6/38.8	0.17	0.6739	69.46/70.07	36.6/30.3	-0.013	0.6376
APOC2p1229-C4p4533/rs112698600	C4-3'FR/C2-5'FR	2b	0.014	CC/CT	714/21	171.91/173.08	38.9/45.0	0.04	0.9328	70.05/69.98	30.2/37.8	-0.007	0.8154
APOC2p1275-C4p4579/rs111356234	C4-3'FR/C2-5'FR	4	0.0352	GA/GG	52/687	163.72/172.87	33.9/39.2	-0.48	0.0954	72.04/70.06	33.8/30.4	0.006	0.7493
APOC2p1357-C4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	0.2581	CC/GC/GG	50/288/411	175.4/176.37/169.04	37.4/39.7/38.1	0.28	0.0153	65.22/70.65/70.21	30.3/31.5/30.0	-0.007	0.3614
APOC2p1540-C4p4844/rs75463753	C2-intron1	4	0.1079	AA/GA/GG	11/128/558	185.45/177.57/169.95	36.9/38.3/39.1	0.42	0.0111	75.36/68.12/70.53	26.4/30.9/30.3	-0.008	0.5
APOC2p2486/rs9304645	intron1	4	0.3655	AA/GA/GG	89/364/292	169.03/170.07/174.92	40.7/37.6/39.2	-0.20	0.0737	74.7/70.34/68.75	32.0/31.3/28.9	0.011	0.1406
APOC2p2935/rs11879392	intron1	2b	0.0135	CC/GC	707/19	171.98/177.14	39.0/41.7	0.27	0.5399	70.68/56.3	31.0/15.3	-0.069	0.0285
APOC2p3010/rs10419086	intron1	6	0.1253	AA/AG/GG	539/150/14	172.94/171.72/170.36	39.8/38.0/28.3	-0.05	0.7439	70.9/64.67/80.16	30.9/24.1/47.0	-0.017	0.1272
APOC2p3692/rs12721060	intron1	No Data	0.0172	GT/TT	23/633	171.96/172.46	43.3/39.3	-0.04	0.9297	67.99/70.4	36.3/30.8	-0.015	0.6229
APOC2p3778/rs5120	intron1	4	0.1845	AA/AT/TT	500/232/23	170.12/175.39/183.12	39.3/38.1/30.7	0.33	0.0129	70.55/69.54/73.52	30.5/29.8/37.5	-0.0001	0.9937
APOC2p3805/rs7257095	intron1	2a	0.1649	CC/CG/GG	509/213/16	171.27/172.82/181.24	38.3/40.8/33.6	0.13	0.3551	70.52/69.28/62.61	32.0/27.7/21.0	-0.003	0.7465
APOC2p3814/rs10422603	intron1	2b	0.3008	GG/GT/TT	63/309/352	171.23/171.5/173.16	45.9/37.8/38.8	-0.08	0.4714	73.55/70.31/68.57	31.9/30.5/29.8	0.012	0.1454
APOC2p3892/rs5121	exon2	5	0.0358	CC/TC/TT	675/50/1	172.5/167.84/201.55	39.7/28.7/NA	-0.11	0.6979	70.57/68.38/86.62	31.2/26.5/NA	0.004	0.8416
APOC2p4086/rs114780592	intron2	4	0.0278	GA/GG	42/700	172.27/171.92	43.0/38.7	-0.02	0.9506	68.73/70.31	28.2/30.8	-0.004	0.8486

Cont. Table 26

APOC2p4118/rs201709243	exon3	4	0.0007	GA/GG	1/722	179.84/172.13	NA/39.1	0.52	0.7926	***	***	***	***
APOC2p4319/rs5123	intron3	No Data	0.0592	AA/GA/GG	6/74/649	176.63/174.09/171.69	17.9/38.9/39.1	0.15	0.4796	79.96/66.14/70.1	30.0/28.4/30.6	-0.008	0.6025
APOC2p4513/rs180809422	intron3	5	0.0135	AA/AC/CC	666/17/1	171.48/182.63/147.07	38.7/42.8/NA	0.34	0.438	69.7/74.06/39.14	30.2/40.3/NA	-0.021	0.5011
APOC2p4587/rs5126	exon4	5	0.0499	AA/CA/CC	636/70/1	172.47/174.05/87.92	39.1/39.1/NA	-0.07	0.771	70.44/69.87/43.72	30.8/32.5/NA	-0.011	0.5193
APOC2p4754/rs7253690	exon4	5	0.0606	AA/GA/GG	6/79/670	176.79/176.46/171.75	17.9/37.8/38.9	0.25	0.2212	80.33/67.52/70.67	30.0/28.0/30.9	-0.004	0.787
APOC2p4853/rs150448996	3'flamking	No Data	0.2736	DD/WD/WW	386/284/57	171.97/173.3/169.32	37.4/40.9/41.4	-0.02	0.8445	70.45/70.09/69.45	32.4/28.1/31.5	0.001	0.9083
APOC2p4973/rs199828513	3'flamking	No Data	0.0082	WI/WW	12/704	158.47/172.45	42.8/38.5	-0.79	0.1664	76.49/70.11	46.3/30.4	0.010	0.8053
APOC2p5004/rs10421404	3'flanking	No Data	0.2908	CC/CT/TT	370/326/56	173.36/170.73/171	38.5/37.8/44.3	-0.11	0.3371	69.07/71.11/74.63	29.8/31.4/32.8	0.011	0.1599
APOC2p5018/rs78403558	3'flanking	5	0.0352	DD/WD/WW	1/51/708	201.27/176.34/171.67	NA/39.6/38.7	0.30	0.2761	63.63/64.03/70.79	NA/21.8/31.1	-0.024	0.2111
APOC2p5310/rs7258345	3'flanking	No Data	0.3067	GG/GT/TT	326/313/57	170.54/172.14/177.55	40.3/38.2/29.6	0.17	0.1497	70.87/69.31/68.65	29.8/31.4/33.4	-0.010	0.216
APOC2p5398/rs12709889	3'flanking	6	0.2587	AA/GA/GG	50/279/405	169.1/173.21/171.05	37.8/40.8/37.6	0.02	0.8441	66.62/70.44/70.46	28.7/28.3/32.4	-0.001	0.9294
APOC2p5491	3'flanking	6	0.0007	CC/TC	742/1	171.71/265.05	38.6/NA	4.21	0.0315	70.01/55.11	30.5/NA	-0.040	0.775
APOC2p5512/rs12721064	3'flanking	6	0.0083	CC/CT	753/13	172.17/170.04	38.7/35.3	-0.10	0.8634	70.02/87.21	30.5/33.9	0.087	0.0297
APOC2p5562	3'flanking	No Data	0.0175	CG/GG	24/704	168.35/171.94	38.4/39.0	-0.21	0.5949	67.09/70.25	31.1/30.5	-0.015	0.6109
APOC2p5586/rs73558127	3'flanking	No Data	0.1001	GG/GT/TT	9/127/589	154.43/170.57/172.77	45.8/40.7/38.7	-0.23	0.1778	80.41/67.13/70.25	39.2/30.0/29.8	-0.008	0.485
APOC2p5771	3'flanking	6	***	***	***	***	***	***	***	78.25/70.26	39.4/30.4	0.031	0.5541
APOC2p5815/rs10423208	3'flanking	5	0.3164	AA/GA/GG	340/323/72	170.83/172.31/178	40.4/39.2/30.3	0.18	0.117	70.84/70.33/67.09	29.8/31.1/32.8	-0.010	0.203
APOC2p5922/rs10422888	3'flanking	5	0.0784	AA/AG/GG	597/99/5	170.44/182.24/164.13	38.3/40.1/51.6	0.48	0.0129	69.37/72.64/72.93	30.1/31.3/31.5	0.015	0.2582
APOC2p5965	3'flanking	5	0.0013	GA/GG	2/743	208.01/171.97	93.3/38.7	1.58	0.2542	61.69/70.14	10.6/30.6	-0.006	0.9512
APOC2p6334	3'flanking	No Data	0.0096	GA/GG	15/746	188.71/171.92	31.0/38.7	0.94	0.0628	73.45/70.12	28.7/30.6	0.014	0.6886

TG:triglyceride; TC: total cholesterol; [a] Cox-Box transformed variables; Age, Gender, Smoking, BMI, Waist, Jobmin, Staff level were included in the final model as covariates.GTcount: genotype count; AdjMean: adjusted means; GT-SD: genotype standard deviation.

Table 27. Genotype-specific means (± SD) of ApoB and ApoA1 genotyped SNPs in African Blacks

						ApoB[a]				ApoA1[a]			
Variant name	**Function**	**regulome db score**	**MAF**	**Genotype**	**GT Count**	**AdjMean**	**GT_SD**	**Beta**	**p_value**	**AdjMean**	**GT_SD**	**Beta**	**p_value**
APOE73/rs1081101	5'flanking	4	0.0611	CC/CT/TT	660/82/5	66.45/67.4/73.43	21.5/24.7/7.9	0.65	0.54877	136.86/138.93/121.99	27.3/30.5/23.6	-0.003	0.99719
APOE173	5'flanking	3a	0.002	AA/GA	746/3	66.5/72.76	21.8/14.2	3.20	0.59226	136.65/157.72	27.6/32.9	6.86	0.19127
APOE308/rs769445	5'flanking	4	0.0072	CC/TC	739/10	66.47/70.18	21.8/21.5	1.87	0.55135	136.6/146.23	27.6/28.1	3.21	0.2461
APOE560/rs449647	5'flanking	5	0.3663	AA/AT/TT	300/334/105	65.41/66.78/69.26	22.9/21.9/18.9	0.92	0.09509	137.15/136.83/133.49	28.1/27.1/30.4	-0.49	0.31886
APOE618	5'flanking	4	0.0006	GC/GG	1/763	74.68/66.72	NA/21.8	4.15	0.68762	83.01/136.66	NA/27.7	-18.42	0.04342
APOE624/rs769446	5'flanking	3a	0.0077	TC/TT	9/690	57.76/66.77	13.5/21.9	-4.19	0.20373	146.85/136.47	18.7/27.9	3.55	0.20204
APOE832/rs405509	5'flanking	1f	0.2561	GG/GT/TT	428/267/61	65.72/68.69/66.11	21.6/22.1/21.5	0.66	0.26113	137.58/136.56/132.03	28.2/27.3/26.8	-0.67	0.19928
APOE1109/rs9282609	Splice site	4	0.0415	CC/TC/TT	686/55/4	66.07/71.5/56.8	21.4/24.4/28.8	1.38	0.27683	136.58/139.25/126.95	27.4/32.1/27.3	0.24	0.83418
APOE1163/rs440446	intron1	4	0.1004	CC/CG/GG	8/126/569	73.38/71.01/66.01	15.1/22.5/21.6	2.30	0.01093	131.72/136.2/137.15	25.8/27.4/27.9	-0.44	0.58046
APOE1231	intron1	2b	0.0125	GA/GG	19/729	62.87/66.6	18.1/21.9	-1.71	0.47484	133.54/136.87	28.3/27.6	-1.12	0.59594
APOE1279/rs877973	intron1	4	0.0597	AA/CA/CC	3/81/664	51.79/67.05/66.53	6.6/24.2/21.6	-0.45	0.68467	129.68/140.9/136.39	33.5/25.8/27.8	1.06	0.27597
APOE1539/rs184686013	intron1	4	0.0086	AA/AG/GG	733/11/1	66.43/70.12/48.6	21.8/20.5/NA	0.23	0.93296	136.35/156.58/122.97	27.6/31.3/NA	4.24	0.0738
APOE2072/rs189660912	intron 2	4	0.0079	GA/GG	12/734	67.45/66.55	10.5/22.0	0.70	0.81486	133.01/136.88	31.9/27.7	-1.35	0.61188
APOE2269/rs6135770	intron 2	5	0.0169	GA/GG	25/723	61.69/66.98	19.9/21.8	-2.56	0.22005	140/136.7	29.2/27.8	1.09	0.55027
APOE2440/rs769450	intron 2	5	0.387	AA/AG/GG	107/308/261	65.5/67.83/67.87	22.4/21.8/20.9	-0.50	0.37248	134.99/138.74/137.19	26.9/28.3/28.4	-0.17	0.73856
APOE3673/rs769453	intron 3	5	0.0066	CC/GC	738/9	66.4/70.47	21.7/22.5	2.02	0.5386	136.5/148.37	27.7/28.4	3.93	0.17574
APOE3937/rs429358	exon 4	5	0.2656	CC/CT/TT	58/285/406	65.25/67.46/66.46	20.4/22.6/21.6	0.05	0.9371	128.85/136.59/137.88	25.0/27.5/28.2	-1.00	0.05924
APOE4036/rs769455	exon 4	5	0.02	CC/TC/TT	708/27/1	66.89/60.39/48.19	21.7/22.7/NA	-3.45	0.06644	136.77/138.61/79.6	27.4/27.5/NA	-0.71	0.66412
APOE4075/rs7412	exon 4	5	0.0605	AA/GA/GG	2/84/670	45.96/63.02/67.16	27.7/18.2/22.2	-2.35	0.03564	172.7/145.92/135.3	47.7/26.7/27.4	3.85	0.00008
APOE4569	3'UTR	5	0.0007	GG/GT	746/1	66.46/96.65	21.8/NA	14.25	0.1684	136.83/185.08	27.7/NA	15.53	0.08835
APOE5223	3'flanking	2b	0.0051	CC/CG	758/8	66.75/61.28	21.9/17.7	-2.54	0.51655	136.65/140.31	27.7/22.0	1.29	0.70886
APOE5231	3'flanking	2b	0.027	GG/GT/TT	2/36/708	50.22/66.27/66.55	17.5/21.6/21.9	-0.82	0.60359	125.57/138.13/136.85	88.2/22.9/27.8	-0.03	0.98493
rs439401	intragenic region	1b	0.1092	CC/CT/TT	587/130/15	65.65/69.73/66.92	21.8/22.6/17.8	1.42	0.0862	137.09/135.48/134.62	27.8/27.8/25.6	-0.50	0.50161
APOC1rs445925	intragenic region	No Data	0.299	AA/GA/GG	68/310/367	67.55/65.84/67.5	23.1/21.2/22.2	-0.31	0.59161	137.99/137.53/136.18	27.3/27.7/28.1	0.36	0.48026
APOC1p720ins4/rs71962921	5'flanking	4	0.2737	II/WI/WW	60/279/396	62.61/65.77/67.67	21.4/21.6/22.1	-1.10	0.06438	135.77/140.58/134.24	24.5/27.4/28.3	1.03	0.04836
APOC1p894/rs190454394	5'flanking	4	0.002	CC/CT	740/3	66.39/83.3	21.8/18.1	8.19	0.17048	136.85/137.78	27.7/28.4	0.40	0.93927
APOC1p1166/rs72654452	intron1	2b	0.0308	CC/CT/TT	715/42/2	66.43/69.71/58.03	21.8/23.5/6.5	0.98	0.51091	136.77/133.56/128.31	27.8/27.3/12.3	-1.09	0.40589

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APOC1p1331/rs10408994	intron2	4	0.0666	AG/GG	98/639	65.22/66.91	20.9/22.0	-0.83	0.46727	134.89/136.82	29.1/27.5	-0.66	0.50656
APOC1p1526/rs5114	intron2	4	0.0579	CC/CT/TT	657/77/3	66.45/67.64/51.76	21.6/24.8/6.6	-0.22	0.84865	136.21/141.93/129.69	28.0/26.1/33.5	1.38	0.165
APOC1p1642	intron2	4	0.0103	CC/CT	742/16	66.75/62.78	21.9/19.4	-1.86	0.47702	136.9/131.29	27.7/29.6	-1.90	0.4104
APOC1p1684/rs12709881	intron2	4	0.0973	AA/GA/GG	8/130/617	49.71/65.76/67	9.7/23.1/21.7	-1.48	0.09465	128.67/140.21/136.26	23.6/26.2/28.0	0.73	0.34454
APOC1p3358	intron3	No Data	0.0021	AA/GA	706/3	66.41/59	22.0/31.7	-3.96	0.50955	136.79/129.19	28.0/16.1	-2.34	0.6601
APOC1p3423/rs389261	intron3	No Data	0.331	AA/GA/GG	79/317/318	65.53/67.06/66.54	20.1/21.6/22.6	-0.04	0.94719	133.68/137.66/137.23	29.8/28.0/26.9	-0.36	0.48713
APOC1p3573/rs10424339	intron3	No Data	0.1396	AA/GA/GG	16/174/541	63.34/65.58/67.09	14.8/19.7/22.7	-0.71	0.36467	128.38/139.71/136.32	19.1/29.5/27.3	0.40	0.55931
APOC1p5006/rs112528434	intron3	No Data	0.085	GG/GT/TT	573/101/7	67.71/67.25/49.23	21.7/22.7/9.0	-1.22	0.2099	136.73/139.26/137.09	27.9/28.5/15.1	0.67	0.44123
APOC1p5053/rs12721052	intron3	No Data	0.22	DD/WD/WW	42/247/465	70.33/66.93/66.24	22.6/21.8/21.9	0.66	0.29256	133.78/136.4/137.22	24.3/28.9/27.0	-0.42	0.4506
APOC1p5667/rs12721054	3'UTR	6	0.1446	AA/GA/GG	507/163/18	67.33/67.34/55.54	21.9/21.2/19.3	-1.01	0.18808	135.85/140.83/134.9	28.3/26.6/29.6	1.01	0.14096
APOC1p5926/rs56131196	3'flanking	No Data	0.1745	AA/AG/GG	21/214/494	58.05/66.99/66.81	26.0/21.8/21.8	-0.70	0.33774	141.08/138.62/136.05	25.0/27.1/28.2	0.87	0.17334
rs4803770	HCR-1	5	0.2695	CC/GC/GG	393/278/57	65.83/66.43/71.57	21.7/21.6/24.4	0.90	0.13554	137.95/135.57/136.07	26.5/30.1/24.9	-0.53	0.32036
HCR1p424/rs117664574	HCR-1	4	0.0073	AG/GG	11/733	71.83/66.46	37.0/21.6	2.07	0.5106	154.41/136.55	36.0/27.5	5.74	0.04801
HCR1p575/rs157599	HCR-1	3a	0.3595	AA/AG/GG	282/309/92	66.91/66.92/68.27	22.7/20.7/22.2	0.27	0.64249	139.3/136.05/136.6	27.1/28.9/26.5	-0.63	0.22016
rs5112	APC1P1	4	0.4797	CC/GC/GG	201/331/166	66.7/67.09/68.92	22.6/21.7/21.6	0.54	0.31703	133.36/139.51/137.98	26.1/29.0/27.0	0.80	0.0924
rs7259004	APC1P1	6	0.302	CC/CG/GG	74/289/368	67.71/66.77/66.22	19.5/21.6/22.6	0.37	0.51449	138.36/138.41/134.76	30.2/25.5/28.8	0.83	0.10102
HCR2p188/rs35136575	HCR-2	2a	0.1546	CC/GC/GG	530/178/25	67.35/63.27/73.02	22.0/21.2/22.5	-0.61	0.4015	135.93/138.83/139.95	27.5/28.4/22.1	0.85	0.18117
HCR2p286	HCR-2	2a	0.0457	AA/AG/GG	3/62/676	39.84/72.35/66.09	25.4/23.5/21.6	1.37	0.27692	99.8/138.38/136.61	39.6/28.1/27.5	-0.59	0.59403
HCR2p523/rs118004808	HCR-2	2b	0.0026	CC/TC	742/4	66.44/80.18	21.9/14.8	6.71	0.19588	136.79/135.78	27.8/23.2	-0.21	0.96328
APOC4p368	5’ flanking	6	0.0019	TC/TT	3/749	63.48/66.95	3.8/21.7	-1.39	0.81479	135.24/136.61	47.1/27.7	-0.69	0.8967
APOC4p637/rs113814026	5’ flanking	No Data	0.0452	GG/GT/TT	685/68/1	66.4/69.81/52.26	21.5/23.3/NA	1.34	0.29549	136.63/138.36/93.9	27.8/26.0/NA	0.14	0.90262
APOC4p757/rs12721105	5’ flanking	5	0.0376	GG/GT/TT	708/53/2	66.65/67.05/74.54	21.9/21.2/2.9	0.45	0.7436	137.13/132.16/137.02	27.9/24.5/52.0	-1.40	0.23935
APOC4p1088	intron1	2b	0.0013	GT/TT	2/736	61.84/66.56	12.6/21.9	-2.07	0.7775	122.5/136.86	33.6/27.8	-4.80	0.45794
APOC4p1130	intron1	5	0.0007	CT/TT	1/744	25.33/66.55	NA/21.8	-21.03	0.04207	181.19/136.78	NA/27.7	14.38	0.11483
APOC4p1192/rs113745034	intron1	4	0.0124	GA/GG	18/695	72.18/66.29	25.1/21.8	2.83	0.26681	146.73/136.51	24.1/28.1	3.44	0.12841
APOC4p1325del3	intron1	4	0.0245	WD/WW	36/706	69.67/66.4	18.1/22.0	1.71	0.33255	136.28/136.88	34.2/27.3	-0.31	0.84012
APOC4p1430ins	intron1	5	0.0341	II/WI/WW	1/45/622	74.06/68.25/65.56	NA/21.6/22.1	1.43	0.35841	92.72/146.32/135.42	NA/24.5/28.2	2.68	0.05543
APOC4p2099/rs111339708	intron1	No Data	0.0141	GG/GT	735/22	66.63/69.07	21.8/23.8	1.19	0.59549	136.41/145.3	27.9/22.1	3.04	0.13403
APOC4p2467/rs115225947	intron1	5	0.0141	GA/GG	21/736	65.91/66.7	24.1/21.9	-0.42	0.85407	129.33/136.92	28.4/27.7	-2.52	0.2125
APOC4p2559/rs5155	intron1	4	0.0986	CC/CT/TT	616/132/7	66.99/65/61.61	22.2/20.6/13.4	-0.98	0.27438	137.4/134.05/118.2	27.6/28.4/21.3	-1.47	0.06609
APOC4p2607/rs5156	intron1	4	0.0129	AG/GG	19/702	69.78/66.44	24.9/21.9	1.60	0.50775	147.1/136.41	23.5/28.1	3.60	0.10172
APOC4p2623/rs5157	intron1	4	0.1723	CC/CT/TT	506/220/20	65.29/70.07/63.46	21.6/22.7/15.2	1.43	0.04428	135.23/140.47/127.95	27.9/27.0/25.3	0.78	0.21466

Cont. Table 27

APOC4p2640/rs5158	intron1	2b	0.0213	CC/CT	723/31	66.45/69.11	22.0/17.3	1.44	0.44596	136.85/133.75	27.5/32.3	-1.12	0.4997
APOC4p2678/rs148564866	intron1	2b	0.0086	GC/GG	13/726	68.5/66.46	27.4/21.7	0.87	0.76308	145.03/136.63	35.1/27.6	2.67	0.29564
APOC4p2767/rs127721107	intron1	4	0.0254	GG/GT	697/38	66.3/72.91	21.7/25.5	3.15	0.07284	136.45/143.13	27.6/30.5	2.17	0.1601
APOC4p3348	intron1	5	0.0007	AG/GG	1/742	46/66.52	NA/21.9	-9.98	0.33555	181.29/136.74	NA/27.6	14.52	0.11008
APOC2p75-C4p3380/rs12721104	C4-intron1	5	0.1368	AA/GA/GG	14/174/562	66.87/66.3/66.63	14.1/21.7/22.2	-0.07	0.92847	119.74/135.5/137.55	23.1/27.2/27.9	-1.25	0.06839
APOC2p194-C4p3498/rs1132899	C4-exon2	5	0.2368	CC/CT/TT	434/282/40	65.25/68.96/64.74	21.6/22.9/15.7	0.95	0.13191	134.91/140.58/133.11	27.4/27.5/29.4	0.88	0.11098
APOC2p228/rs5164	C4-exon2	5	0.0066	AG/GA/GG	9/1/730	71.19/78.12/66.48	29.3/NA/21.8	2.49	0.4501	151.28/103.03/136.67	18.4/NA/27.8	3.31	0.25501
APOC2p288-C4p3592/rs12691090	C4-exon2	5	0.0272	CC/CT	698/41	66.31/70.55	21.7/25.9	1.96	0.24561	136.44/142.55	27.6/29.1	2.00	0.17721
APOC2p396-C4p3700	C4-intron2	5	0.0007	GA/GG	1/719	47.55/66.81	NA/21.9	-9.04	0.38386	172.07/136.63	NA/27.9	11.51	0.21156
APOC2p488-C4p3792/rs5165	C4-intron2	5	0.0146	GA/GG	22/715	64.63/66.62	17.4/22.0	-0.83	0.71058	132.2/136.93	25.4/27.7	-1.54	0.43321
APOC2p623-C4p3927/rs5167	C4-exon3	5	0.4594	GG/GT/TT	164/367/223	63.91/68.02/66.36	22.8/22.5/20.1	-0.54	0.31017	134.53/138.92/134.05	27.8/27.4/27.7	0.19	0.6794
APOC2p665-C4p3969/rs138548797	C4-exon3	No Data	0.0086	AA/CA	729/13	66.32/75.01	21.8/26.4	4.09	0.15807	136.97/130.35	27.8/18.5	-2.07	0.41707
APOC2p708-C4p4012	C4-exon3	6	0.0007	GA/GG	1/739	79.3/66.53	NA/21.9	6.46	0.53306	108.23/136.83	NA/27.7	-9.42	0.30174
APOC2p853-C4p4157/rs10425530	C4-3' UTR	6	0.11	AA/GA/GG	7/153/587	58.99/66.53/66.84	17.7/24.4/21.2	-0.53	0.5399	123.03/141.36/135.63	37.6/28.3/27.4	1.17	0.12757
APOC2p1042-C4p4346/rs12709885	C4-3'FR/C2-5'FR	5	0.0178	AA/TA/TT	720/23/1	66.89/57.22/62.23	21.6/26.5/NA	-4.39	0.02431	136.16/156.91/140.36	27.5/29.9/NA	5.95	0.00071
APOC2p1187-C4p4491/rs111782345	C4-3'FR/C2-5'FR	5	0.0178	AG/GG	26/691	72.68/66.23	21.6/21.8	3.17	0.13276	146.19/136.63	22.5/28.0	3.23	0.08379
APOC2p1229-C4p4533/rs112698600	C4-3'FR/C2-5'FR	2b	0.014	CC/CT	714/21	66.32/72.07	21.8/24.4	2.78	0.23927	136.53/145.91	27.9/20.9	3.20	0.12314
APOC2p1275-C4p4579/rs111356234	C4-3'FR/C2-5'FR	4	0.0352	GA/GG	52/687	66.08/66.63	20.4/22.0	-0.23	0.87888	137.8/136.61	30.2/27.6	0.35	0.79182
APOC2p1357-C4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	0.2581	CC/GC/GG	50/288/411	66.99/69.37/64.75	17.8/22.7/21.3	1.37	0.02344	130.59/141.26/134.21	27.7/27.0/27.6	0.80	0.13323
APOC2p1540-C4p4844/rs75463753	C2-intron1	4	0.1079	AA/GA/GG	11/128/558	67.06/68.51/65.68	14.8/23.3/21.8	1.08	0.21814	132.61/138.59/135.96	29.5/27.3/28.4	0.48	0.5384
APOC2p2486/rs9304645	intron1	4	0.3655	AA/GA/GG	89/364/292	66.34/66.3/66.87	23.7/22.1/21.0	-0.21	0.7176	142.16/135.72/135.49	34.5/26.2/26.9	0.75	0.13555
APOC2p2935/rs11879392	intron1	2b	0.0135	CC/GC	707/19	66.34/66.92	22.0/16.8	0.44	0.85516	136.85/137.68	27.6/32.7	0.18	0.93035
APOC2p3010/rs10419086	intron1	6	0.1253	AA/AG/GG	539/150/14	67.99/64.76/69.3	22.3/20.8/15.5	-0.91	0.2581	138.46/132.88/136.43	28.7/24.9/26.7	-1.32	0.06568
APOC2p3692/rs12721060	intron1	No Data	0.0172	GT/TT	23/633	71.63/66.93	23.9/21.4	2.28	0.31473	145.71/136.94	20.4/28.2	3.01	0.14108
APOC2p3778/rs5120	intron1	4	0.1845	AA/AT/TT	500/232/23	66/68.31/69.94	22.2/21.8/12.2	1.11	0.10763	135.48/138.99/135.74	28.2/26.9/28.6	0.79	0.19964
APOC2p3805/rs7257095	intron1	2a	0.1649	CC/CG/GG	509/213/16	66.08/67.81/68.2	21.3/23.2/23.9	0.72	0.33716	137.15/135.93/131.19	28.0/26.7/28.2	-0.55	0.40568
APOC2p3814/rs10422603	intron1	2b	0.3008	GG/GT/TT	63/309/352	67.74/66.13/66.92	24.3/22.8/20.7	-0.10	0.87424	141.98/137.67/135.22	32.6/27.0/27.5	0.97	0.06515
APOC2p3892/rs5121	exon2	5	0.0358	CC/TC/TT	675/50/1	66.57/65.72/76.29	22.3/16.6/NA	-0.03	0.98356	136.66/136.88/142.71	28.1/24.5/NA	0.20	0.87741
APOC2p4086/rs114780592	intron2	4	0.0278	GA/GG	42/700	72.68/66.2	25.8/21.6	3.05	0.0669	141.16/136.52	28.7/27.6	1.53	0.29745

Cont. Table 27

APOC2p4118/rs201709243	exon3	4	0.0007	GA/GG	1/722	60.37/66.56	NA/22.0	-2.87	0.7826	***	***	***	***
APOC2p4319/rs5123	intron3	No Data	0.0592	AA/GA/GG	6/74/649	72.9/64.68/66.64	18.3/19.5/22.1	-0.25	0.82293	138.85/138.09/136.47	27.8/29.2/27.6	0.49	0.61561
APOC2p4513/rs180809422	intron3	5	0.0135	AA/AC/CC	666/17/1	65.74/73.83/55.79	21.9/24.1/NA	2.64	0.26202	136.12/146.66/154.65	27.8/22.4/NA	3.47	0.09379
APOC2p4587/rs5126	exon4	5	0.0499	AA/CA/CC	636/70/1	66.24/70.29/52.22	21.9/20.8/NA	1.71	0.18011	136.48/139.92/94.63	2798/27.0/NA	0.68	0.54818
APOC2p4754/rs7253690	exon4	5	0.0606	AA/GA/GG	6/79/670	72.96/66.14/66.87	18.3/18.1/22.2	0.19	0.85817	138.53/140.71/136.3	27.8/30.2/27.5	1.17	0.22087
APOC2p4853/rs150448996	3'flamking	No Data	0.2736	DD/WD/WW	386/284/57	65.87/68.51/61.64	20.7/23.7/20.5	-0.05	0.93724	138.01/136.14/131.65	28.1/27.0/29.2	-0.86	0.10718
APOC2p4973/rs199828513	3'flamking	No Data	0.0082	WI/WW	12/704	74.02/66.82	25.3/21.5	3.46	0.24889	137.16/137.23	11.9/28.1	0.16	0.95293
APOC2p5004/rs10421404	3'flanking	No Data	0.2908	CC/CT/TT	370/326/56	66.9/66.25/68.08	20.7/22.6/23.8	-0.04	0.94186	135.82/136.31/141.93	27.8/26.7/32.4	0.61	0.24821
APOC2p5018/rs78403558	3'flanking	5	0.0352	DD/WD/WW	1/51/708	81.34/68.78/66.53	NA/22.5/21.8	1.27	0.37773	137.17/138.07/136.62	NA/34.0/27.3	0.36	0.77793
APOC2p5310/rs7258345	3'flanking	No Data	0.3067	GG/GT/TT	326/313/57	66.36/67.39/66.36	23.1/21.2/16.0	0.29	0.63627	138.01/137.46/134.06	29.1/27.2/24.4	-0.42	0.44209
APOC2p5398/rs12709889	3'flanking	6	0.2587	AA/GA/GG	50/279/405	61.99/68.59/65.74	21.1/23.1/20.9	0.16	0.79862	132.9/136/137.54	28.8/26.3/28.3	-0.63	0.24337
APOC2p5491	3'flanking	6	0.0007	CC/TC	742/1	66.49/49.23	21.9/NA	-8.06	0.43745	136.83/119.12	27.7/NA	-5.71	0.53224
APOC2p5512/rs12721064	3'flanking	6	0.0083	CC/CT	753/13	66.78/61.92	21.9/17.5	-2.23	0.43911	136.65/136.54	27.9/17.3	0.10	0.96886
APOC2p5562	3'flanking	No Data	0.0175	CG/GG	24/704	64.44/66.45	19.8/22.0	-0.92	0.67145	139.29/136.71	39.5/27.4	0.65	0.73492
APOC2p5586/rs73558127	3'flanking	No Data	0.1001	GG/GT/TT	9/127/589	71.92/66.13/66.69	28.0/21.4/22.1	0.13	0.88663	146/138.61/136.4	29.2/25.2/28.3	1.00	0.20571
APOC2p5771	3'flanking	6	***	***	***	***	***	***	***	133.2/136.85	20.8/27.7	-1.10	0.74972
APOC2p5815/rs10423208	3'flanking	5	0.3164	AA/GA/GG	340/323/72	66.03/66.9/66.84	23.3/21.5/17.8	0.34	0.55855	137.38/136.77/133.59	29.4/27.0/23.8	-0.43	0.41044
APOC2p5922/rs10422888	3'flanking	5	0.0784	AA/AG/GG	597/99/5	66.04/70.45/60.04	21.7/21.5/30.7	1.47	0.14838	136.82/137.93/129.97	27.2/30.2/38.3	0.05	0.95405
APOC2p5965	3'flanking	5	0.0013	GA/GG	2/743	44.73/66.55	10.8/21.9	-10.45	0.15456	127.8/136.82	7.9/27.8	-2.79	0.66578
APOC2p6334	3'flanking	No Data	0.0096	GA/GG	15/746	72.76/66.62	15.3/21.9	3.15	0.2415	130.12/136.79	30.5/27.5	-2.30	0.33277

LDL-C: low-density lipoprotein cholesterol; ApoB: Apolipoprotein B; TG: triglyceride; HDL-C: high-density lipoprotein cholesterol.
[a] Cox-Box transformed variables.
Age, Gender, Smoking, BMI, Waist, Jobmin, Staff level were included in the final model as covariates.
GTcount: genotype count; AdjMean: adjusted means; GT-SD: genotype standard deviation.

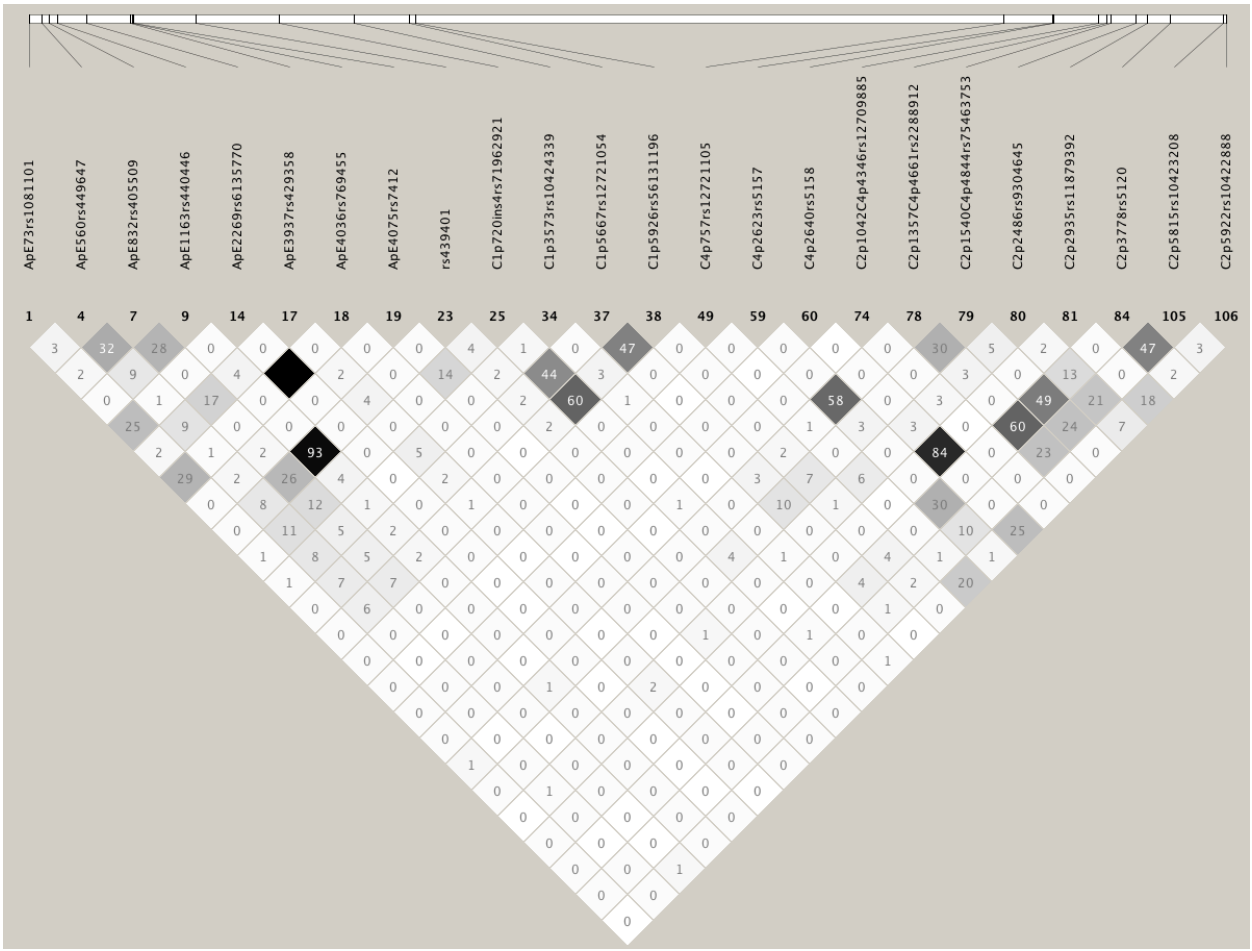


Figure 22. LD plot of the 24 common variants (MAF>1%) with significant associations in Blacks

3.6.2 Gene-based association analysis

3.6.2.1 NHWs

Table 28 presents the gene-based association results with lipid traits in NHWs. The genetic variation of *APOE-C1-C4-C2* gene cluster showed significant associations with LDL-C, TC and apoB and the association signal seems to be derived from *APOE2* allele.

Table 28. Gene-based association results with lipid traits in NHWs

Gene-based test based on all 63 SNPs							
Lipid trait	**Chr**	**Gene**	**nSNPs**	**Test**	**P-value**	**Best.SNP**	**SNP.p-value**
HDL_C	19	APOE	63	86.15598	0.136	APOC1p1317/rs12721048	0.016159
LDL_C	19	APOE	63	164.5623	0.000428	APOE4075/rs7412	1.84E-07
TG	19	APOE	63	91.74789	0.07955	APOC1p2041/rs3826688	0.001125
TC	19	APOE	63	170.0197	0.000288	APOE4075/rs7412	9.51E-06
ApoB	19	APOE	63	200.5421	3.60E-05	APOE4075/rs7412	9.65E-13
ApoA1	19	APOE	63	56.50568	0.607	APOC1p1317/rs12721048	0.00423
Gene-based test based on 29 common SNPs (MAF≥5%)							
lipid trait	**Chr**	**Gene**	**nSNPs**	**Test**	**P-value**	**Best.SNP**	**SNP.p-value**
HDL_C	19	APOE	29	26.29908	0.507	HCR2p188/rs35136575	0.033039
LDL_C	19	APOE	29	110.0057	0.00105	APOE4075/rs7412	1.84E-07
TG	19	APOE	29	56.96919	0.05774	APOC1p2041/rs3826688	0.001125
TC	19	APOE	29	96.86054	0.00276	APOE4075/rs7412	9.51E-06
ApoB	19	APOE	29	150.0422	4.00E-05	APOE4075/rs7412	9.65E-13
ApoA1	19	APOE	29	20.71344	0.634	rs7259004	0.04602

yellow-highlighted values represent significant p-value;
nSNPs: represents the number of SNPs included in the analysis; Test: represent the overall test statistic; Pvalue: the overall p-value; SNP.pvalue: p-value of the best SNPs contributed to the significance.

3.6.2.2 African Blacks

Table 29 gives the gene-based association results with lipid traits in Blacks. The genetic variation of *APOE-C1-C4-C2* gene cluster showed significant associations with LDL-C, TC, and apoA1 and the association signal seems to be derived from *APOE2* allele.

Table 29. Gene-based association results with lipid traits in Blacks

Gene-based test on all 106 SNPs							
Lipid Trait	**Chr**	**Gene**	**nSNPs**	**Test**	**Pvalue**	**Best.SNP**	**SNP.pvalue**
HDL_C	19	APOE	106	123.1083	0.231	APOE618	0.00079
LDL_C	19	APOE	106	215.9868	0.001159	APOE4075/rs7412	5.35E-07
TG	19	APOE	106	134.5834	0.134	APOC4p757/rs12721105	0.000522
TC	19	APOE	106	159.0945	0.03628	APOE4075/rs7412	0.000118
ApoB	19	APOE	106	121.2497	0.23	APOE1163/rs440446	0.010931
ApoA1	19	APOE	106	163.1894	0.02868	APOE4075/rs7412	8.47E-05
Gene-based test on 47 SNPs with MAF≥5%							
Lipid Trait	**Chr**	**Gene**	**nSNPs**	**Test**	**Pvalue**	**Best.SNP**	**SNP.pvalue**
HDL_C	19	APOE	47	46.73669	0.452	rs439401	0.044476
LDL_C	19	APOE	47	137.8881	0.000652	APOE4075/rs7412	5.35E-07
TG	19	APOE	47	62.28504	0.167	APOC1p5667/rs12721054	0.006986
TC	19	APOE	47	94.13141	0.01742	APOE4075/rs7412	0.000118
ApoB	19	APOE	47	60.36205	0.208	APOE1163/rs440446	0.010931
ApoA1	19	APOE	47	84.34323	0.03789	APOE4075/rs7412	8.47E-05

yellow-highlighted values represent significant p-value;
nSNPs: represents the number of SNPs included in the analysis; Test: represent the overall test statistic; Pvalue: the overall p-value; SNP.pvalue: p-value of the best SNPs contributed to the significance.

3.6.3 Haplotype-based association analysis

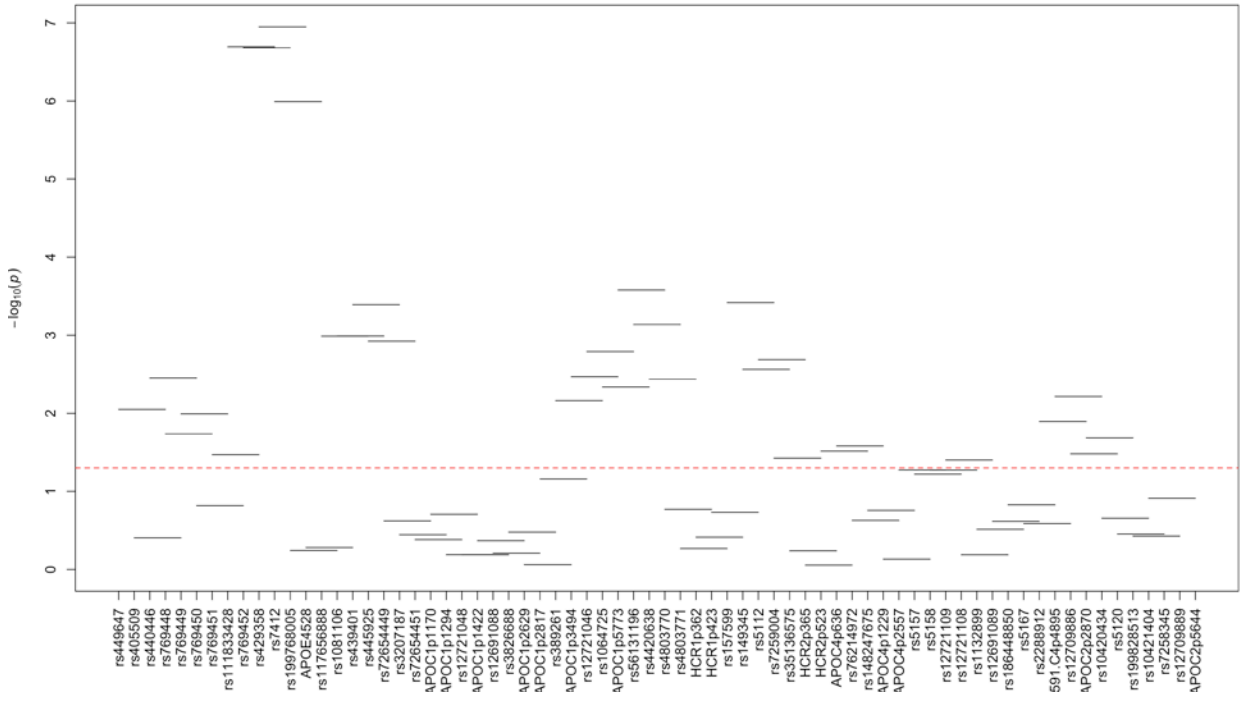
3.6.3.1 NHWs

The haplotype-based association results with lipid traits are summarized in **Tables 30-38** and their corresponding p-values of 4-SNP windows plots are summarized in **Figure 23**. Multiple windows showed significant global p-values with LDL-C, TC, and apoB, confirming the single-locus association results. The top significant global p-values with LDL-C were seen with windows 8, 9, 10, and 11 that were mapped to *APOE2/E4* alleles. The significant haplotype associations in the remaining windows were derived from common/uncommon variants with significant single association with LDL-C. On the other hand, the significant associations seen with the windows 60-63, seem to be attributed to a rare variant *APOC2*p2870. We observed similar pattern of haplotype association results with TC as it was seen with LDL-C. Multiple

windows showed significant global p-value with apoB, confirming the single effect of common/uncommon variants with MAF>1%, except one region that mapped to windows 19 and 20 where the association seems to come from a rare variant with MAF<1% (*APOC1*p1317/rs12721048).

We observed multiple windows to be associated with HDL-C, where common/uncommon variants (MAF>1%) contributed to the observed effects. However, three regions that are mapped to windows 19, 20, 49, and 57, the effects seem to be derived from rare variants with MAF<1% (*APOC1*p1170, *APOC1*p1317/rs12721048, *APOC4*p1229, and *APOC2*p543C4p3847/rs186448850). Likewise, multiple windows showed significant association with apoA1, confirming the single effect of common/uncommon variants with MAF>1%, except two regions mapped to windows 18, 19, and 20 where the effects seem to be derived from rare variants (MAF<1%), including *APOC1*p703/rs3207187, and *APOC1*p1317/rs12721048. For TG, we also observed association in multiple windows containing common/uncommon variants (MAF>1%) that showed associations in single-locus analyses. In addition, we observed association with TG in windows 33, 47, 48, 49, and 58 that contained rare variants (MAF<1%), *APOC1*p5773, *APOC4*p1229, and *APOC2*p543C4p3847/rs186448850.

a) LDL-C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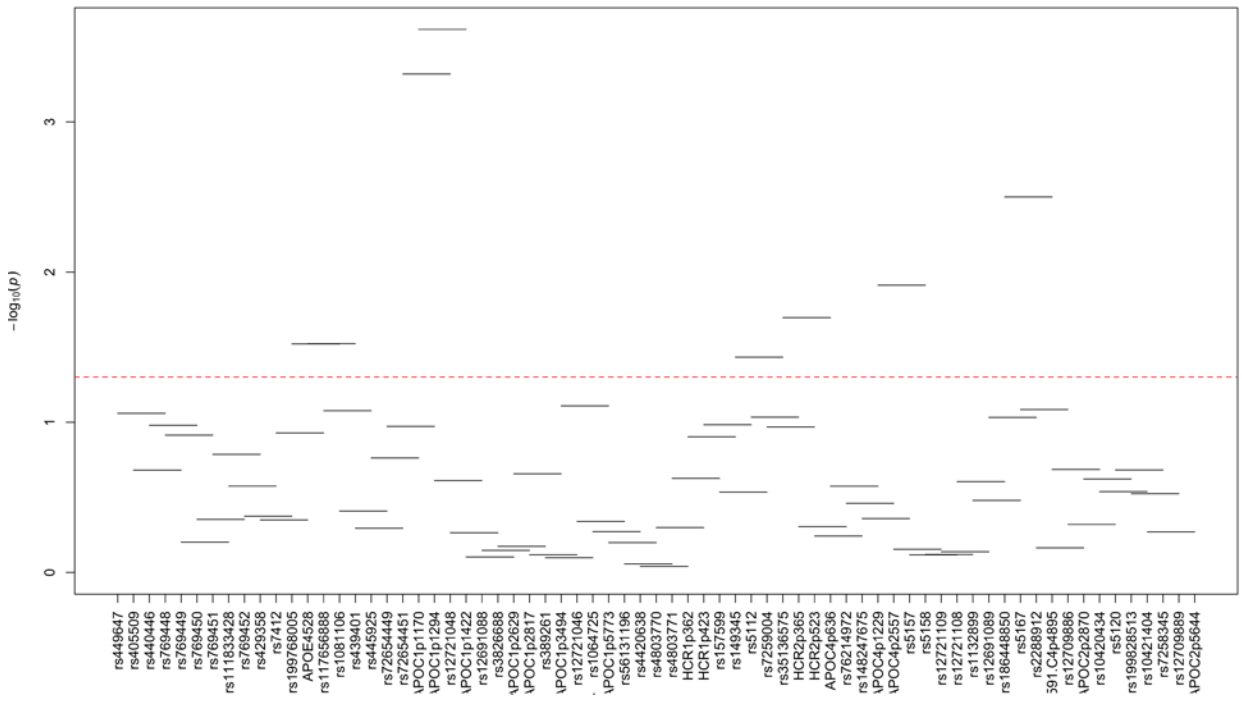
b) HDL-C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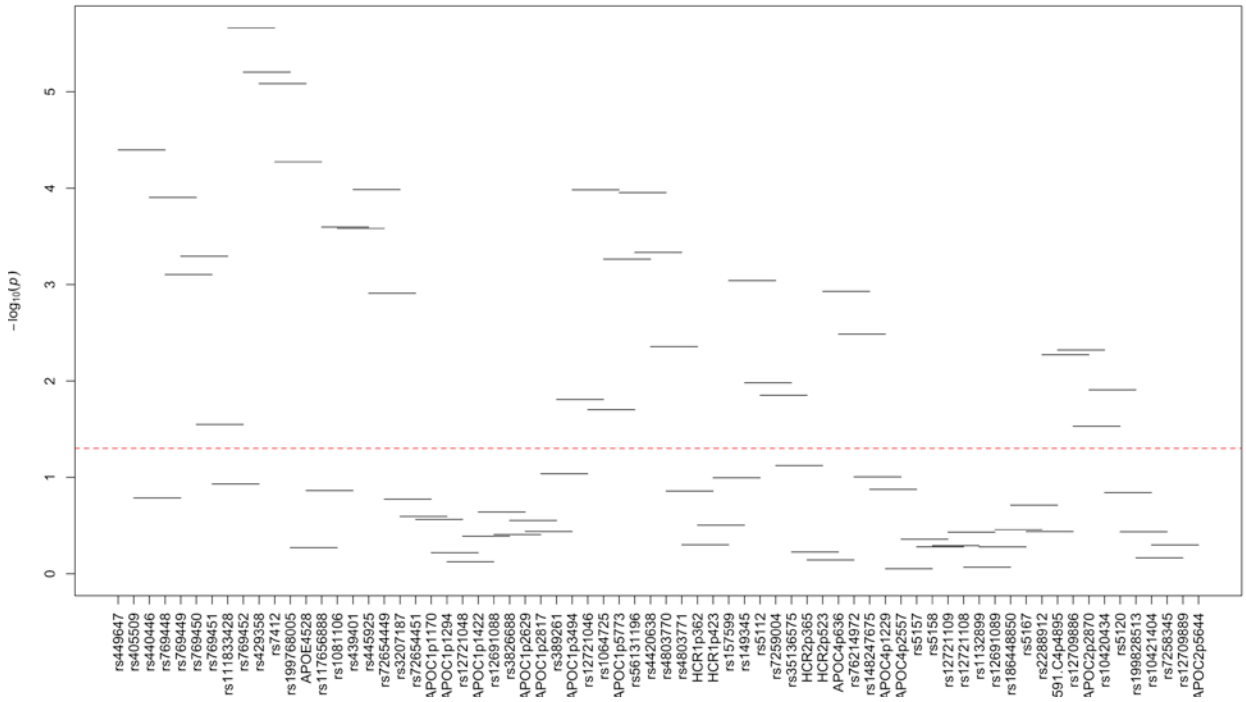
c) TC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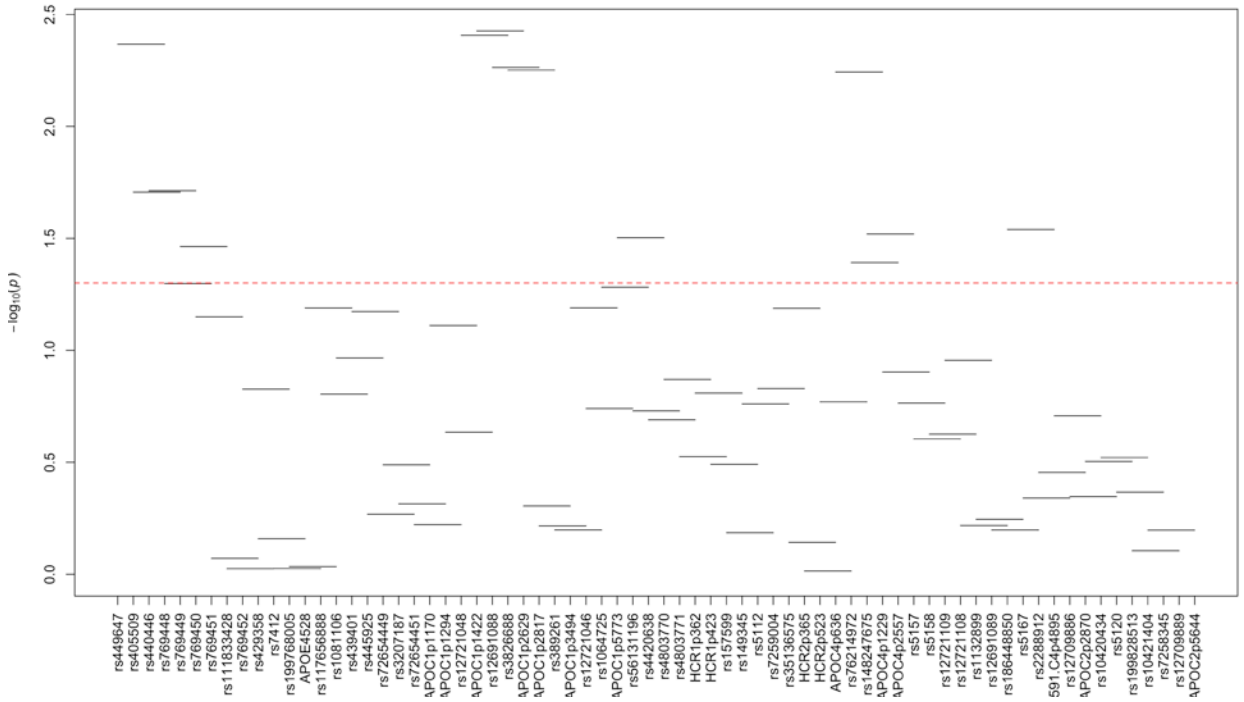
d) TG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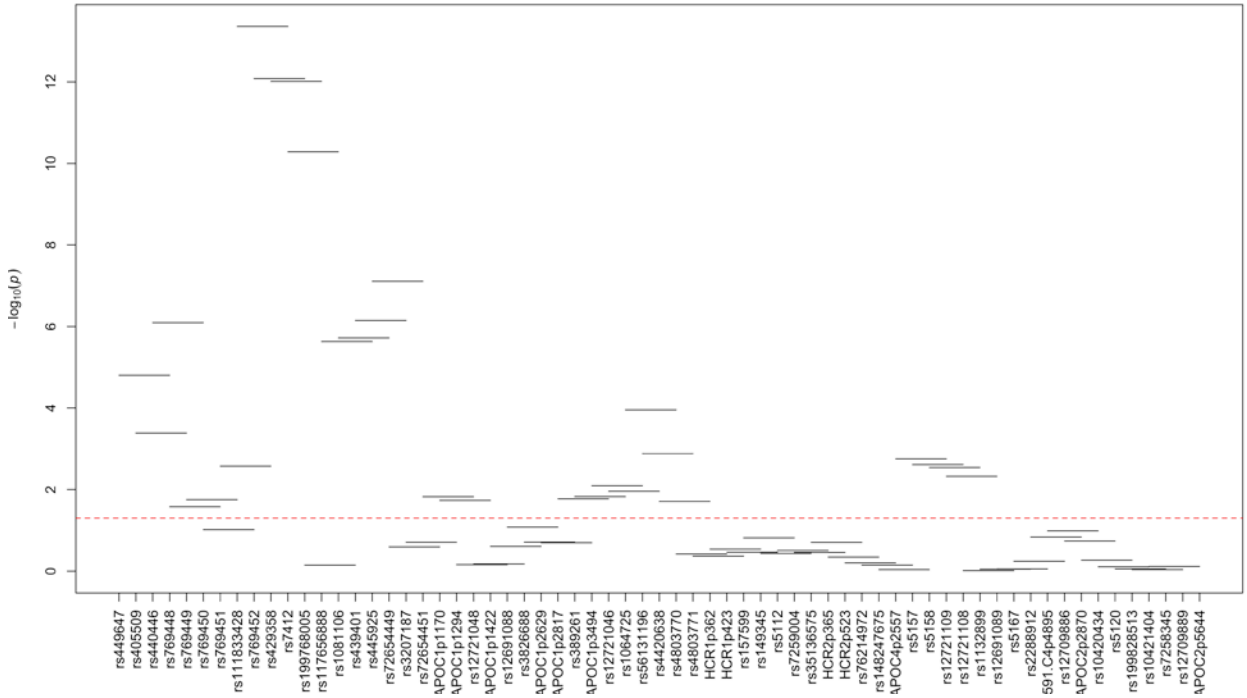
e) ApoB



f) ApoA1

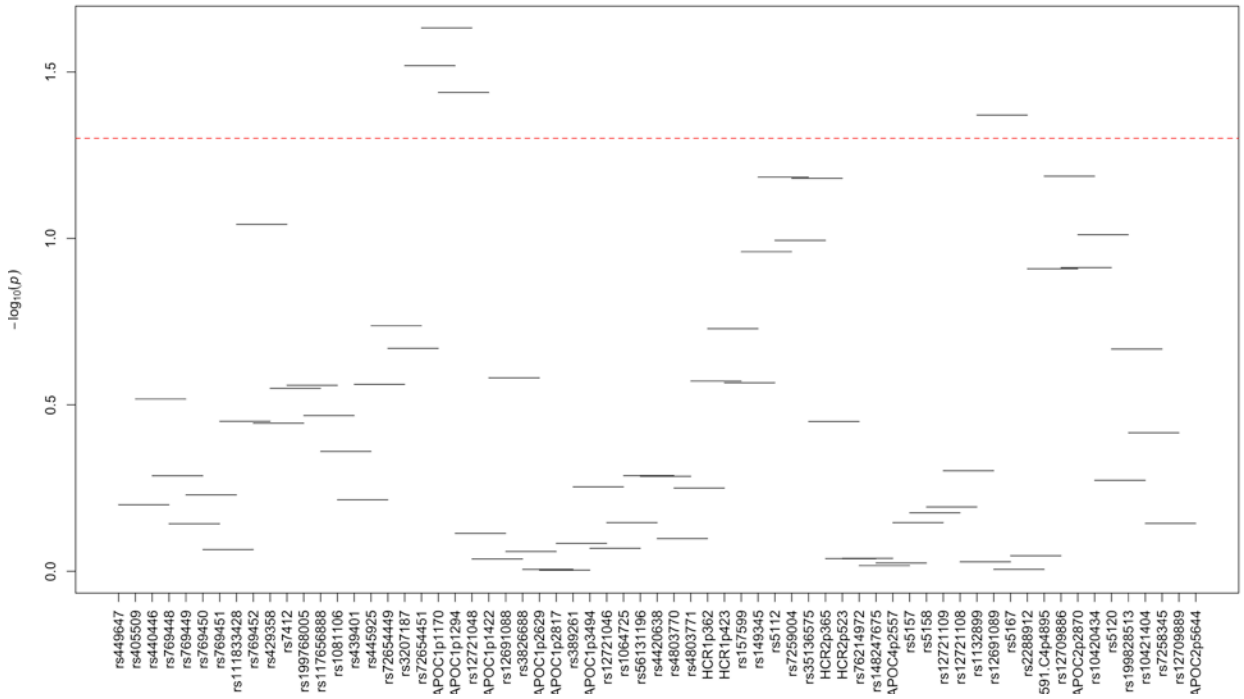


Figure 23. Haplotype based association plots with lipid traits in NHWs

The X-axis has the genotyped markers that included in each window and the Y-axis has the –log (global p-value), the red line represent the significance threshold of the global haplotype p-value, each line is corresponding to one window, all lines underneath the red line means non- significant global p-value and vice versa.

Table 30. Haplotype-based association results with LDL-C, TC, and TG in NHWs

HAPLOTYPE WINDOWS						LDL-C			TC			TG[a]		
wind	w.snp	Function	Regulome DB score	Genotype	MAF	Beta	Single-p	hap_P	Beta	Single-p	hap_P	Beta	Single-p	hap_P
1	APOE560/rs449647	5' flanking	5	AA/AT/TT	0.16103	-7.12	0.02468	0.0089	-6.71	0.042839	0.00004	-0.02	0.52293	0.00429
1	APOE832/rs405509	5' flanking	1f	GG/GT/TT	0.47749	0.42	0.85418	NA	-0.68	0.77567	NA	-0.07	0.00333	NA
1	APOE1163/rs440446	intron 1	4	CC/GC/GG	0.36035	-2.59	0.28095	NA	-4.26	0.089292	NA	-0.08	0.00181	NA
1	APOE1575/rs769448	intron 1	4	CC/CT/TT	0.02097	0.75	0.92317	NA	1.88	0.816453	NA	-0.09	0.23228	NA
2	APOE832/rs405509	5' flanking	1f	GG/GT/TT	0.47749	0.42	0.85418	0.39226	-0.68	0.77567	0.163716	-0.07	0.00333	0.01963
2	APOE1163/rs440446	intron 1	4	CC/GC/GG	0.36035	-2.59	0.28095	NA	-4.26	0.089292	NA	-0.08	0.00181	NA
2	APOE1575/rs769448	intron 1	4	CC/CT/TT	0.02097	0.75	0.92317	NA	1.88	0.816453	NA	-0.09	0.23228	NA
2	APOE1998/rs769449	intron 2	4	AA/AG/GG	0.1165	6.95	0.05505	NA	8.31	0.028503	NA	0.01	0.68668	NA
3	APOE1163/rs440446	intron 1	4	CC/GC/GG	0.36035	-2.59	0.28095	0.00352	-4.26	0.089292	0.000125	-0.08	0.00181	0.01936
3	APOE1575/rs769448	intron 1	4	CC/CT/TT	0.02097	0.75	0.92317	NA	1.88	0.816453	NA	-0.09	0.23228	NA
3	APOE1998/rs769449	intron 2	4	AA/AG/GG	0.1165	6.95	0.05505	NA	8.31	0.028503	NA	0.01	0.68668	NA
3	APOE2440/rs769450	intron 2	5	AA/GA/GG	0.40145	4.89	0.03784	NA	6.88	0.005137	NA	0.06	0.00823	NA
4	APOE1575/rs769448	intron 1	4	CC/CT/TT	0.02097	0.75	0.92317	0.01832	1.88	0.816453	0.000787	-0.09	0.23228	0.05026
4	APOE1998/rs769449	intron 2	4	AA/AG/GG	0.1165	6.95	0.05505	NA	8.31	0.028503	NA	0.01	0.68668	NA
4	APOE2440/rs769450	intron 2	5	AA/GA/GG	0.40145	4.89	0.03784	NA	6.88	0.005137	NA	0.06	0.00823	NA
4	APOE2907/rs769451	intron 2	5	GT/TT	0.01124	0.45	0.96677	NA	-1.93	0.864877	NA	-0.05	0.61567	NA
5	APOE1998/rs769449	intron 2	4	AA/AG/GG	0.1165	6.95	0.05505	0.01014	8.31	0.028503	0.000508	0.01	0.68668	0.03436
5	APOE2440/rs769450	intron 2	5	AA/GA/GG	0.40145	4.89	0.03784	NA	6.88	0.005137	NA	0.06	0.00823	NA
5	APOE2907/rs769451	intron 2	5	GT/TT	0.01124	0.45	0.96677	NA	-1.93	0.864877	NA	-0.05	0.61567	NA
5	APOE3038/rs111833428	exon 3	5	AG/GG	0.00162	27.34	0.33535	NA	33.8	0.256747	NA	0.16	0.57655	NA
6	APOE2440/rs769450	intron 2	5	AA/GA/GG	0.40145	4.89	0.03784	0.15188	6.88	0.005137	0.028183	0.06	0.00823	0.07083
6	APOE2907/rs769451	intron 2	5	GT/TT	0.01124	0.45	0.96677	NA	-1.93	0.864877	NA	-0.05	0.61567	NA
6	APOE3038/rs111833428	exon 3	5	AG/GG	0.00162	27.34	0.33535	NA	33.8	0.256747	NA	0.16	0.57655	NA
6	APOE3106/rs769452	exon 3	5	TC/TT	0.00081	18.03	0.65224	NA	21.3	0.611017	NA	-0.22	0.5865	NA
7	APOE2907/rs769451	intron 2	5	GT/TT	0.01124	0.45	0.96677	0.03391	-1.93	0.864877	0.116849	-0.05	0.61567	0.84883

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7	APOE3038/rs111833428	exon 3	5	AG/GG	0.00162	27.34	0.33535	NA	33.8	0.256747	NA	0.16	0.57655	NA
7	APOE3106/rs769452	exon 3	5	TC/TT	0.00081	18.03	0.65224	NA	21.3	0.611017	NA	-0.22	0.5865	NA
7	APOE3937/rs429358	exon 4	5	CC/CT/TT	0.15253	8.10	0.01033	NA	6.82	0.038251	NA	0.01	0.70692	NA
8	APOE3038/rs111833428	exon 3	5	AG/GG	0.00162	27.34	0.33535	2.03E-07	33.8	0.256747	0.000002	0.16	0.57655	0.94386
8	APOE3106/rs769452	exon 3	5	TC/TT	0.00081	18.03	0.65224	NA	21.3	0.611017	NA	-0.22	0.5865	NA
8	APOE3937/rs429358	exon 4	5	CC/CT/TT	0.15253	8.10	0.01033	NA	6.82	0.038251	NA	0.01	0.70692	NA
8	APOE4075/rs7412	exon 4	5	CC/TC/TT	0.08065	-21.84	1.84E-07	NA	-19.46	9.51E-06	NA	0.01	0.74378	NA
9	APOE3106/rs769452	exon 3	5	TC/TT	0.00081	18.03	0.65224	2.09E-07	21.3	0.611017	0.000006	-0.22	0.5865	0.14904
9	APOE3937/rs429358	exon 4	5	CC/CT/TT	0.15253	8.10	0.01033	NA	6.82	0.038251	NA	0.01	0.70692	NA
9	APOE4075/rs7412	exon 4	5	CC/TC/TT	0.08065	-21.84	1.84E-07	NA	-19.46	9.51E-06	NA	0.01	0.74378	NA
9	APOE4310/rs199768005	exon 4	5	TA/TT	0.00402	-32.56	0.07050	NA	-46.88	0.012787	NA	-0.4	0.02603	NA
10	APOE3937/rs429358	exon 4	5	CC/CT/TT	0.15253	8.10	0.01033	1.12E-07	6.82	0.038251	0.000008	0.01	0.70692	0.69342
10	APOE4075/rs7412	exon 4	5	CC/TC/TT	0.08065	-21.84	1.84E-07	NA	-19.46	9.51E-06	NA	0.01	0.74378	NA
10	APOE4310/rs199768005	exon 4	5	TA/TT	0.00402	-32.56	0.07050	NA	-46.88	0.012787	NA	-0.4	0.02603	NA
10	APOE4528	3'UTR (exon 4)	5	CC/CT	0.0008	-12.30	0.75854	NA	36.03	0.389779	NA	0.92	0.02316	NA
11	APOE4075/rs7412	exon 4	5	CC/TC/TT	0.08065	-21.84	1.84E-07	1.02E-06	-19.46	9.51E-06	0.000053	0.01	0.74378	0.94227
11	APOE4310/rs199768005	exon 4	5	TA/TT	0.00402	-32.56	0.07050	NA	-46.88	0.012787	NA	-0.4	0.02603	NA
11	APOE4528	3'UTR (exon 4)	5	CC/CT	0.0008	-12.30	0.75854	NA	36.03	0.389779	NA	0.92	0.02316	NA
11	APOE4737/rs117656888	3'flanking	5	CC/GC	0.00806	13.58	0.28672	NA	23.15	0.083533	NA	0.09	0.50843	NA
12	APOE4310/rs199768005	exon 4	5	TA/TT	0.00402	-32.56	0.07050	0.57192	-46.88	0.012787	0.535682	-0.4	0.02603	0.92319
12	APOE4528	3'UTR (exon 4)	5	CC/CT	0.0008	-12.30	0.75854	NA	36.03	0.389779	NA	0.92	0.02316	NA
12	APOE4737/rs117656888	3'flanking	5	CC/GC	0.00806	13.58	0.28672	NA	23.15	0.083533	NA	0.09	0.50843	NA
12	APOE5361/rs1081106	3'flanking	3a	CC/TC/TT	0.08521	4.00	0.32719	NA	4.62	0.279139	NA	-0.01	0.89282	NA
13	APOE4528	3'UTR (exon 4)	5	CC/CT	0.0008	-12.30	0.75854	0.52351	36.03	0.389779	0.136851	0.92	0.02316	0.0646
13	APOE4737/rs117656888	3'flanking	5	CC/GC	0.00806	13.58	0.28672	NA	23.15	0.083533	NA	0.09	0.50843	NA

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13	APOE5361/rs1081106	3'flanking	3a	CC/TC/TT	0.08521	4.00	0.32719	NA	4.62	0.279139	NA	-0.01	0.89282	NA
13	rs439401	intergenic	1b	CC/CT/TT	0.35961	-1.76	0.45214	NA	-2.82	0.248555	NA	-0.06	0.01936	NA
14	APOE4737/rs117656888	3'flanking	5	CC/GC	0.00806	13.58	0.28672	0.00103	23.15	0.083533	0.000253	0.09	0.50843	0.15678
14	APOE5361/rs1081106	3'flanking	3a	CC/TC/TT	0.08521	4.00	0.32719	NA	4.62	0.279139	NA	-0.01	0.89282	NA
14	rs439401	intergenic	1b	CC/CT/TT	0.35961	-1.76	0.45214	NA	-2.82	0.248555	NA	-0.06	0.01936	NA
14	rs445925	intergenic	no data	AA/GA/GG	0.1094	-12.58	0.00047	NA	-13.53	0.000315	NA	0.01	0.8251	NA
15	APOE5361/rs1081106	3'flanking	3a	CC/TC/TT	0.08521	4.00	0.32719	0.00103	4.62	0.279139	0.000262	-0.01	0.89282	0.10807
15	rs439401	intergenic	1b	CC/CT/TT	0.35961	-1.76	0.45214	NA	-2.82	0.248555	NA	-0.06	0.01936	NA
15	rs445925	intergenic	no data	AA/GA/GG	0.1094	-12.58	0.00047	NA	-13.53	0.000315	NA	0.01	0.8251	NA
15	APOC1p698/rs72654449	5'flanking	4	CA/CC	0.00405	-14.29	0.42751	NA	-23.7	0.208777	NA	-0.17	0.34254	NA
16	rs439401	intergenic	1b	CC/CT/TT	0.35961	-1.76	0.45214	0.00041	-2.82	0.248555	0.000103	-0.06	0.01936	0.06712
16	rs445925	intergenic	no data	AA/GA/GG	0.1094	-12.58	0.00047	NA	-13.53	0.000315	NA	0.01	0.8251	NA
16	APOC1p698/rs72654449	5'flanking	4	CA/CC	0.00405	-14.29	0.42751	NA	-23.7	0.208777	NA	-0.17	0.34254	NA
16	APOC1p703/rs3207187	5'flanking	4	CC/CT	0.00081	12.09	0.76286	NA	52.4	0.212361	NA	-0.07	0.86073	NA
17	rs445925	intergenic	no data	AA/GA/GG	0.1094	-12.58	0.00047	0.00119	-13.53	0.000315	0.001228	0.01	0.8251	0.53944
17	APOC1p698/rs72654449	5'flanking	4	CA/CC	0.00405	-14.29	0.42751	NA	-23.7	0.208777	NA	-0.17	0.34254	NA
17	APOC1p703/rs3207187	5'flanking	4	CC/CT	0.00081	12.09	0.76286	NA	52.4	0.212361	NA	-0.07	0.86073	NA
17	APOC1p720/rs72654451	5'flanking	4	II/WI/WW	0.2299	-3.67	0.17680	NA	-4.42	0.120168	NA	0.01	0.73507	NA
18	APOC1p698/rs72654449	5'flanking	4	CA/CC	0.00405	-14.29	0.42751	0.23845	-23.7	0.208777	0.168715	-0.17	0.34254	0.3244
18	APOC1p703/rs3207187	5'flanking	4	CC/CT	0.00081	12.09	0.76286	NA	52.4	0.212361	NA	-0.07	0.86073	NA
18	APOC1p720/rs72654451	5'flanking	4	II/WI/WW	0.2299	-3.67	0.17680	NA	-4.42	0.120168	NA	0.01	0.73507	NA
18	APOC1p1170	intron 1	2b	GA/GG	0.00082	-41.75	0.29561	NA	-29.4	0.483929	NA	-0.61	0.12814	NA
19	APOC1p703/rs3207187	5'flanking	4	CC/CT	0.00081	12.09	0.76286	0.35821	52.4	0.212361	0.253998	-0.07	0.86073	0.48431
19	APOC1p720/rs72654451	5'flanking	4	II/WI/WW	0.2299	-3.67	0.17680	NA	-4.42	0.120168	NA	0.01	0.73507	NA
19	APOC1p1170	intron 1	2b	GA/GG	0.00082	-41.75	0.29561	NA	-29.4	0.483929	NA	-0.61	0.12814	NA
19	APOC1p1294	intron 2	4	AA/AC	0.00081	-6.76	0.86595	NA	13.45	0.748544	NA	-0.1	0.80361	NA
20	APOC1p720/rs72654451	5'flanking	4	II/WI/WW	0.2299	-3.67	0.17680	0.41389	-4.42	0.120168	0.27284	0.01	0.73507	0.59971

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20	APOC1p1170	intron 1	2b	GA/GG	0.00082	-41.75	0.29561	NA	-29.4	0.483929	NA	-0.61	0.12814	NA
20	APOC1p1294	intron 2	4	AA/AC	0.00081	-6.76	0.86595	NA	13.45	0.748544	NA	-0.1	0.80361	NA
20	APOC1p1317/rs12721048	intron 2	4	GA/GG	0.00164	13.48	0.63208	NA	34.5	0.244241	NA	-0.01	0.9701	NA
21	APOC1p1170	intron 1	2b	GA/GG	0.00082	-41.75	0.29561	0.19634	-29.4	0.483929	0.604101	-0.61	0.12814	0.07733
21	APOC1p1294	intron 2	4	AA/AC	0.00081	-6.76	0.86595	NA	13.45	0.748544	NA	-0.1	0.80361	NA
21	APOC1p1317/rs12721048	intron 2	4	GA/GG	0.00164	13.48	0.63208	NA	34.5	0.244241	NA	-0.01	0.9701	NA
21	APOC1p1422	intron 2	4	GA/GG	0.00161	-51.98	0.06572	NA	-53.33	0.072147	NA	-0.49	0.0838	NA
22	APOC1p1294	intron 2	4	AA/AC	0.00081	-6.76	0.86595	0.64566	13.45	0.748544	0.748724	-0.1	0.80361	0.23179
22	APOC1p1317/rs12721048	intron 2	4	GA/GG	0.00164	13.48	0.63208	NA	34.5	0.244241	NA	-0.01	0.9701	NA
22	APOC1p1422	intron 2	4	GA/GG	0.00161	-51.98	0.06572	NA	-53.33	0.072147	NA	-0.49	0.0838	NA
22	APOC1p1566/rs12691088	intron 2	2b	GA/GG	0.00579	3.19	0.83505	NA	-2.77	0.862436	NA	-0.08	0.61826	NA
23	APOC1p1317/rs12721048	intron 2	4	GA/GG	0.00164	13.48	0.63208	0.6467	34.5	0.244241	0.408575	-0.01	0.9701	0.00392
23	APOC1p1422	intron 2	4	GA/GG	0.00161	-51.98	0.06572	NA	-53.33	0.072147	NA	-0.49	0.0838	NA
23	APOC1p1566/rs12691088	intron 2	2b	GA/GG	0.00579	3.19	0.83505	NA	-2.77	0.862436	NA	-0.08	0.61826	NA
23	APOC1p2041/rs3826688	intron 2	5	AA/GA/GG	0.34241	-2.38	0.32461	NA	-3.6	0.154054	NA	-0.08	0.00113	NA
24	APOC1p1422	intron 2	4	GA/GG	0.00161	-51.98	0.06572	0.42704	-53.33	0.072147	0.228581	-0.49	0.0838	0.00374
24	APOC1p1566/rs12691088	intron 2	2b	GA/GG	0.00579	3.19	0.83505	NA	-2.77	0.862436	NA	-0.08	0.61826	NA
24	APOC1p2041/rs3826688	intron 2	5	AA/GA/GG	0.34241	-2.38	0.32461	NA	-3.6	0.154054	NA	-0.08	0.00113	NA
24	APOC1p2629	exon 3	4	GA/GG	0.00081	-47.60	0.23493	NA	-24.89	0.552467	NA	-0.02	0.96335	NA
25	APOC1p1566/rs12691088	intron 2	2b	GA/GG	0.00579	3.19	0.83505	0.61842	-2.77	0.862436	0.391799	-0.08	0.61826	0.00545
25	APOC1p2041/rs3826688	intron 2	5	AA/GA/GG	0.34241	-2.38	0.32461	NA	-3.6	0.154054	NA	-0.08	0.00113	NA
25	APOC1p2629	exon 3	4	GA/GG	0.00081	-47.60	0.23493	NA	-24.89	0.552467	NA	-0.02	0.96335	NA
25	APOC1p2817	intron 3	2b	CC/CT	0.00329	-5.57	0.77937	NA	8.17	0.694332	NA	0.04	0.83338	NA
26	APOC1p2041/rs3826688	intron 2	5	AA/GA/GG	0.34241	-2.38	0.32461	0.33229	-3.6	0.154054	0.279497	-0.08	0.00113	0.0056
26	APOC1p2629	exon 3	4	GA/GG	0.00081	-47.60	0.23493	NA	-24.89	0.552467	NA	-0.02	0.96335	NA
26	APOC1p2817	intron 3	2b	CC/CT	0.00329	-5.57	0.77937	NA	8.17	0.694332	NA	0.04	0.83338	NA
26	APOC1p3423/rs389261	intron 3	no data	GA/GG	0.00247	-18.83	0.41632	NA	-32.02	0.18592	NA	-0.02	0.91687	NA

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27	APOC1p2629	exon 3	4	GA/GG	0.00081	-47.60	0.23493	0.86905	-24.89	0.552467	0.365178	-0.02	0.96335	0.4951
27	APOC1p2817	intron 3	2b	CC/CT	0.00329	-5.57	0.77937	NA	8.17	0.694332	NA	0.04	0.83338	NA
27	APOC1p3423/rs389261	intron 3	no data	GA/GG	0.00247	-18.83	0.41632	NA	-32.02	0.18592	NA	-0.02	0.91687	NA
27	APOC1p3494	intron 3	no data	CC/CT	0.00161	73.63	0.00916	NA	103.78	0.000437	NA	0.4	0.16425	NA
28	APOC1p2817	intron 3	2b	CC/CT	0.00329	-5.57	0.77937	0.0693	8.17	0.694332	0.091732	0.04	0.83338	0.60749
28	APOC1p3423/rs389261	intron 3	no data	GA/GG	0.00247	-18.83	0.41632	NA	-32.02	0.18592	NA	-0.02	0.91687	NA
28	APOC1p3494	intron 3	no data	CC/CT	0.00161	73.63	0.00916	NA	103.78	0.000437	NA	0.4	0.16425	NA
28	APOC1p4334/rs12721046	intron 3	6	AA/GA/GG	0.15221	6.93	0.03064	NA	5.95	0.077337	NA	0.02	0.47873	NA
29	APOC1p3423/rs389261	intron 3	no data	GA/GG	0.00247	-18.83	0.41632	0.0069	-32.02	0.18592	0.015589	-0.02	0.91687	0.63268
29	APOC1p3494	intron 3	no data	CC/CT	0.00161	73.63	0.00916	NA	103.78	0.000437	NA	0.4	0.16425	NA
29	APOC1p4334/rs12721046	intron 3	6	AA/GA/GG	0.15221	6.93	0.03064	NA	5.95	0.077337	NA	0.02	0.47873	NA
29	APOC1p5641/rs1064725	3'UTR	no data	GG/GT/TT	0.03883	11.99	0.04148	NA	13.65	0.026307	NA	-0.05	0.40638	NA
30	C1p3494	intron 3	no data	CC/CT	0.00161	73.63	0.00916	0.0034	103.78	0.000437	0.000104	0.4	0.16425	0.06454
30	C1p4334/rs12721046	intron 3	6	AA/GA/GG	0.15221	6.93	0.03064	NA	5.95	0.077337	NA	0.02	0.47873	NA
30	APOC1p5641/rs1064725	3'UTR	no data	GG/GT/TT	0.03883	11.99	0.04148	NA	13.65	0.026307	NA	-0.05	0.40638	NA
30	C1p5773	3' flanking	no data	GA/GG	0.00083	-11.49	0.77418	NA	37.56	0.369912	NA	0.93	0.02109	NA
31	C1p4334/rs12721046	intron 3	6	AA/GA/GG	0.15221	6.93	0.03064	0.00162	5.95	0.077337	0.019841	0.02	0.47873	0.18191
31	APOC1p5641/rs1064725	3'UTR	no data	GG/GT/TT	0.03883	11.99	0.04148	NA	13.65	0.026307	NA	-0.05	0.40638	NA
31	APOC1p5773	3' flanking	no data	GA/GG	0.00083	-11.49	0.77418	NA	37.56	0.369912	NA	0.93	0.02109	NA
31	APOC1p5926/rs56131196	3' flanking	no data	AA/GA/GG	0.18851	7.24	0.01416	NA	6.69	0.030458	NA	0.01	0.76774	NA
32	APOC1p5641/rs1064725	3'UTR	no data	GG/GT/TT	0.03883	11.99	0.04148	0.0046	13.65	0.026307	0.000544	-0.05	0.40638	0.05217
32	C1p5773	3' flanking	no data	GA/GG	0.00083	-11.49	0.77418	NA	37.56	0.369912	NA	0.93	0.02109	NA
32	APOC1p5926/rs56131196	3' flanking	no data	AA/GA/GG	0.18851	7.24	0.01416	NA	6.69	0.030458	NA	0.01	0.76774	NA
32	APOC1p6026/rs4420638	3 'flanking	no data	AA/GA/GG	0.15558	6.97	0.02600	NA	6.79	0.040182	NA	0.03	0.39236	NA
33	APOC1p5773	3' flanking	no data	GA/GG	0.00083	-11.49	0.77418	0.00026	37.56	0.369912	0.000111	0.93	0.02109	0.0314
33	APOC1p5926/rs56131196	3' flanking	no data	AA/GA/GG	0.18851	7.24	0.01416	NA	6.69	0.030458	NA	0.01	0.76774	NA
33	APOC1p6026/rs4420638	3 'flanking	no data	AA/GA/GG	0.15558	6.97	0.02600	NA	6.79	0.040182	NA	0.03	0.39236	NA

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33	rs4803770	HCR1	5	CC/GC/GG	0.37795	5.52	0.01966	NA	6.08	0.01385	NA	0.04	0.0801	NA
34	APOC1p5926/rs56131196	3' flanking	no data	AA/GA/GG	0.18851	7.24	0.01416	0.00073	6.69	0.030458	0.000464	0.01	0.76774	0.18627
34	APOC1p6026/rs4420638	3 'flanking	no data	AA/GA/GG	0.15558	6.97	0.02600	NA	6.79	0.040182	NA	0.03	0.39236	NA
34	rs4803770	HCR1	5	CC/GC/GG	0.37795	5.52	0.01966	NA	6.08	0.01385	NA	0.04	0.0801	NA
34	HCR1p292/rs4803771	HCR1	4	CC/CG/GG	0.02451	3.86	0.59596	NA	1.4	0.854119	NA	0.02	0.81882	NA
35	rs4420638	3 'flanking	no data	AA/GA/GG	0.15558	6.97	0.02600	0.00365	6.79	0.040182	0.004402	0.03	0.39236	0.20392
35	rs4803770	HCR1	5	CC/GC/GG	0.37795	5.52	0.01966	NA	6.08	0.01385	NA	0.04	0.0801	NA
35	HCR1p292/rs4803771	HCR1	4	CC/CG/GG	0.02451	3.86	0.59596	NA	1.4	0.854119	NA	0.02	0.81882	NA
35	HCR1p362	HCR1	2a	CA/CC	0.00247	-14.29	0.53623	NA	-3.8	0.874948	NA	0.3	0.20302	NA
36	rs4803770	HCR1	5	CC/GC/GG	0.37795	5.52	0.01966	0.17009	6.08	0.01385	0.138271	0.04	0.0801	0.13468
36	HCR1p292/rs4803771	HCR1	4	CC/CG/GG	0.02451	3.86	0.59596	NA	1.4	0.854119	NA	0.02	0.81882	NA
36	HCR1p362	HCR1	2a	CA/CC	0.00247	-14.29	0.53623	NA	-3.8	0.874948	NA	0.3	0.20302	NA
36	HCR1p423	HCR1	4	CC/CG/GG	0.02581	-6.26	0.36857	NA	-7.84	0.28132	NA	-0.12	0.07997	NA
37	HCR1p292/rs4803771	HCR1	4	CC/CG/GG	0.02451	3.86	0.59596	0.54038	1.4	0.854119	0.499584	0.02	0.81882	0.29791
37	HCR1p362	HCR1	2a	CA/CC	0.00247	-14.29	0.53623	NA	-3.8	0.874948	NA	0.3	0.20302	NA
37	HCR1p423	HCR1	4	CC/CG/GG	0.02581	-6.26	0.36857	NA	-7.84	0.28132	NA	-0.12	0.07997	NA
37	HCR1p575/rs157599	HCR1	3a	AA/AG	0.00242	-19.28	0.40626	NA	-32.24	0.184365	NA	-0.02	0.92604	NA
38	HCR1p362	HCR1	2a	CA/CC	0.00247	-14.29	0.53623	0.38555	-3.8	0.874948	0.312672	0.3	0.20302	0.1552
38	HCR1p423	HCR1	4	CC/CG/GG	0.02581	-6.26	0.36857	NA	-7.84	0.28132	NA	-0.12	0.07997	NA
38	HCR1p575/rs157599	HCR1	3a	AA/AG	0.00242	-19.28	0.40626	NA	-32.24	0.184365	NA	-0.02	0.92604	NA
38	HCR1p727/rs149345	HCR1	3a	TG/TT	0.00244	-19.80	0.39188	NA	-33.23	0.169457	NA	-0.03	0.90531	NA
39	HCR1p423	HCR1	4	CC/CG/GG	0.02581	-6.26	0.36857	0.18545	-7.84	0.28132	0.101051	-0.12	0.07997	0.3228
39	HCR1p575/rs157599	HCR1	3a	AA/AG	0.00242	-19.28	0.40626	NA	-32.24	0.184365	NA	-0.02	0.92604	NA
39	HCR1p727/rs149345	HCR1	3a	TG/TT	0.00244	-19.80	0.39188	NA	-33.23	0.169457	NA	-0.03	0.90531	NA
39	rs5112	APOC1P1	4	CC/GC/GG	0.46329	-4.61	0.05150	NA	-4.95	0.04462	NA	-0.02	0.32168	NA
40	HCR1p575/rs157599	HCR1	3a	AA/AG	0.00242	-19.28	0.40626	0.00038	-32.24	0.184365	0.00091	-0.02	0.92604	0.65253
40	HCR1p727/rs149345	HCR1	3a	TG/TT	0.00244	-19.80	0.39188	NA	-33.23	0.169457	NA	-0.03	0.90531	NA

Cont. Table 30

40	rs5112	APOC1P1	4	CC/GC/GG	0.46329	-4.61	0.05150	NA	-4.95	0.04462	NA	-0.02	0.32168	NA
40	rs7259004	APOC1P1	6	CC/CG/GG	0.11765	-9.78	0.00499	NA	-9.06	0.013416	NA	0.05	0.21034	NA
41	HCR1p727/rs149345	HCR1	3a	TG/TT	0.00244	-19.80	0.39188	0.00274	-33.23	0.169457	0.010431	-0.03	0.90531	0.17356
41	rs5112	APOC1P1	4	CC/GC/GG	0.46329	-4.61	0.05150	NA	-4.95	0.04462	NA	-0.02	0.32168	NA
41	rs7259004	APOC1P1	6	CC/CG/GG	0.11765	-9.78	0.00499	NA	-9.06	0.013416	NA	0.05	0.21034	NA
41	HR2p188/rs35136575	HCR2	2a	CC/GC/GG	0.22742	-3.15	0.23237	NA	-2.25	0.41394	NA	-0.03	0.28305	NA
42	rs5112	APOC1P1	4	CC/GC/GG	0.46329	-4.61	0.05150	0.00205	-4.95	0.04462	0.014051	-0.02	0.32168	0.14811
42	rs7259004	APOC1P1	6	CC/CG/GG	0.11765	-9.78	0.00499	NA	-9.06	0.013416	NA	0.05	0.21034	NA
42	HCR2p188/rs35136575	HCR2	2a	CC/GC/GG	0.22742	-3.15	0.23237	NA	-2.25	0.41394	NA	-0.03	0.28305	NA
42	HCR2p365	HCR2	2b	CA/CC	0.00409	2.62	0.88437	NA	-6.5	0.729513	NA	-0.2	0.26595	NA
43	rs7259004	APOC1P1	6	CC/CG/GG	0.11765	-9.78	0.00499	0.03754	-9.06	0.013416	0.075596	0.05	0.21034	0.06479
43	HCR2p188/rs35136575	HCR2	2a	CC/GC/GG	0.22742	-3.15	0.23237	NA	-2.25	0.41394	NA	-0.03	0.28305	NA
43	HCR2p365	HCR2	2b	CA/CC	0.00409	2.62	0.88437	NA	-6.5	0.729513	NA	-0.2	0.26595	NA
43	HCR2p523	HCR2	2b	CC/CT	0.02258	3.50	0.65774	NA	8.1	0.326605	NA	0.02	0.76638	NA
44	HCR2p188/rs35136575	HCR2	2a	CC/GC/GG	0.22742	-3.15	0.23237	0.57661	-2.25	0.41394	0.594348	-0.03	0.28305	0.71972
44	HCR2p365	HCR2	2b	CA/CC	0.00409	2.62	0.88437	NA	-6.5	0.729513	NA	-0.2	0.26595	NA
44	HCR2p523	HCR2	2b	CC/CT	0.02258	3.50	0.65774	NA	8.1	0.326605	NA	0.02	0.76638	NA
44	APOC4p636	5' flanking	no data	CC/CT	0.00083	54.33	0.17687	NA	63.55	0.130313	NA	0.73	0.07317	NA
45	HCR2p365	HCR2	2b	CA/CC	0.00409	2.62	0.88437	0.88247	-6.5	0.729513	0.71721	-0.2	0.26595	0.96689
45	HCR2p523	HCR2	2b	CC/CT	0.02258	3.50	0.65774	NA	8.1	0.326605	NA	0.02	0.76638	NA
45	APOC4p636	5' flanking	no data	CC/CT	0.00083	54.33	0.17687	NA	63.55	0.130313	NA	0.73	0.07317	NA
45	APOC4p968/rs76214972	5'UTR	4	AA/AG	0.03623	-1.85	0.76580	NA	-5.6	0.387837	NA	0.02	0.80852	NA
46	HCR2p523	HCR2	2b	CC/CT	0.02258	3.50	0.65774	0.03044	8.1	0.326605	0.001176	0.02	0.76638	0.16964
46	APOC4p636	5' flanking	no data	CC/CT	0.00083	54.33	0.17687	NA	63.55	0.130313	NA	0.73	0.07317	NA
46	APOC4p968/rs76214972	5'UTR	4	AA/AG	0.03623	-1.85	0.76580	NA	-5.6	0.387837	NA	0.02	0.80852	NA
46	APOC4p1150/rs148247675	intron 1	5	AA/GA	0.00166	73.90	0.00896	NA	103.8	0.000431	NA	0.39	0.16983	NA
47	APOC4p636	5' flanking	no data	CC/CT	0.00083	54.33	0.17687	0.02617	63.55	0.130313	0.003271	0.73	0.07317	0.00572

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47	APOC4p968/rs76214972	5'UTR	4	AA/AG	0.03623	-1.85	0.76580	NA	-5.6	0.387837	NA	0.02	0.80852	NA
47	APOC4p1150/rs148247675	intron 1	5	AA/GA	0.00166	73.90	0.00896	NA	103.8	0.000431	NA	0.39	0.16983	NA
47	APOC4p1229	intron 1	2b	GC/GG	0.00161	18.29	0.52047	NA	16.99	0.570069	NA	0.68	0.01859	NA
48	APOC4p968/rs76214972	5' UTR	4	AA/AG	0.03623	-1.85	0.76580	0.23507	-5.6	0.387837	0.098741	0.02	0.80852	0.04053
48	APOC4p1150/rs148247675	intron 1	5	AA/GA	0.00166	73.90	0.00896	NA	103.8	0.000431	NA	0.39	0.16983	NA
48	APOC4p1229	intron 1	2b	GC/GG	0.00161	18.29	0.52047	NA	16.99	0.570069	NA	0.68	0.01859	NA
48	APOC4p2557	intron 1	4	CA/CC	0.00081	-35.35	0.37814	NA	-57.38	0.172729	NA	0.12	0.7681	NA
49	APOC4p1150/rs148247675	intron 1	5	AA/GA	0.00166	73.90	0.00896	0.17526	103.8	0.000431	0.133074	0.39	0.16983	0.03019
49	APOC4p1229	intron 1	2b	GC/GG	0.00161	18.29	0.52047	NA	16.99	0.570069	NA	0.68	0.01859	NA
49	APOC4p2557	intron 1	4	CA/CC	0.00081	-35.35	0.37814	NA	-57.38	0.172729	NA	0.12	0.7681	NA
49	APOC4p2623/rs5157	intron 1	4	CC/CT/TT	0.49759	-1.55	0.49622	NA	-0.35	0.885145	NA	0.02	0.3751	NA
50	APOC4p1229	intron 1	2b	GC/GG	0.00161	18.29	0.52047	0.73404	16.99	0.570069	0.888123	0.68	0.01859	0.12497
50	APOC4p2557	intron 1	4	CA/CC	0.00081	-35.35	0.37814	NA	-57.38	0.172729	NA	0.12	0.7681	NA
50	APOC4p2623/rs5157	intron 1	4	CC/CT/TT	0.49759	-1.55	0.49622	NA	-0.35	0.885145	NA	0.02	0.3751	NA
50	APOC4p2640/rs5158	intron 1	2b	CC/CT/TT	0.13813	-1.55	0.64078	NA	-1.79	0.607587	NA	-0.04	0.22194	NA
51	APOC4p2557	intron 1	4	CA/CC	0.00081	-35.35	0.37814	0.05301	-57.38	0.172729	0.438605	0.12	0.7681	0.17205
51	APOC4p2623/rs5157	intron 1	4	CC/CT/TT	0.49759	-1.55	0.49622	NA	-0.35	0.885145	NA	0.02	0.3751	NA
51	APOC4p2640/rs5158	intron 1	2b	CC/CT/TT	0.13813	-1.55	0.64078	NA	-1.79	0.607587	NA	-0.04	0.22194	NA
51	APOC4p2683/rs12721109	intron 1	2b	AA/AG/GG	0.02369	-19.14	0.00923	NA	-12.75	0.097846	NA	-0.16	0.03289	NA
52	APOC4p2623/rs5157	intron 1	4	CC/CT/TT	0.49759	-1.55	0.49622	0.06026	-0.35	0.885145	0.5248	0.02	0.3751	0.24847
52	APOC4p2640/rs5158	intron 1	2b	CC/CT/TT	0.13813	-1.55	0.64078	NA	-1.79	0.607587	NA	-0.04	0.22194	NA
52	APOC4p2683/rs12721109	intron 1	2b	AA/AG/GG	0.02369	-19.14	0.00923	NA	-12.75	0.097846	NA	-0.16	0.03289	NA
52	APOC4p2703/rs12721108	intron 1	2a	GG/GT	0.00808	1.93	0.87976	NA	-9.51	0.476026	NA	-0.15	0.23842	NA
53	APOC4p2640/rs5158	intron 1	2b	CC/CT/TT	0.13813	-1.55	0.64078	0.05313	-1.79	0.607587	0.510489	-0.04	0.22194	0.23658
53	APOC4p2683/rs12721109	intron 1	2b	AA/AG/GG	0.02369	-19.14	0.00923	NA	-12.75	0.097846	NA	-0.16	0.03289	NA
53	APOC4p2703/rs12721108	intron 1	2a	GG/GT	0.00808	1.93	0.87976	NA	-9.51	0.476026	NA	-0.15	0.23842	NA
53	APOC2p194APOC4p3498/rs1132899	C4-exon2	5	CC/CT/TT	0.48629	-1.91	0.40706	NA	-0.62	0.797285	NA	0.02	0.34646	NA

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54	APOC4p2683/rs12721109	intron 1	2b	AA/AG/GG	0.02369	-19.14	0.00923	0.03968	-12.75	0.097846	0.370766	-0.16	0.03289	0.11065
54	APOC4p2703/rs12721108	intron 1	2a	GG/GT	0.00808	1.93	0.87976	NA	-9.51	0.476026	NA	-0.15	0.23842	NA
54	APOC2p194APOC4p3498/rs1132899	C4-exon2	5	CC/CT/TT	0.48629	-1.91	0.40706	NA	-0.62	0.797285	NA	0.02	0.34646	NA
54	APOC2p242APOC4p3546/rs12691089	C4-exon2	5	AG/GG	0.00322	2.18	0.91357	NA	-5.18	0.805514	NA	-0.16	0.44443	NA
55	APOC4p2703/rs12721108	intron 1	2a	GG/GT	0.00808	1.93	0.87976	0.64722	-9.51	0.476026	0.855425	-0.15	0.23842	0.60501
55	APOC2p194APOC4p3498/rs1132899	C4-exon2	5	CC/CT/TT	0.48629	-1.91	0.40706	NA	-0.62	0.797285	NA	0.02	0.34646	NA
55	APOC2p242APOC4p3546/rs12691089	C4-exon2	5	AG/GG	0.00322	2.18	0.91357	NA	-5.18	0.805514	NA	-0.16	0.44443	NA
55	APOC2p543APOC4p3847/rs186448850	C4-intron2	5	CT/TT	0.00164	18.71	0.51026	NA	17.51	0.557831	NA	0.68	0.01713	NA
56	APOC2p194APOC4p3498/rs1132899	C4-exon2	5	CC/CT/TT	0.48629	-1.91	0.40706	0.30687	-0.62	0.797285	0.526107	0.02	0.34646	0.56818
56	APOC2p242APOC4p3546/rs12691089	C4-exon2	5	AG/GG	0.00322	2.18	0.91357	NA	-5.18	0.805514	NA	-0.16	0.44443	NA
56	APOC2p543APOC4p3847/rs186448850	C4-intron2	5	CT/TT	0.00164	18.71	0.51026	NA	17.51	0.557831	NA	0.68	0.01713	NA
56	APOC2p623APOC4p3927/rs5167	C4-exon3	5	GG/TG/TT	0.35955	4.19	0.08239	NA	2.94	0.244306	NA	-0.003	0.8759	NA
57	APOC2p242APOC4p3546/rs12691089	C4-exon2	5	AG/GG	0.00322	2.18	0.91357	0.24138	-5.18	0.805514	0.348494	-0.16	0.44443	0.63305
57	APOC2p543APOC4p3847/rs186448850	C4-intron2	5	CT/TT	0.00164	18.71	0.51026	NA	17.51	0.557831	NA	0.68	0.01713	NA
57	APOC2p623APOC4p3927/rs5167	C4-exon3	5	GG/TG/TT	0.35955	4.19	0.08239	NA	2.94	0.244306	NA	-0.003	0.8759	NA
57	APOC2p1357APOC4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	CC/CG/GG	0.49678	0.74	0.74503	NA	-0.65	0.785955	NA	-0.02	0.38126	NA
58	APOC2p543APOC4p3847/rs186448850	C4-intron2	5	CT/TT	0.00164	18.71	0.51026	0.14814	17.51	0.557831	0.194087	0.68	0.01713	0.02882
58	APOC2p623APOC4p3927/rs5167	C4-exon3	5	GG/TG/TT	0.35955	4.19	0.08239	NA	2.94	0.244306	NA	-0.003	0.8759	NA
58	APOC2p1357APOC4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	CC/CG/GG	0.49678	0.74	0.74503	NA	-0.65	0.785955	NA	-0.02	0.38126	NA
58	APOC2p1591APOC4p4895	C2-intron1	4	GA/GG	0.00081	54.17	0.17639	NA	62.97	0.132918	NA	0.73	0.0712	NA
59	APOC2p623APOC4p3927/rs5167	C4-exon3	5	GG/TG/TT	0.35955	4.19	0.08239	0.25789	2.94	0.244306	0.365463	-0.003	0.8759	0.45685
59	APOC2p1357APOC4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	CC/CG/GG	0.49678	0.74	0.74503	NA	-0.65	0.785955	NA	-0.02	0.38126	NA
59	APOC4p4895C2p1591	C2-intron1	4	GA/GG	0.00081	54.17	0.17639	NA	62.97	0.132918	NA	0.73	0.0712	NA

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59	APOC2p1851/rs12709886	intron 1	6	GA/GG	0.03722	-1.31	0.83107	NA	-4.49	0.484754	NA	0.03	0.58453	NA
60	APOC2p1357APOC4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	CC/CG/GG	0.49678	0.74	0.74503	0.01273	-0.65	0.785955	0.005339	-0.02	0.38126	0.35045
60	APOC2p1591APOC4p4895	C2-intron1	4	GA/GG	0.00081	54.17	0.17639	NA	62.97	0.132918	NA	0.73	0.0712	NA
60	APOC2p1851/rs12709886	intron 1	6	GA/GG	0.03722	-1.31	0.83107	NA	-4.49	0.484754	NA	0.03	0.58453	NA
60	APOC2p2870	intron 1	4	GG/GT	0.00403	53.09	0.00302	NA	58.43	0.001792	NA	0.12	0.51156	NA
61	APOC4p4895C2p1591	C2-intron1	4	GA/GG	0.00081	54.17	0.17639	0.00606	62.97	0.132918	0.004771	0.73	0.0712	0.19575
61	APOC2p1851/rs12709886	intron 1	6	GA/GG	0.03722	-1.31	0.83107	NA	-4.49	0.484754	NA	0.03	0.58453	NA
61	APOC2p2870	intron 1	4	GG/GT	0.00403	53.09	0.00302	NA	58.43	0.001792	NA	0.12	0.51156	NA
61	APOC2p3348/rs10420434	intron 1	no data	GA/GG	0.0371	-6.86	0.26403	NA	-2.44	0.704321	NA	-0.09	0.17358	NA
62	APOC2p1851/rs12709886	intron 1	6	GA/GG	0.03722	-1.31	0.83107	0.03314	-4.49	0.484754	0.029432	0.03	0.58453	0.44984
62	APOC2p2870	intron 1	4	GG/GT	0.00403	53.09	0.00302	NA	58.43	0.001792	NA	0.12	0.51156	NA
62	APOC2p3348/rs10420434	intron 1	no data	GA/GG	0.0371	-6.86	0.26403	NA	-2.44	0.704321	NA	-0.09	0.17358	NA
62	APOC2p3778/rs5120	intron 1	4	AA/AT/TT	0.49756	1.24	0.58450	NA	-1.32	0.578429	NA	-0.02	0.28092	NA
63	APOC2p2870	intron 1	4	GG/GT	0.00403	53.09	0.00302	0.02068	58.43	0.001792	0.012336	0.12	0.51156	0.31341
63	APOC2p3348/rs10420434	intron 1	no data	GA/GG	0.0371	-6.86	0.26403	NA	-2.44	0.704321	NA	-0.09	0.17358	NA
63	APOC2p3778/rs5120	intron 1	4	AA/AT/TT	0.49756	1.24	0.58450	NA	-1.32	0.578429	NA	-0.02	0.28092	NA
63	APOC2p4853/rs199828513	3' flanking	no data	DD/WD/WW	0.27832	4.36	0.09431	NA	2.44	0.370769	NA	0.01	0.67415	NA
64	APOC2p3348/rs10420434	intron 1	no data	GA/GG	0.0371	-6.86	0.26403	0.22036	-2.44	0.704321	0.143722	-0.09	0.17358	0.30086
64	APOC2p3778/rs5120	intron 1	4	AA/AT/TT	0.49756	1.24	0.58450	NA	-1.32	0.578429	NA	-0.02	0.28092	NA
64	APOC2p4853/rs199828513	3' flanking	no data	DD/WD/WW	0.27832	4.36	0.09431	NA	2.44	0.370769	NA	0.01	0.67415	NA
64	APOC2p5004/rs10421404	3' flanking	no data	CC/CT/TT	0.18233	-2.35	0.41805	NA	-3.09	0.30928	NA	-0.03	0.35914	NA
65	APOC2p3778/rs5120	intron 1	4	AA/AT/TT	0.49756	1.24	0.58450	0.35134	-1.32	0.578429	0.367397	-0.02	0.28092	0.42887
65	APOC2p4853/rs199828513	3' flanking	no data	DD/WD/WW	0.27832	4.36	0.09431	NA	2.44	0.370769	NA	0.01	0.67415	NA
65	APOC2p5004/rs10421404	3' flanking	no data	CC/CT/TT	0.18233	-2.35	0.41805	NA	-3.09	0.30928	NA	-0.03	0.35914	NA
65	APOC2p5310/rs7258345	3' flanking	no data	GG/TG/TT	0.46487	1.99	0.38168	NA	-0.13	0.956125	NA	-0.01	0.81914	NA
66	APOC2p4853/rs199828513	3' flanking	no data	DD/WD/WW	0.27832	4.36	0.09431	0.37269	2.44	0.370769	0.682314	0.01	0.67415	0.78539
66	APOC2p5004/rs10421404	3' flanking	no data	CC/CT/TT	0.18233	-2.35	0.41805	NA	-3.09	0.30928	NA	-0.03	0.35914	NA

Cont. Table 30

66	APOC2p5310/rs7258345	3' flanking	no data	GG/TG/TT	0.46487	1.99	0.38168	NA	-0.13	0.956125	NA	-0.01	0.81914	NA
66	APOC2p5398/rs12709889	3' flanking	6	AA/GA/GG	0.27603	3.95	0.13225	NA	1.98	0.470115	NA	0.01	0.59738	NA
67	APOC2p5004/rs10421404	3' flanking	no data	CC/CT/TT	0.18233	-2.35	0.41805	0.12235	-3.09	0.30928	0.50223	-0.03	0.35914	0.63438
67	APOC2p5310/rs7258345	3' flanking	no data	GG/TG/TT	0.46487	1.99	0.38168	NA	-0.13	0.956125	NA	-0.01	0.81914	NA
67	APOC2p5398/rs12709889	3' flanking	6	AA/GA/GG	0.27603	3.95	0.13225	NA	1.98	0.470115	NA	0.01	0.59738	NA
67	APOC2p5644	3' flanking	6	AG/GG	0.00923	20.49	0.09475	NA	14.86	0.245457	NA	-0.1	0.41034	NA

wind: 4-SNPs haplotype window; w.snps: SNPs that were included in each window; p-value: single-locus p-value; hap-P: haplotype global p-value; [a] Cox-Box transformed data.

Table 31. Haplotype-based association results with HDL-C in NHWs

				HDL-C[a]				
wind	w.snp	Function	RegulomeDB score	Genotype	MAF	Beta	Single-p	hap_P
1	APOE560/rs449647	5' flanking	5	AA/AT/TT	0.16103	-0.01	0.35257	0.08734
1	APOE832/rs405509	5' flanking	1f	GG/GT/TT	0.47749	0.01	0.40306	NA
1	APOE1163/rs440446	intron 1	4	CC/GC/GG	0.36035	0.01	0.2865	NA
1	APOE1575rs769448	intron 1	4	CC/CT/TT	0.02097	0.08	0.01974	NA
2	APOE832/rs405509	5' flanking	1f	GG/GT/TT	0.47749	0.01	0.40306	0.20875
2	APOE1163/rs440446	intron 1	4	CC/GC/GG	0.36035	0.01	0.2865	NA
2	APOE1575/rs769448	intron 1	4	CC/CT/TT	0.02097	0.08	0.01974	NA
2	APOE1998/rs769449	intron 2	4	AA/AG/GG	0.1165	-0.01	0.58003	NA
3	APOE1163/rs440446	intron 1	4	CC/GC/GG	0.36035	0.01	0.2865	0.10469
3	APOE1575/rs769448	intron 1	4	CC/CT/TT	0.02097	0.08	0.01974	NA
3	APOE1998/rs769449	intron 2	4	AA/AG/GG	0.1165	-0.01	0.58003	NA
3	APOE2440/rs769450	intron 2	5	AA/GA/GG	0.40145	0.003	0.77245	NA
4	APOE1575/rs769448	intron 1	4	CC/CT/TT	0.02097	0.08	0.01974	0.12196
4	APOE1998/rs769449	intron 2	4	AA/AG/GG	0.1165	-0.01	0.58003	NA
4	APOE2440/rs769450	intron 2	5	AA/GA/GG	0.40145	0.003	0.77245	NA
4	APOE2907/rs769451	intron 2	5	GT/TT	0.01124	0.05	0.33896	NA
5	APOE1998/rs769449	intron 2	4	AA/AG/GG	0.1165	-0.01	0.58003	0.62753
5	APOE2440/rs769450	intron 2	5	AA/GA/GG	0.40145	0.003	0.77245	NA

Cont. Table 31

5	APOE2907/rs769451	intron 2	5	GT/TT	0.01124	0.05	0.33896	NA
5	APOE3038/rs111833428	exon 3	5	AG/GG	0.00162	0.1	0.43657	NA
6	APOE2440/rs769450	intron 2	5	AA/GA/GG	0.40145	0.003	0.77245	0.44317
6	APOE2907/rs769451	intron 2	5	GT/TT	0.01124	0.05	0.33896	NA
6	APOE3038/rs111833428	exon 3	5	AG/GG	0.00162	0.1	0.43657	NA
6	APOE3106/rs769452	exon 3	5	TC/TT	0.00081	0.2	0.27872	NA
7	APOE2907/rs769451	intron 2	5	GT/TT	0.01124	0.05	0.33896	0.16371
7	APOE3038/rs111833428	exon 3	5	AG/GG	0.00162	0.1	0.43657	NA
7	APOE3106/rs769452	exon 3	5	TC/TT	0.00081	0.2	0.27872	NA
7	APOE3937/rs429358	exon 4	5	CC/CT/TT	0.15253	-0.02	0.22334	NA
8	APOE3038/rs111833428	exon 3	5	AG/GG	0.00162	0.1	0.43657	0.26639
8	APOE3106/rs769452	exon 3	5	TC/TT	0.00081	0.2	0.27872	NA
8	APOE3937/rs429358	exon 4	5	CC/CT/TT	0.15253	-0.02	0.22334	NA
8	APOE4075/rs7412	exon 4	5	CC/TC/TT	0.08065	-0.01	0.45241	NA
9	APOE3106/rs769452	exon 3	5	TC/TT	0.00081	0.2	0.27872	0.42211
9	APOE3937/rs429358	exon 4	5	CC/CT/TT	0.15253	-0.02	0.22334	NA
9	APOE4075/rs7412	exon 4	5	CC/TC/TT	0.08065	-0.01	0.45241	NA
9	APOE4310/rs199768005	exon 4	5	TA/TT	0.00402	0.01	0.89267	NA
10	APOE3937/rs429358	exon 4	5	CC/CT/TT	0.15253	-0.02	0.22334	0.44664
10	APOE4075/rs7412	exon 4	5	CC/TC/TT	0.08065	-0.01	0.45241	NA
10	APOE4310/rs199768005	exon 4	5	TA/TT	0.00402	0.01	0.89267	NA
10	APOE4528	3'UTR (exon 4)	5	CC/CT	0.0008	0.24	0.19264	NA
11	APOE4075/rs7412	exon 4	5	CC/TC/TT	0.08065	-0.01	0.45241	0.11795
11	APOE4310/rs199768005	exon 4	5	TA/TT	0.00402	0.01	0.89267	NA
11	APOE4528	3'UTR (exon 4)	5	CC/CT	0.0008	0.24	0.19264	NA
11	APOE4737/rs117656888	3'flanking	5	CC/GC	0.00806	0.12	0.04872	NA
12	APOE4310/rs199768005	exon 4	5	TA/TT	0.00402	0.01	0.89267	0.03008
12	APOE4528	3'UTR (exon 4)	5	CC/CT	0.0008	0.24	0.19264	NA
12	APOE4737/rs117656888	3'flanking	5	CC/GC	0.00806	0.12	0.04872	NA
12	APOE5361/rs1081106	3'flanking	3a	CC/TC/TT	0.08521	0.03	0.09145	NA
13	APOE4528	3'UTR (exon 4)	5	CC/CT	0.0008	0.24	0.19264	0.02997
13	APOE4737/rs117656888	3'flanking	5	CC/GC	0.00806	0.12	0.04872	NA
13	APOE5361/rs1081106	3'flanking	3a	CC/TC/TT	0.08521	0.03	0.09145	NA

Cont. Table 31

13	rs439401	intergenic	1b	CC/CT/TT	0.35961	0.01	0.54485	NA
14	APOE4737/rs117656888	3'flanking	5	CC/GC	0.00806	0.12	0.04872	0.08392
14	APOE5361/rs1081106	3'flanking	3a	CC/TC/TT	0.08521	0.03	0.09145	NA
14	rs439401	intergenic	1b	CC/CT/TT	0.35961	0.01	0.54485	NA
14	APOC1rs445925	intergenic	no data	AA/GA/GG	0.1094	-0.02	0.27231	NA
15	APOE5361/rs1081106	3'flanking	3a	CC/TC/TT	0.08521	0.03	0.09145	0.39059
15	rs439401	intergenic	1b	CC/CT/TT	0.35961	0.01	0.54485	NA
15	APOC1rs445925	intergenic	no data	AA/GA/GG	0.1094	-0.02	0.27231	NA
15	APOC1p698	5'flanking	4	CA/CC	0.00405	-0.02	0.78922	NA
16	rs439401	intergenic	1b	CC/CT/TT	0.35961	0.01	0.54485	0.50844
16	APOC1rs445925	intergenic	no data	AA/GA/GG	0.1094	-0.02	0.27231	NA
16	APOC1p698/rs72654449	5'flanking	4	CA/CC	0.00405	-0.02	0.78922	NA
16	APOC1p720/rs72654451	5'flanking	4	II/WI/WW	0.2299	-0.02	0.08599	NA
17	APOC1rs445925	intergenic	no data	AA/GA/GG	0.1094	-0.02	0.27231	0.17293
17	APOC1p698/rs72654449	5'flanking	4	CA/CC	0.00405	-0.02	0.78922	NA
17	APOC1p720/rs72654451	5'flanking	4	II/WI/WW	0.2299	-0.02	0.08599	NA
17	APOC1p1170	intron 1	2b	GA/GG	0.00082	0.4	0.03328	NA
18	APOC1p698/rs72654449	5'flanking	4	CA/CC	0.00405	-0.02	0.78922	0.1064
18	APOC1p720/rs72654451	5'flanking	4	II/WI/WW	0.2299	-0.02	0.08599	NA
18	APOC1p1170	intron 1	2b	GA/GG	0.00082	0.4	0.03328	NA
18	APOC1p1294	intron 2	4	AA/AC	0.00081	0.27	0.15333	NA
19	APOC1p720/rs72654451	5'flanking	4	II/WI/WW	0.2299	-0.02	0.08599	0.00048
19	APOC1p1170	intron 1	2b	GA/GG	0.00082	0.4	0.03328	NA
19	APOC1p1294	intron 2	4	AA/AC	0.00081	0.27	0.15333	NA
19	APOC1p1317/rs12721048	intron 2	4	GA/GG	0.00164	0.32	0.01616	NA
20	APOC1p1170	intron 1	2b	GA/GG	0.00082	0.4	0.03328	0.00024
20	APOC1p1294	intron 2	4	AA/AC	0.00081	0.27	0.15333	NA
20	APOC1p1317/rs12721048	intron 2	4	GA/GG	0.00164	0.32	0.01616	NA
20	APOC1p1422	intron 2	4	GA/GG	0.00161	0.18	0.18304	NA
21	APOC1p1294	intron 2	4	AA/AC	0.00081	0.27	0.15333	0.24439
21	APOC1p1317/rs12721048	intron 2	4	GA/GG	0.00164	0.32	0.01616	NA
21	APOC1p1422	intron 2	4	GA/GG	0.00161	0.18	0.18304	NA
21	APOC1p1566/rs12691088	intron 2	2b	GA/GG	0.00579	-0.07	0.30637	NA

Cont. Table 31

22	APOC1p1317/rs12721048	intron 2	4	GA/GG	0.00164	0.32	0.01616	0.54426
22	APOC1p1422	intron 2	4	GA/GG	0.00161	0.18	0.18304	NA
22	APOC1p1566/rs12691088	intron 2	2b	GA/GG	0.00579	-0.07	0.30637	NA
22	APOC1p2041/rs3826688	intron 2	5	AA/GA/GG	0.34241	0.01	0.39851	NA
23	APOC1p1422	intron 2	4	GA/GG	0.00161	0.18	0.18304	0.78818
23	APOC1p1566/rs12691088	intron 2	2b	GA/GG	0.00579	-0.07	0.30637	NA
23	APOC1p2041/rs3826688	intron 2	5	AA/GA/GG	0.34241	0.01	0.39851	NA
23	APOC1p2629	exon 3	4	GA/GG	0.00081	0.3	0.11169	NA
24	APOC1p1566/rs12691088	intron 2	2b	GA/GG	0.00579	-0.07	0.30637	0.71336
24	APOC1p2041/rs3826688	intron 2	5	AA/GA/GG	0.34241	0.01	0.39851	NA
24	APOC1p2629	exon 3	4	GA/GG	0.00081	0.3	0.11169	NA
24	APOC1p2817	intron 3	2b	CC/CT	0.00329	0.13	0.2246	NA
25	APOC1p2041/rs3826688	intron 2	5	AA/GA/GG	0.34241	0.01	0.39851	0.67141
25	APOC1p2629	exon 3	4	GA/GG	0.00081	0.3	0.11169	NA
25	APOC1p2817	intron 3	2b	CC/CT	0.00329	0.13	0.2246	NA
25	APOC1p3423/rs389261	intron 3	no data	GA/GG	0.00247	-0.18	0.09939	NA
26	APOC1p2629	exon 3	4	GA/GG	0.00081	0.3	0.11169	0.22049
26	APOC1p2817	intron 3	2b	CC/CT	0.00329	0.13	0.2246	NA
26	APOC1p3423/rs389261	intron 3	no data	GA/GG	0.00247	-0.18	0.09939	NA
26	APOC1p3494	intron 3	no data	CC/CT	0.00161	0.26	0.04784	NA
27	APOC1p2817	intron 3	2b	CC/CT	0.00329	0.13	0.2246	0.76271
27	APOC1p3423/rs389261	intron 3	no data	GA/GG	0.00247	-0.18	0.09939	NA
27	APOC1p3494	intron 3	no data	CC/CT	0.00161	0.26	0.04784	NA
27	APOC1p4334/rs12721046	intron 3	6	AA/GA/GG	0.15221	-0.0001	0.99672	NA
28	APOC1p3423/rs389261	intron 3	no data	GA/GG	0.00247	-0.18	0.09939	0.79698
28	APOC1p3494	intron 3	no data	CC/CT	0.00161	0.26	0.04784	NA
28	APOC1p4334/rs12721046	intron 3	6	AA/GA/GG	0.15221	-0.0001	0.99672	NA
28	APOC1p5641/rs1064725	3'UTR	no data	GG/GT/TT	0.03883	0.03	0.32535	NA
29	APOC1p3494	intron 3	no data	CC/CT	0.00161	0.26	0.04784	0.07767
29	APOC1p4334/rs12721046	intron 3	6	AA/GA/GG	0.15221	-0.0001	0.99672	NA
29	APOC1p5641/rs1064725	3'UTR	no data	GG/GT/TT	0.03883	0.03	0.32535	NA
29	APOC1p5773	3' flanking	no data	GA/GG	0.00083	0.24	0.19556	NA
30	APOC1p4334/rs12721046	intron 3	6	AA/GA/GG	0.15221	-0.0001	0.99672	0.45722

Cont. Table 31

30	APOC1p5641/rs1064725	3'UTR	no data	GG/GT/TT	0.03883	0.03	0.32535	NA
30	APOC1p5773	3' flanking	no data	GA/GG	0.00083	0.24	0.19556	NA
30	APOC1p5926/rs56131196	3' flanking	no data	AA/GA/GG	0.18851	-0.01	0.6146	NA
31	APOC1p5641/rs1064725	3'UTR	no data	GG/GT/TT	0.03883	0.03	0.32535	0.53541
31	APOC1p5773	3' flanking	no data	GA/GG	0.00083	0.24	0.19556	NA
31	APOC1p5926/rs56131196	3' flanking	no data	AA/GA/GG	0.18851	-0.01	0.6146	NA
31	APOC1p6026/rs4420638	3 'flanking	no data	AA/GA/GG	0.15558	-0.01	0.56998	NA
32	APOC1p5773	3' flanking	no data	GA/GG	0.00083	0.24	0.19556	0.63232
32	APOC1p5926/rs56131196	3' flanking	no data	AA/GA/GG	0.18851	-0.01	0.6146	NA
32	APOC1p6026/rs4420638	3 'flanking	no data	AA/GA/GG	0.15558	-0.01	0.56998	NA
32	rs4803770	HCR1	5	CC/GC/GG	0.37795	0.003	0.76528	NA
33	APOC1p5926/rs56131196	3' flanking	no data	AA/GA/GG	0.18851	-0.01	0.6146	0.87834
33	APOC1p6026/rs4420638	3 'flanking	no data	AA/GA/GG	0.15558	-0.01	0.56998	NA
33	rs4803770	HCR1	5	CC/GC/GG	0.37795	0.003	0.76528	NA
33	HCR1p292/rs4803771	HCR1	4	CC/CG/GG	0.02451	-0.02	0.54022	NA
34	APOC1p6026/rs4420638	3 'flanking	no data	AA/GA/GG	0.15558	-0.01	0.56998	0.91218
34	rs4803770	HCR1	5	CC/GC/GG	0.37795	0.003	0.76528	NA
34	HCR1p292/rs4803771	HCR1	4	CC/CG/GG	0.02451	-0.02	0.54022	NA
34	HCR1p362	HCR1	2a	CA/CC	0.00247	0.001	0.99148	NA
35	rs4803770	HCR1	5	CC/GC/GG	0.37795	0.003	0.76528	0.50275
35	HCR1p292/rs4803771	HCR1	4	CC/CG/GG	0.02451	-0.02	0.54022	NA
35	HCR1p362	HCR1	2a	CA/CC	0.00247	0.001	0.99148	NA
35	HCR1p423	HCR1	4	CC/CG/GG	0.02581	0.06	0.09096	NA
36	HCR1p292/rs4803771	HCR1	4	CC/CG/GG	0.02451	-0.02	0.54022	0.23626
36	HCR1p362	HCR1	2a	CA/CC	0.00247	0.001	0.99148	NA
36	HCR1p423	HCR1	4	CC/CG/GG	0.02581	0.06	0.09096	NA
36	HCR1p575/rs157599	HCR1	3a	AA/AG	0.00242	-0.18	0.09959	NA
37	HCR1p362	HCR1	2a	CA/CC	0.00247	0.001	0.99148	0.12504
37	HCR1p423	HCR1	4	CC/CG/GG	0.02581	0.06	0.09096	NA
37	HCR1p575/rs157599	HCR1	3a	AA/AG	0.00242	-0.18	0.09959	NA
37	HCR1p727/rs149345	HCR1	3a	TG/TT	0.00244	-0.18	0.10151	NA
38	HCR1p423	HCR1	4	CC/CG/GG	0.02581	0.06	0.09096	0.10382
38	HCR1p575/rs157599	HCR1	3a	AA/AG	0.00242	-0.18	0.09959	NA

Cont. Table 31

38	HCR1p727/rs149345	HCR1	3a	TG/TT	0.00244	-0.18	0.10151	NA
38	rs5112	APOC1P1	4	CC/GC/GG	0.46329	-0.01	0.65328	NA
39	HCR1p575/rs157599	HCR1	3a	AA/AG	0.00242	-0.18	0.09959	0.2921
39	HCR1p727/rs149345	HCR1	3a	TG/TT	0.00244	-0.18	0.10151	NA
39	rs5112	APOC1P1	4	CC/GC/GG	0.46329	-0.01	0.65328	NA
39	rs7259004	APOC1P1	6	CC/CG/GG	0.11765	0.01	0.71147	NA
40	HCR1p727/rs149345	HCR1	3a	TG/TT	0.00244	-0.18	0.10151	0.03689
40	rs5112	APOC1P1	4	CC/GC/GG	0.46329	-0.01	0.65328	NA
40	rs7259004	APOC1P1	6	CC/CG/GG	0.11765	0.01	0.71147	NA
40	HCR2p188/rs35136575	HCR2	2a	CC/GC/GG	0.22742	0.03	0.03304	NA
41	rs5112	APOC1P1	4	CC/GC/GG	0.46329	-0.01	0.65328	0.09258
41	rs7259004	APOC1P1	6	CC/CG/GG	0.11765	0.01	0.71147	NA
41	HCR2p188/rs35136575	HCR2	2a	CC/GC/GG	0.22742	0.03	0.03304	NA
41	HCR2p365	HCR2	2b	CA/CC	0.00409	-0.02	0.81824	NA
42	rs7259004	APOC1P1	6	CC/CG/GG	0.11765	0.01	0.71147	0.10734
42	HCR2p188/rs35136575	HCR2	2a	CC/GC/GG	0.22742	0.03	0.03304	NA
42	HCR2p365	HCR2	2b	CA/CC	0.00409	-0.02	0.81824	NA
42	HCR2p523	HCR2	2b	CC/CT	0.02258	-0.03	0.37507	NA
43	HCR2p188/rs35136575	HCR2	2a	CC/GC/GG	0.22742	0.03	0.03304	0.02013
43	HCR2p365	HCR2	2b	CA/CC	0.00409	-0.02	0.81824	NA
43	HCR2p523	HCR2	2b	CC/CT	0.02258	-0.03	0.37507	NA
43	APOC4p636	5' flanking	no data	CC/CT	0.00083	-0.36	0.0564	NA
44	HCR2p365	HCR2	2b	CA/CC	0.00409	-0.02	0.81824	0.49618
44	HCR2p523	HCR2	2b	CC/CT	0.02258	-0.03	0.37507	NA
44	APOC4p636	5' flanking	no data	CC/CT	0.00083	-0.36	0.0564	NA
44	APOC4p968/rs76214972	5'UTR	4	AA/AG	0.03623	-0.03	0.34336	NA
45	HCR2p523	HCR2	2b	CC/CT	0.02258	-0.03	0.37507	0.57223
45	APOC4p636	5' flanking	no data	CC/CT	0.00083	-0.36	0.0564	NA
45	APOC4p968/rs76214972	5'UTR	4	AA/AG	0.03623	-0.03	0.34336	NA
45	APOC4p1150/rs148247675	intron 1	5	AA/GA	0.00166	0.26	0.04737	NA
46	APOC4p636	5' flanking	no data	CC/CT	0.00083	-0.36	0.0564	0.26683
46	APOC4p968/rs76214972	5'UTR	4	AA/AG	0.03623	-0.03	0.34336	NA
46	APOC4p1150/rs148247675	intron 1	5	AA/GA	0.00166	0.26	0.04737	NA

Cont. Table 31

46	APOC4p1229	intron 1	2b	GC/GG	0.00161	-0.36	0.00733	NA
47	APOC4p968/rs76214972	5'UTR	4	AA/AG	0.03623	-0.03	0.34336	0.3462
47	APOC4p1150/rs148247675	intron 1	5	AA/GA	0.00166	0.26	0.04737	NA
47	APOC4p1229	intron 1	2b	GC/GG	0.00161	-0.36	0.00733	NA
47	APOC4p2557	intron 1	4	CA/CC	0.00081	-0.27	0.14545	NA
48	APOC4p1150/rs148247675	intron 1	5	AA/GA	0.00166	0.26	0.04737	0.43724
48	APOC4p1229	intron 1	2b	GC/GG	0.00161	-0.36	0.00733	NA
48	APOC4p2557	intron 1	4	CA/CC	0.00081	-0.27	0.14545	NA
48	APOC4p2623/rs5157	intron 1	4	CC/CT/TT	0.49759	-0.01	0.48156	NA
49	APOC4p1229	intron 1	2b	GC/GG	0.00161	-0.36	0.00733	0.01224
49	APOC4p2557	intron 1	4	CA/CC	0.00081	-0.27	0.14545	NA
49	APOC4p2623/rs5157	intron 1	4	CC/CT/TT	0.49759	-0.01	0.48156	NA
49	APOC4p2640/rs5158	intron 1	2b	CC/CT/TT	0.13813	0.02	0.14018	NA
50	APOC4p2557	intron 1	4	CA/CC	0.00081	-0.27	0.14545	0.7013
50	APOC4p2623/rs5157	intron 1	4	CC/CT/TT	0.49759	-0.01	0.48156	NA
50	APOC4p2640/rs5158	intron 1	2b	CC/CT/TT	0.13813	0.02	0.14018	NA
50	APOC4p2683/rs12721109	intron 1	2b	AA/AG/GG	0.02369	0.03	0.38586	NA
51	APOC4p2623/rs5157	intron 1	4	CC/CT/TT	0.49759	-0.01	0.48156	0.76319
51	APOC4p2640/rs5158	intron 1	2b	CC/CT/TT	0.13813	0.02	0.14018	NA
51	APOC4p2683/rs12721109	intron 1	2b	AA/AG/GG	0.02369	0.03	0.38586	NA
51	APOC4p2703/rs12721108	intron 1	2a	GG/GT	0.00808	-0.04	0.53441	NA
52	APOC4p2640/rs5158	intron 1	2b	CC/CT/TT	0.13813	0.02	0.14018	0.75905
52	APOC4p2683/rs12721109	intron 1	2b	AA/AG/GG	0.02369	0.03	0.38586	NA
52	APOC4p2703/rs12721108	intron 1	2a	GG/GT	0.00808	-0.04	0.53441	NA
52	APOC4p3498C2p194/rs1132899	C4-exon2	5	CC/CT/TT	0.48629	-0.01	0.42951	NA
53	APOC4p2683/rs12721109	intron 1	2b	AA/AG/GG	0.02369	0.03	0.38586	0.72787
53	APOC4p2703/rs12721108	intron 1	2a	GG/GT	0.00808	-0.04	0.53441	NA
53	APOC2p194C4p3498/rs1132899	C4-exon2	5	CC/CT/TT	0.48629	-0.01	0.42951	NA
53	APOC2p242C4p3546/rs12691089	C4-exon2	5	AG/GG	0.00322	-0.01	0.91107	NA
54	APOC4p2703/rs12721108	intron 1	2a	GG/GT	0.00808	-0.04	0.53441	0.24838
54	APOC2p194C4p3498/rs1132899	C4-exon2	5	CC/CT/TT	0.48629	-0.01	0.42951	NA
54	APOC2p242C4p3546/rs12691089	C4-exon2	5	AG/GG	0.00322	-0.01	0.91107	NA
54	APOC2p543C4p3847/rs186448850	C4-intron2	5	CT/TT	0.00164	-0.36	0.0074	NA

Cont. Table 31

55	APOC2p194C4p3498/rs1132899	C4-exon2	5	CC/CT/TT	0.48629	-0.01	0.42951	0.33125
55	APOC2p242C4p3546/rs12691089	C4-exon2	5	AG/GG	0.00322	-0.01	0.91107	NA
55	APOC2p543C4p3847/rs186448850	C4-intron2	5	CT/TT	0.00164	-0.36	0.0074	NA
55	APOC2p623C4p3927/rs5167	C4-exon3	5	GG/TG/TT	0.35955	-0.001	0.92518	NA
56	APOC2p242C4p3546/rs12691089	C4-exon2	5	AG/GG	0.00322	-0.01	0.91107	0.09285
56	APOC2p543C4p3847/rs186448850	C4-intron2	5	CT/TT	0.00164	-0.36	0.0074	NA
56	APOC2p623C4p3927/rs5167	C4-exon3	5	GG/TG/TT	0.35955	-0.001	0.92518	NA
56	APOC2p1357C4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	CC/CG/GG	0.49678	0.01	0.58956	NA
57	APOC2p543C4p3847/rs186448850	C4-intron2	5	CT/TT	0.00164	-0.36	0.0074	0.00316
57	APOC2p623C4p3927/rs5167	C4-exon3	5	GG/TG/TT	0.35955	-0.001	0.92518	NA
57	APOC2p1357C4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	CC/CG/GG	0.49678	0.01	0.58956	NA
57	APOC2p1591C4p4895	C2-intron1	4	GA/GG	0.00081	-0.36	0.05115	NA
58	APOC2p623C4p3927/rs5167	C4-exon3	5	GG/TG/TT	0.35955	-0.001	0.92518	0.0822
58	APOC2p1357C4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	CC/CG/GG	0.49678	0.01	0.58956	NA
58	APOC2p1591C4p4895	C2-intron1	4	GA/GG	0.00081	-0.36	0.05115	NA
58	APOC2p1851/rs12709886	intron 1	6	GA/GG	0.03722	-0.02	0.41183	NA
59	APOC2p1357C4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	CC/CG/GG	0.49678	0.01	0.58956	0.68608
59	APOC2p1591C4p4895	C2-intron1	4	GA/GG	0.00081	-0.36	0.05115	NA
59	APOC2p1851/rs12709886	intron 1	6	GA/GG	0.03722	-0.02	0.41183	NA
59	APOC2p2870	intron 1	4	GG/GT	0.00403	0.03	0.7577	NA
60	APOC2p1591C4p4895	C2-intron1	4	GA/GG	0.00081	-0.36	0.05115	0.2064
60	APOC2p1851/rs12709886	intron 1	6	GA/GG	0.03722	-0.02	0.41183	NA
60	APOC2p2870	intron 1	4	GG/GT	0.00403	0.03	0.7577	NA
60	APOC2p3348/rs10420434	intron 1	no data	GA/GG	0.0371	0.05	0.10518	NA
61	APOC2p1851/rs12709886	intron 1	6	GA/GG	0.03722	-0.02	0.41183	0.47918
61	APOC2p2870	intron 1	4	GG/GT	0.00403	0.03	0.7577	NA
61	APOC2p3348/rs10420434	intron 1	no data	GA/GG	0.0371	0.05	0.10518	NA
61	APOC2p3778/rs5120	intron 1	4	AA/AT/TT	0.49756	0.01	0.51351	NA
62	APOC2p2870	intron 1	4	GG/GT	0.00403	0.03	0.7577	0.23867
62	APOC2p3348/rs10420434	intron 1	no data	GA/GG	0.0371	0.05	0.10518	NA
62	APOC2p3778/rs5120	intron 1	4	AA/AT/TT	0.49756	0.01	0.51351	NA
62	APOC2p4853/rs199828513	3' flanking	no data	DD/WD/WW	0.27832	-0.01	0.32077	NA
63	APOC2p3348/rs10420434	intron 1	no data	GA/GG	0.0371	0.05	0.10518	0.28973

Cont. Table 31

63	APOC2p3778/rs5120	intron 1	4	AA/AT/TT	0.49756	0.01	0.51351	NA
63	APOC2p4853/rs199828513	3' flanking	no data	DD/WD/WW	0.27832	-0.01	0.32077	NA
63	APOC2p5004/rs10421404	3' flanking	no data	CC/CT/TT	0.18233	0.02	0.25579	NA
64	APOC2p3778/rs5120	intron 1	4	AA/AT/TT	0.49756	0.01	0.51351	0.20798
64	APOC2p4853/rs199828513	3' flanking	no data	DD/WD/WW	0.27832	-0.01	0.32077	NA
64	APOC2p5004/rs10421404	3' flanking	no data	CC/CT/TT	0.18233	0.02	0.25579	NA
64	APOC2p5310/rs7258345	3' flanking	no data	GG/TG/TT	0.46487	-0.002	0.84552	NA
65	APOC2p4853/rs199828513	3' flanking	no data	DD/WD/WW	0.27832	-0.01	0.32077	0.299
65	APOC2p5004/rs10421404	3' flanking	no data	CC/CT/TT	0.18233	0.02	0.25579	NA
65	APOC2p5310/rs7258345	3' flanking	no data	GG/TG/TT	0.46487	-0.002	0.84552	NA
65	APOC2p5398/rs12709889	3' flanking	6	AA/GA/GG	0.27603	-0.01	0.27402	NA
66	APOC2p5004/rs10421404	3' flanking	no data	CC/CT/TT	0.18233	0.02	0.25579	0.53685
66	APOC2p5310/rs7258345	3' flanking	no data	GG/TG/TT	0.46487	-0.002	0.84552	NA
66	APOC2p5398/rs12709889	3' flanking	6	AA/GA/GG	0.27603	-0.01	0.27402	NA
66	APOC2p5644	3' flanking	6	AG/GG	0.00923	0.01	0.89469	NA

wind: 4-SNPs haplotype window; w.snps: SNPs that were included in each window; p-value: single-locus p-value; hap-P: haplotype global p-value; [a] Cox-Box transformed data.

Table 32. Haplotype-based association results with ApoB, and ApoA1 in NHWs

HAPLOTYPE WINDOWS						ApoB[a]			ApoA1		
wind	w.snp	Function	RegulomeDB svore	Genotype	MAF	Beta	Single-p	hap_P	Beta	Single-p	hap_P
1	APOE560/rs449647	5' flanking	5	AA/AT/TT	0.16103	-0.95	0.12896	0.00002	-1.57	0.61755	0.63079
1	APOE832rs405509	5' flanking	1f	GG/GT/TT	0.47749	1.46	0.0009	NA	-1.8	0.41735	NA
1	APOE1163/rs440446	intron 1	4	CC/GC/GG	0.36035	0.56	0.23194	NA	-0.19	0.9349	NA
1	APOE1575rs769448	intron 1	4	CC/CT/TT	0.02097	0.94	0.52039	NA	3.44	0.63942	NA
2	APOE832rs405509	5' flanking	1f	GG/GT/TT	0.47749	1.46	0.0009	0.00041	-1.8	0.41735	0.30357
2	APOE1163/rs440446	intron 1	4	CC/GC/GG	0.36035	0.56	0.23194	NA	-0.19	0.9349	NA
2	APOE1575rs769448	intron 1	4	CC/CT/TT	0.02097	0.94	0.52039	NA	3.44	0.63942	NA
2	APOE1998/rs769449	intron 2	4	AA/AG/GG	0.1165	2.03	0.00297	NA	-4.38	0.20481	NA
3	APOE1163/rs440446	intron 1	4	CC/GC/GG	0.36035	0.56	0.23194	8.05E-07	-0.19	0.9349	0.51661
3	APOE1575rs769448	intron 1	4	CC/CT/TT	0.02097	0.94	0.52039	NA	3.44	0.63942	NA
3	APOE1998/rs769449	intron 2	4	AA/AG/GG	0.1165	2.03	0.00297	NA	-4.38	0.20481	NA
3	APOE2440/rs769450	intron 2	5	AA/GA/GG	0.40145	0.15	0.74223	NA	0.7	0.76559	NA
4	APOE1575rs769448	intron 1	4	CC/CT/TT	0.02097	0.94	0.52039	0.02649	3.44	0.63942	0.71919
4	APOE1998/rs769449	intron 2	4	AA/AG/GG	0.1165	2.03	0.00297	NA	-4.38	0.20481	NA
4	APOE2440/rs769450	intron 2	5	AA/GA/GG	0.40145	0.15	0.74223	NA	0.7	0.76559	NA
4	APOE2907/rs769451	intron 2	5	GT/TT	0.01124	-0.22	0.9196	NA	3.7	0.73794	NA
5	APOE1998/rs769449	intron 2	4	AA/AG/GG	0.1165	2.03	0.00297	0.01761	-4.38	0.20481	0.5894
5	APOE2440/rs769450	intron 2	5	AA/GA/GG	0.40145	0.15	0.74223	NA	0.7	0.76559	NA
5	APOE2907/rs769451	intron 2	5	GT/TT	0.01124	-0.22	0.9196	NA	3.7	0.73794	NA
5	APOE3038/rs111833428	exon 3	5	AG/GG	0.00162	13.81	0.03418	NA	3.29	0.92048	NA
6	APOE2440/rs769450	intron 2	5	AA/GA/GG	0.40145	0.15	0.74223	0.09646	0.7	0.76559	0.86069
6	APOE2907/rs769451	intron 2	5	GT/TT	0.01124	-0.22	0.9196	NA	3.7	0.73794	NA
6	APOE3038/rs111833428	exon 3	5	AG/GG	0.00162	13.81	0.03418	NA	3.29	0.92048	NA
6	APOE3106/rs769452	exon 3	5	TC/TT	0.00081	9.15	0.1602	NA	29.79	0.3649	NA
7	APOE2907/rs769451	intron 2	5	GT/TT	0.01124	-0.22	0.9196	0.00266	3.7	0.73794	0.35441
7	APOE3038/rs111833428	exon 3	5	AG/GG	0.00162	13.81	0.03418	NA	3.29	0.92048	NA
7	APOE3106/rs769452	exon 3	5	TC/TT	0.00081	9.15	0.1602	NA	29.79	0.3649	NA
7	APOE3937/rs429358	exon 4	5	CC/CT/TT	0.15253	2.14	0.0005	NA	-3.66	0.23988	NA
8	APOE3038/rs111833428	exon 3	5	AG/GG	0.00162	13.81	0.03418	4.37E-14	3.29	0.92048	0.0907
8	APOE3106/rs769452	exon 3	5	TC/TT	0.00081	9.15	0.1602	NA	29.79	0.3649	NA

Cont. Table 32

8	APOE3937/rs429358	exon 4	5	CC/CT/TT	0.15253	2.14	0.0005	NA	-3.66	0.23988	NA
8	APOE4075/rs7412	exon 4	5	CC/TC/TT	0.08065	-5.6	9.65E-13	NA	5.12	0.20813	NA
9	APOE3106/rs769452	exon 3	5	TC/TT	0.00081	9.15	0.1602	8.32E-13	29.79	0.3649	0.35899
9	APOE3937/rs429358	exon 4	5	CC/CT/TT	0.15253	2.14	0.0005	NA	-3.66	0.23988	NA
9	APOE4075/rs7412	exon 4	5	CC/TC/TT	0.08065	-5.6	9.65E-13	NA	5.12	0.20813	NA
9	APOE4310/rs199768005	exon 4	5	TA/TT	0.00402	1.05	0.82199	NA	-35.74	0.12454	NA
10	APOE3937/rs429358	exon 4	5	CC/CT/TT	0.15253	2.14	0.0005	9.72E-13	-3.66	0.23988	0.28206
10	APOE4075/rs7412	exon 4	5	CC/TC/TT	0.08065	-5.6	9.65E-13	NA	5.12	0.20813	NA
10	APOE4310/rs199768005	exon 4	5	TA/TT	0.00402	1.05	0.82199	NA	-35.74	0.12454	NA
10	APOE4737/rs117656888	3'flanking	5	CC/GC	0.00806	1.6	0.5203	NA	-5.55	0.6576	NA
11	APOE4075/rs7412	exon 4	5	CC/TC/TT	0.08065	-5.6	9.65E-13	5.19E-11	5.12	0.20813	0.27626
11	APOE4310/rs199768005	exon 4	5	TA/TT	0.00402	1.05	0.82199	NA	-35.74	0.12454	NA
11	APOE4737/rs117656888	3'flanking	5	CC/GC	0.00806	1.6	0.5203	NA	-5.55	0.6576	NA
11	APOE5361/rs1081106	3'flanking	3a	CC/TC/TT	0.08521	0.12	0.88128	NA	3.3	0.43184	NA
12	APOE4310/rs199768005	exon 4	5	TA/TT	0.00402	1.05	0.82199	0.71494	-35.74	0.12454	0.34024
12	APOE4737/rs117656888	3'flanking	5	CC/GC	0.00806	1.6	0.5203	NA	-5.55	0.6576	NA
12	APOE5361/rs1081106	3'flanking	3a	CC/TC/TT	0.08521	0.12	0.88128	NA	3.3	0.43184	NA
12	rs439401	intergenic	1b	CC/CT/TT	0.35961	0.39	0.39749	NA	0.91	0.69151	NA
13	APOE4737/rs117656888	3'flanking	5	CC/GC	0.00806	1.6	0.5203	2.35E-06	-5.55	0.6576	0.43609
13	APOE5361/rs1081106	3'flanking	3a	CC/TC/TT	0.08521	0.12	0.88128	NA	3.3	0.43184	NA
13	rs439401	intergenic	1b	CC/CT/TT	0.35961	0.39	0.39749	NA	0.91	0.69151	NA
13	APOC1rs445925	intergenic	no data	AA/GA/GG	0.1094	-3.78	5.17E-08	NA	3.53	0.32306	NA
14	APOE5361/rs1081106	3'flanking	3a	CC/TC/TT	0.08521	0.12	0.88128	1.91E-06	3.3	0.43184	0.60969
14	rs439401	intergenic	1b	CC/CT/TT	0.35961	0.39	0.39749	NA	0.91	0.69151	NA
14	APOC1rs445925	intergenic	no data	AA/GA/GG	0.1094	-3.78	5.17E-08	NA	3.53	0.32306	NA
14	APOC1p698/rs72654449	5'flanking	4	CA/CC	0.00405	-2.77	0.55052	NA	-4.7	0.84127	NA
15	rs439401	intergenic	1b	CC/CT/TT	0.35961	0.39	0.39749	7.14E-07	0.91	0.69151	0.27455
15	APOC1rs445925	intergenic	no data	AA/GA/GG	0.1094	-3.78	5.17E-08	NA	3.53	0.32306	NA
15	APOC1p698/rs72654449	5'flanking	4	CA/CC	0.00405	-2.77	0.55052	NA	-4.7	0.84127	NA
15	APOC1p703/rs3207187	5'flanking	4	CC/CT	0.00081	-0.88	0.89283	NA	102.96	0.00165	NA
16	APOC1rs445925	intergenic	no data	AA/GA/GG	0.1094	-3.78	5.17E-08	7.77E-08	3.53	0.32306	0.18289
16	APOC1p698/rs72654449	5'flanking	4	CA/CC	0.00405	-2.77	0.55052	NA	-4.7	0.84127	NA

Cont. Table 32

16	APOC1p703/rs3207187	5'flanking	4	CC/CT	0.00081	-0.88	0.89283	NA	102.96	0.00165	NA
16	APOC1p720/rs72654451	5'flanking	4	II/WI/WW	0.2299	-0.82	0.11683	NA	-0.46	0.86119	NA
17	APOC1p698/rs72654449	5'flanking	4	CA/CC	0.00405	-2.77	0.55052	0.25344	-4.7	0.84127	0.21401
17	APOC1p703/rs3207187	5'flanking	4	CC/CT	0.00081	-0.88	0.89283	NA	102.96	0.00165	NA
17	APOC1p720/rs72654451	5'flanking	4	II/WI/WW	0.2299	-0.82	0.11683	NA	-0.46	0.86119	NA
17	APOC1p1170	intron 1	2b	GA/GG	0.00082	7.14	0.27763	NA	18.3	0.57227	NA
18	APOC1p703/rs3207187	5'flanking	4	CC/CT	0.00081	-0.88	0.89283	0.19599	102.96	0.00165	0.03024
18	APOC1p720/rs72654451	5'flanking	4	II/WI/WW	0.2299	-0.82	0.11683	NA	-0.46	0.86119	NA
18	APOC1p1170	intron 1	2b	GA/GG	0.00082	7.14	0.27763	NA	18.3	0.57227	NA
18	APOC1p1294	intron 2	4	AA/AC	0.00081	3.07	0.63865	NA	27.03	0.4118	NA
19	APOC1p720/rs72654451	5'flanking	4	II/WI/WW	0.2299	-0.82	0.11683	0.01494	-0.46	0.86119	0.02329
19	APOC1p1170	intron 1	2b	GA/GG	0.00082	7.14	0.27763	NA	18.3	0.57227	NA
19	APOC1p1294	intron 2	4	AA/AC	0.00081	3.07	0.63865	NA	27.03	0.4118	NA
19	APOC1p1317/rs12721048	intron 2	4	GA/GG	0.00164	11.18	0.01598	NA	66.89	0.00423	NA
20	APOC1p1170	intron 1	2b	GA/GG	0.00082	7.14	0.27763	0.01839	18.3	0.57227	0.03642
20	APOC1p1294	intron 2	4	AA/AC	0.00081	3.07	0.63865	NA	27.03	0.4118	NA
20	APOC1p1317/rs12721048	intron 2	4	GA/GG	0.00164	11.18	0.01598	NA	66.89	0.00423	NA
20	APOC1p1422	intron 2	4	GA/GG	0.00161	1.88	0.77425	NA	-26.52	0.42032	NA
21	APOC1p1294	intron 2	4	AA/AC	0.00081	3.07	0.63865	0.69399	27.03	0.4118	0.76922
21	APOC1p1317/rs12721048	intron 2	4	GA/GG	0.00164	11.18	0.01598	NA	66.89	0.00423	NA
21	APOC1p1422	intron 2	4	GA/GG	0.00161	1.88	0.77425	NA	-26.52	0.42032	NA
21	APOC1p1566/rs12691088	intron 2	2b	GA/GG	0.00579	-4.95	0.12948	NA	-27.45	0.09146	NA
22	APOC1p1317/rs12721048	intron 2	4	GA/GG	0.00164	11.18	0.01598	0.66989	66.89	0.00423	0.91771
22	APOC1p1422	intron 2	4	GA/GG	0.00161	1.88	0.77425	NA	-26.52	0.42032	NA
22	APOC1p1566/rs12691088	intron 2	2b	GA/GG	0.00579	-4.95	0.12948	NA	-27.45	0.09146	NA
22	APOC1p2041/rs3826688	intron 2	5	AA/GA/GG	0.34241	0.3	0.51703	NA	0.24	0.91759	NA
23	APOC1p1422	intron 2	4	GA/GG	0.00161	1.88	0.77425	0.24701	-26.52	0.42032	0.26215
23	APOC1p1566/rs12691088	intron 2	2b	GA/GG	0.00579	-4.95	0.12948	NA	-27.45	0.09146	NA
23	APOC1p2041/rs3826688	intron 2	5	AA/GA/GG	0.34241	0.3	0.51703	NA	0.24	0.91759	NA
23	APOC1p2629	exon 3	4	GA/GG	0.00081	-5.12	0.43402	NA	2.54	0.93833	NA
24	APOC1p1566/rs12691088	intron 2	2b	GA/GG	0.00579	-4.95	0.12948	0.08378	-27.45	0.09146	0.87228
24	APOC1p2041/rs3826688	intron 2	5	AA/GA/GG	0.34241	0.3	0.51703	NA	0.24	0.91759	NA

Cont. Table 32

24	APOC1p2629	exon 3	4	GA/GG	0.00081	-5.12	0.43402	NA	2.54	0.93833	NA
24	APOC1p2817	intron 3	2b	CC/CT	0.00329	-4.46	0.23676	NA	21.2	0.27005	NA
25	APOC1p2041/rs3826688	intron 2	5	AA/GA/GG	0.34241	0.3	0.51703	0.19514	0.24	0.91759	0.98712
25	APOC1p2629	exon 3	4	GA/GG	0.00081	-5.12	0.43402	NA	2.54	0.93833	NA
25	APOC1p2817	intron 3	2b	CC/CT	0.00329	-4.46	0.23676	NA	21.2	0.27005	NA
25	APOC1p3423rs389261	intron 3	no data	GA/GG	0.00247	-3.5	0.35153	NA	-21.68	0.2583	NA
26	APOC1p2629	exon 3	4	GA/GG	0.00081	-5.12	0.43402	0.20128	2.54	0.93833	0.9918
26	APOC1p2817	intron 3	2b	CC/CT	0.00329	-4.46	0.23676	NA	21.2	0.27005	NA
26	APOC1p3423rs389261	intron 3	no data	GA/GG	0.00247	-3.5	0.35153	NA	-21.68	0.2583	NA
26	APOC1p3494	intron 3	no data	CC/CT	0.00161	5.38	0.41256	NA	-1.39	0.96622	NA
27	APOC1p2817	intron 3	2b	CC/CT	0.00329	-4.46	0.23676	0.01678	21.2	0.27005	0.82389
27	APOC1p3423rs389261	intron 3	no data	GA/GG	0.00247	-3.5	0.35153	NA	-21.68	0.2583	NA
27	APOC1p3494	intron 3	no data	CC/CT	0.00161	5.38	0.41256	NA	-1.39	0.96622	NA
27	APOC1p4334/rs12721046	intron 3	6	AA/GA/GG	0.15221	1.59	0.00983	NA	-2.11	0.49556	NA
28	APOC1p3423rs389261	intron 3	no data	GA/GG	0.00247	-3.5	0.35153	0.01486	-21.68	0.2583	0.55738
28	APOC1p3494	intron 3	no data	CC/CT	0.00161	5.38	0.41256	NA	-1.39	0.96622	NA
28	APOC1p4334/rs12721046	intron 3	6	AA/GA/GG	0.15221	1.59	0.00983	NA	-2.11	0.49556	NA
28	APOC1p5641/rs1064725	3'UTR	no data	GG/GT/TT	0.03883	2	0.09267	NA	-4.32	0.47284	NA
29	C1p3494	intron 3	no data	CC/CT	0.00161	5.38	0.41256	0.00809	-1.39	0.96622	0.85336
29	C1p4334/rs12721046	intron 3	6	AA/GA/GG	0.15221	1.59	0.00983	NA	-2.11	0.49556	NA
29	APOC1p5641/rs1064725	3'UTR	no data	GG/GT/TT	0.03883	2	0.09267	NA	-4.32	0.47284	NA
29	APOC1p5926/rs56131196	3' flanking	no data	AA/GA/GG	0.18851	1.75	0.00229	NA	-2.59	0.3695	NA
30	APOC1p4334/rs12721046	intron 3	6	AA/GA/GG	0.15221	1.59	0.00983	0.01101	-2.11	0.49556	0.71384
30	APOC1p5641/rs1064725	3'UTR	no data	GG/GT/TT	0.03883	2	0.09267	NA	-4.32	0.47284	NA
30	APOC1p5926/rs56131196	3' flanking	no data	AA/GA/GG	0.18851	1.75	0.00229	NA	-2.59	0.3695	NA
30	APOC1p6026/rs4420638	3 'flanking	no data	AA/GA/GG	0.15558	1.43	0.01775	NA	-1.1	0.71599	NA
31	APOC1p5641/rs1064725	3'UTR	no data	GG/GT/TT	0.03883	2	0.09267	0.00011	-4.32	0.47284	0.51634
31	APOC1p5926/rs56131196	3' flanking	no data	AA/GA/GG	0.18851	1.75	0.00229	NA	-2.59	0.3695	NA
31	APOC1p6026/rs4420638	3 'flanking	no data	AA/GA/GG	0.15558	1.43	0.01775	NA	-1.1	0.71599	NA
31	rs4803770	HCR1	5	CC/GC/GG	0.37795	0.56	0.21851	NA	0.02	0.99367	NA
32	APOC1p5926/rs56131196	3' flanking	no data	AA/GA/GG	0.18851	1.75	0.00229	0.00131	-2.59	0.3695	0.5184
32	APOC1p6026/rs4420638	3 'flanking	no data	AA/GA/GG	0.15558	1.43	0.01775	NA	-1.1	0.71599	NA

Cont. Table 32

32	rs4803770	HCR1	5	CC/GC/GG	0.37795	0.56	0.21851	NA	0.02	0.99367	NA
32	HCR1p292/rs4803771	HCR1	4	CC/CG/GG	0.02451	0.68	0.64404	NA	-5.81	0.42728	NA
33	APOC1p6026/rs4420638	3 'flanking	no data	AA/GA/GG	0.15558	1.43	0.01775	0.01945	-1.1	0.71599	0.79712
33	rs4803770	HCR1	5	CC/GC/GG	0.37795	0.56	0.21851	NA	0.02	0.99367	NA
33	HCR1p292/rs4803771	HCR1	4	CC/CG/GG	0.02451	0.68	0.64404	NA	-5.81	0.42728	NA
33	HCR1p362	HCR1	2a	CA/CC	0.00247	2.07	0.75319	NA	-3.48	0.91586	NA
34	rs4803770	HCR1	5	CC/GC/GG	0.37795	0.56	0.21851	0.3828	0.02	0.99367	0.56196
34	HCR1p292/rs4803771	HCR1	4	CC/CG/GG	0.02451	0.68	0.64404	NA	-5.81	0.42728	NA
34	HCR1p362	HCR1	2a	CA/CC	0.00247	2.07	0.75319	NA	-3.48	0.91586	NA
34	HCR1p423	HCR1	4	CC/CG/GG	0.02581	2.1	0.14804	NA	11.09	0.12932	NA
35	HCR1p292/rs4803771	HCR1	4	CC/CG/GG	0.02451	0.68	0.64404	0.43162	-5.81	0.42728	0.26826
35	HCR1p362	HCR1	2a	CA/CC	0.00247	2.07	0.75319	NA	-3.48	0.91586	NA
35	HCR1p423	HCR1	4	CC/CG/GG	0.02581	2.1	0.14804	NA	11.09	0.12932	NA
35	HCR1p575/rs157599	HCR1	3a	AA/AG	0.00242	-3.48	0.35815	NA	-21.8	0.25308	NA
36	HCR1p362	HCR1	2a	CA/CC	0.00247	2.07	0.75319	0.2894	-3.48	0.91586	0.18676
36	HCR1p423	HCR1	4	CC/CG/GG	0.02581	2.1	0.14804	NA	11.09	0.12932	NA
36	HCR1p575/rs157599	HCR1	3a	AA/AG	0.00242	-3.48	0.35815	NA	-21.8	0.25308	NA
36	HCR1p727/rs149345	HCR1	3a	TG/TT	0.00244	-3.47	0.35832	NA	-21.7	0.25437	NA
37	HCR1p423	HCR1	4	CC/CG/GG	0.02581	2.1	0.14804	0.34557	11.09	0.12932	0.2714
37	HCR1p575/rs157599	HCR1	3a	AA/AG	0.00242	-3.48	0.35815	NA	-21.8	0.25308	NA
37	HCR1p727/rs149345	HCR1	3a	TG/TT	0.00244	-3.47	0.35832	NA	-21.7	0.25437	NA
37	rs5112	APOC1P1	4	CC/GC/GG	0.46329	-0.15	0.75492	NA	-0.67	0.77688	NA
38	HCR1p575/rs157599	HCR1	3a	AA/AG	0.00242	-3.48	0.35815	0.15272	-21.8	0.25308	0.10958
38	HCR1p727/rs149345	HCR1	3a	TG/TT	0.00244	-3.47	0.35832	NA	-21.7	0.25437	NA
38	rs5112	APOC1P1	4	CC/GC/GG	0.46329	-0.15	0.75492	NA	-0.67	0.77688	NA
38	rs7259004	APOC1P1	6	CC/CG/GG	0.11765	-1.33	0.05153	NA	6.89	0.04602	NA
39	HCR1p727/rs149345	HCR1	3a	TG/TT	0.00244	-3.47	0.35832	0.36908	-21.7	0.25437	0.06537
39	rs5112	APOC1P1	4	CC/GC/GG	0.46329	-0.15	0.75492	NA	-0.67	0.77688	NA
39	rs7259004	APOC1P1	6	CC/CG/GG	0.11765	-1.33	0.05153	NA	6.89	0.04602	NA
39	HCR2p188/rs35136575	HCR2	2a	CC/GC/GG	0.22742	-0.48	0.36635	NA	5.16	0.04957	NA
40	rs5112	APOC1P1	4	CC/GC/GG	0.46329	-0.15	0.75492	0.314	-0.67	0.77688	0.10135
40	rs7259004	APOC1P1	6	CC/CG/GG	0.11765	-1.33	0.05153	NA	6.89	0.04602	NA

Cont. Table 32

40	HCR2p188/rs35136575	HCR2	2a	CC/GC/GG	0.22742	-0.48	0.36635	NA	5.16	0.04957	NA
40	HCR2p365	HCR2	2b	CA/CC	0.00409	3.05	0.41812	NA	10.58	0.58105	NA
41	rs7259004	APOC1P1	6	CC/CG/GG	0.11765	-1.33	0.05153	0.35093	6.89	0.04602	0.06601
41	HCR2p188/rs35136575	HCR2	2a	CC/GC/GG	0.22742	-0.48	0.36635	NA	5.16	0.04957	NA
41	HCR2p365	HCR2	2b	CA/CC	0.00409	3.05	0.41812	NA	10.58	0.58105	NA
41	HCR2p523	HCR2	2b	CC/CT	0.02258	1.04	0.47773	NA	3.82	0.60612	NA
42	HCR2p188/rs35136575	HCR2	2a	CC/GC/GG	0.22742	-0.48	0.36635	0.1967	5.16	0.04957	0.35493
42	HCR2p365	HCR2	2b	CA/CC	0.00409	3.05	0.41812	NA	10.58	0.58105	NA
42	HCR2p523	HCR2	2b	CC/CT	0.02258	1.04	0.47773	NA	3.82	0.60612	NA
42	C4p968/rs76214972	5'UTR	4	AA/AG	0.03623	1.25	0.29092	NA	2.03	0.73303	NA
43	HCR2p365	HCR2	2b	CA/CC	0.00409	3.05	0.41812	0.4537	10.58	0.58105	0.9155
43	HCR2p523	HCR2	2b	CC/CT	0.02258	1.04	0.47773	NA	3.82	0.60612	NA
43	APOC4p968/rs76214972	5'UTR	4	AA/AG	0.03623	1.25	0.29092	NA	2.03	0.73303	NA
43	APOC4p1150/rs148247675	intron 1	5	AA/GA	0.00166	5.53	0.3975	NA	-1.61	0.96085	NA
44	HCR2p523	HCR2	2b	CC/CT	0.02258	1.04	0.47773	0.62842	3.82	0.60612	0.91367
44	APOC4p968/rs76214972	5'UTR	4	AA/AG	0.03623	1.25	0.29092	NA	2.03	0.73303	NA
44	APOC4p1150/rs148247675	intron 1	5	AA/GA	0.00166	5.53	0.3975	NA	-1.61	0.96085	NA
44	APOC4p2557	intron 1	4	CA/CC	0.00081	-5.26	0.42411	NA	-14.77	0.65409	NA
45	APOC4p968/rs76214972	5'UTR	4	AA/AG	0.03623	1.25	0.29092	0.71365	2.03	0.73303	0.96118
45	APOC4p1150/rs148247675	intron 1	5	AA/GA	0.00166	5.53	0.3975	NA	-1.61	0.96085	NA
45	APOC4p2557	intron 1	4	CA/CC	0.00081	-5.26	0.42411	NA	-14.77	0.65409	NA
45	APOC4p2623/rs5157	intron 1	4	CC/CT/TT	0.49759	-0.3	0.49795	NA	0.34	0.87974	NA
46	APOC4p1150/rs148247675	intron 1	5	AA/GA	0.00166	5.53	0.3975	0.91812	-1.61	0.96085	0.94395
46	APOC4p2557	intron 1	4	CA/CC	0.00081	-5.26	0.42411	NA	-14.77	0.65409	NA
46	APOC4p2623/rs5157	intron 1	4	CC/CT/TT	0.49759	-0.3	0.49795	NA	0.34	0.87974	NA
46	APOC4p2640/rs5158	intron 1	2b	CC/CT/TT	0.13813	0.35	0.59389	NA	-1.45	0.66203	NA
47	APOC4p2557	intron 1	4	CA/CC	0.00081	-5.26	0.42411	0.00177	-14.77	0.65409	0.71382
47	APOC4p2623/rs5157	intron 1	4	CC/CT/TT	0.49759	-0.3	0.49795	NA	0.34	0.87974	NA
47	APOC4p2640/rs5158	intron 1	2b	CC/CT/TT	0.13813	0.35	0.59389	NA	-1.45	0.66203	NA
47	APOC4p2683/rs12721109	intron 1	2b	AA/AG/GG	0.02369	-4.99	0.00057	NA	-9.31	0.19641	NA
48	APOC4p2623/rs5157	intron 1	4	CC/CT/TT	0.49759	-0.3	0.49795	0.00245	0.34	0.87974	0.66721
48	APOC4p2640/rs5158	intron 1	2b	CC/CT/TT	0.13813	0.35	0.59389	NA	-1.45	0.66203	NA

Cont. Table 32

48	APOC4p2683/rs12721109	intron 1	2b	AA/AG/GG	0.02369	-4.99	0.00057	NA	-9.31	0.19641	NA
48	APOC4p2703/rs12721108	intron 1	2a	GG/GT	0.00808	-1.23	0.59732	NA	-9	0.44345	NA
49	APOC4p2640/rs5158	intron 1	2b	CC/CT/TT	0.13813	0.35	0.59389	0.00287	-1.45	0.66203	0.6402
49	APOC4p2683/rs12721109	intron 1	2b	AA/AG/GG	0.02369	-4.99	0.00057	NA	-9.31	0.19641	NA
49	APOC4p2703/rs12721108	intron 1	2a	GG/GT	0.00808	-1.23	0.59732	NA	-9	0.44345	NA
49	APOC2p194APOC4p3498/rs1132899	C4-exon2	5	CC/CT/TT	0.48629	-0.12	0.79089	NA	1.35	0.54665	NA
50	APOC4p2683/rs12721109	intron 1	2b	AA/AG/GG	0.02369	-4.99	0.00057	0.00471	-9.31	0.19641	0.49843
50	APOC4p2703/rs12721108	intron 1	2a	GG/GT	0.00808	-1.23	0.59732	NA	-9	0.44345	NA
50	APOC2p194C4p3498/rs1132899	C4-exon2	5	CC/CT/TT	0.48629	-0.12	0.79089	NA	1.35	0.54665	NA
50	APOC2p242C4p3546/rs12691089	C4-exon2	5	AG/GG	0.00322	-1.8	0.69724	NA	0.65	0.97779	NA
51	APOC4p2703/rs12721108	intron 1	2a	GG/GT	0.00808	-1.23	0.59732	0.96882	-9	0.44345	0.93596
51	APOC2p194C4p3498/rs1132899	C4-exon2	5	CC/CT/TT	0.48629	-0.12	0.79089	NA	1.35	0.54665	NA
51	APOC2p242C4p3546/rs12691089	C4-exon2	5	AG/GG	0.00322	-1.8	0.69724	NA	0.65	0.97779	NA
51	APOC2p623C4p3927/rs5167	C4-exon3	5	GG/TG/TT	0.35955	0.11	0.81626	NA	-1.01	0.67218	NA
52	APOC2p194C4p3498/rs1132899	C4-exon2	5	CC/CT/TT	0.48629	-0.12	0.79089	0.89426	1.35	0.54665	0.04259
52	APOC2p242C4p3546/rs12691089	C4-exon2	5	AG/GG	0.00322	-1.8	0.69724	NA	0.65	0.97779	NA
52	APOC2p623C4p3927/rs5167	C4-exon3	5	GG/TG/TT	0.35955	0.11	0.81626	NA	-1.01	0.67218	NA
52	APOC2p1357C4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	CC/CG/GG	0.49678	0.19	0.66177	NA	0.03	0.988	NA
53	APOC2p242C4p3546/rs12691089	C4-exon2	5	AG/GG	0.00322	-1.8	0.69724	0.68765	0.65	0.97779	0.95558
53	APOC2p623C4p3927/rs5167	C4-exon3	5	GG/TG/TT	0.35955	0.11	0.81626	NA	-1.01	0.67218	NA
53	APOC2p1357C4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	CC/CG/GG	0.49678	0.19	0.66177	NA	0.03	0.988	NA
53	APOC2p1851/rs12709886	intron 1	6	GA/GG	0.03722	1.35	0.2357	NA	5.83	0.30785	NA
54	APOC2p623C4p3927/rs5167	C4-exon3	5	GG/TG/TT	0.35955	0.11	0.81626	0.21163	-1.01	0.67218	0.31879
54	APOC2p1357C4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	CC/CG/GG	0.49678	0.19	0.66177	NA	0.03	0.988	NA
54	APOC2p1851/rs12709886	intron 1	6	GA/GG	0.03722	1.35	0.2357	NA	5.83	0.30785	NA
54	APOC2p2870	intron 1	4	GG/GT	0.00403	6.33	0.05291	NA	-36.2	0.02793	NA
55	APOC2p1357C4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	CC/CG/GG	0.49678	0.19	0.66177	0.17473	0.03	0.988	0.11939
55	APOC2p1851/rs12709886	intron 1	6	GA/GG	0.03722	1.35	0.2357	NA	5.83	0.30785	NA
55	APOC2p2870	intron 1	4	GG/GT	0.00403	6.33	0.05291	NA	-36.2	0.02793	NA
55	APOC2p3348/rs10420434	intron 1	no data	GA/GG	0.0371	-1.24	0.3101	NA	6.94	0.2529	NA
56	APOC2p1851/rs12709886	intron 1	6	GA/GG	0.03722	1.35	0.2357	0.18265	5.83	0.30785	0.12229
56	APOC2p2870	intron 1	4	GG/GT	0.00403	6.33	0.05291	NA	-36.2	0.02793	NA

Cont. Table 32

56	APOC2p3348/rs10420434	intron 1	no data	GA/GG	0.0371	-1.24	0.3101	NA	6.94	0.2529	NA
56	APOC2p3778/rs5120	intron 1	4	AA/AT/TT	0.49756	0.14	0.74796	NA	0.29	0.89544	NA
57	APOC2p2870	intron 1	4	GG/GT	0.00403	6.33	0.05291	0.54107	-36.2	0.02793	0.09748
57	APOC2p3348/rs10420434	intron 1	no data	GA/GG	0.0371	-1.24	0.3101	NA	6.94	0.2529	NA
57	APOC2p3778/rs5120	intron 1	4	AA/AT/TT	0.49756	0.14	0.74796	NA	0.29	0.89544	NA
57	APOC2p4853/rs199828513	3' flanking	no data	DD/WD/WW	0.27832	0.21	0.6757	NA	-2.81	0.2692	NA
58	APOC2p3348/rs10420434	intron 1	no data	GA/GG	0.0371	-1.24	0.3101	0.78242	6.94	0.2529	0.53289
58	APOC2p3778/rs5120	intron 1	4	AA/AT/TT	0.49756	0.14	0.74796	NA	0.29	0.89544	NA
58	APOC2p4853/rs199828513	3' flanking	no data	DD/WD/WW	0.27832	0.21	0.6757	NA	-2.81	0.2692	NA
58	APOC2p5004/rs10421404	3' flanking	no data	CC/CT/TT	0.18233	0.26	0.63942	NA	1.64	0.56044	NA
59	APOC2p3778/rs5120	intron 1	4	AA/AT/TT	0.49756	0.14	0.74796	0.88628	0.29	0.89544	0.21504
59	APOC2p4853/rs199828513	3' flanking	no data	DD/WD/WW	0.27832	0.21	0.6757	NA	-2.81	0.2692	NA
59	APOC2p5004/rs10421404	3' flanking	no data	CC/CT/TT	0.18233	0.26	0.63942	NA	1.64	0.56044	NA
59	APOC2p5310/rs7258345	3' flanking	no data	GG/TG/TT	0.46487	0.36	0.41406	NA	-1.16	0.6041	NA
60	APOC2p4853/rs199828513	3' flanking	no data	DD/WD/WW	0.27832	0.21	0.6757	0.9147	-2.81	0.2692	0.38319
60	APOC2p5004/rs10421404	3' flanking	no data	CC/CT/TT	0.18233	0.26	0.63942	NA	1.64	0.56044	NA
60	APOC2p5310/rs7258345	3' flanking	no data	GG/TG/TT	0.46487	0.36	0.41406	NA	-1.16	0.6041	NA
60	APOC2p5398/rs12709889	3' flanking	6	AA/GA/GG	0.27603	0.06	0.91243	NA	-3.11	0.23298	NA
61	APOC2p5004/rs10421404	3' flanking	no data	CC/CT/TT	0.18233	0.26	0.63942	0.77002	1.64	0.56044	0.71778
61	APOC2p5310/rs7258345	3' flanking	no data	GG/TG/TT	0.46487	0.36	0.41406	NA	-1.16	0.6041	NA
61	APOC2p5398/rs12709889	3' flanking	6	AA/GA/GG	0.27603	0.06	0.91243	NA	-3.11	0.23298	NA
61	APOC2p5644	3' flanking	6	AG/GG	0.00923	1.74	0.42698	NA	7.67	0.4929	NA

wind: 4-SNPs haplotype window; w.snps: SNPs that were included in each window; p-value: single-locus p-value; hap-P: haplotype global p-value.

[a] Cox-Box transformed data.

Table 33. Haplotype-based association summary of significant windows with LDL-C in NHWs

LDL-C										
	Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
Geno.3	1	A	T	C	C	0.2591	-6.76	3.01	-2.25	0.02486
Geno.4	1	A	T	C	T	0.0211	-1.35	7.63	-0.18	0.85966
Geno.5	1	A	T	G	C	0.1182	3.48	3.70	0.94	0.34709
Geno.7	1	T	G	G	C	0.0814	-18.23	4.88	-3.74	0.00020
Geno.8	1	T	T	C	C	0.0783	0.97	4.57	0.21	0.83201
Geno.rare	1	*	*	*	*	0.0027	-18.70	0.03	-615.99	<10E-06
haplo.base	1	A	G	G	C	0.4391	NA	NA	NA	NA
Geno.2	3	C	C	G	G	0.3374	-4.93	2.65	-1.86	0.06304
Geno.31	3	C	T	G	G	0.0211	-1.67	7.67	-0.22	0.82803
Geno.52	3	G	C	A	G	0.1150	2.98	3.79	0.79	0.43109
Geno.72	3	G	C	G	G	0.1221	-13.46	3.69	-3.65	0.00029
Geno.rare2	3	*	*	*	*	0.0019	-10.87	0.09	-124.49	<10E-06
haplo.base2	3	G	C	G	A	0.4026	NA	NA	NA	NA
Geno.32	4	C	A	G	T	0.1150	10.18	3.78	2.69	0.00724
Geno.53	4	C	G	A	T	0.4019	7.14	2.48	2.87	0.00419
Geno.9	4	T	G	G	T	0.0210	5.04	7.73	0.65	0.51461
Geno.rare3	4	*	*	*	*	0.0112	3.41	10.84	0.31	0.75341
haplo.base3	4	C	G	G	T	0.4508	NA	NA	NA	NA
Geno.33	5	A	G	T	G	0.1147	9.92	3.76	2.64	0.00850
Geno.61	5	G	A	T	G	0.4002	6.75	2.44	2.76	0.00586
Geno.rare4	5	*	*	*	*	0.0129	6.44	0.24	26.92	<10E-06
haplo.base4	5	G	G	T	G	0.4722	NA	NA	NA	NA
Geno.62	7	T	G	T	C	0.1489	8.17	3.18	2.57	0.01049522
Geno.rare6	7	*	*	*	*	0.0137	6.30	0.11	55.65	<10E-06
haplo.base6	7	T	G	T	T	0.8375	NA	NA	NA	NA
Geno.35	8	G	T	C	C	0.1490	5.03	3.20	1.57	0.11629
Geno.63	8	G	T	T	T	0.0781	-22.79	4.35	-5.24	2.26E-07
Geno.rare7	8	*	*	*	*	0.0048	40.70	0.05	853.88	<10E-06
haplo.base7	8	G	T	T	C	0.7680	NA	NA	NA	NA
Geno.36	9	T	C	C	T	0.1514	5.97	3.12	1.92	0.05594
Geno.73	9	T	T	T	T	0.0805	-20.88	4.13	-5.06	5.62E-07
Geno.rare8	9	*	*	*	*	0.0048	-26.44	0.06	-427.62	<10E-06
haplo.base8	9	T	T	C	T	0.7632	NA	NA	NA	NA
Geno.21	10	C	C	T	C	0.1522	6.01	3.11	1.93	0.05361
Geno.74	10	T	T	T	C	0.0805	-20.91	4.12	-5.07	5.27E-07
Geno.rare9	10	*	*	*	*	0.0048	-31.49	0.06	-507.97	<10E-06
haplo.base9	10	T	C	T	C	0.7624	NA	NA	NA	NA
Geno.54	11	T	T	C	C	0.0805	-21.80	4.12	-5.29	1.68E-07
Geno.rare10	11	*	*	*	*	0.0129	-6.08	10.20	-0.60	0.55144
haplo.base10	11	C	T	C	C	0.9066	NA	NA	NA	NA
Geno.22	14	C	C	C	G	0.0810	0.41	4.31	0.09	0.92476
Geno.43	14	C	T	C	A	0.1101	-15.73	3.90	-4.03	6.17E-05
Geno.64	14	C	T	T	G	0.3559	-5.13	2.56	-2.01	0.04537
Geno.rare13	14	*	*	*	*	0.0095	8.41	0.33	25.81	<10E-06
haplo.base13	14	C	T	C	G	0.4435	NA	NA	NA	NA

Cont. Table 33

Geno.23	15	C	C	G	C	0.0838	0.06	4.25	0.01	0.98920
Geno.44	15	T	C	A	C	0.1101	-16.16	3.91	-4.13	4.10E-05
Geno.81	15	T	T	G	C	0.3579	-5.12	2.54	-2.01	0.04453
Geno.rare14	15	*	*	*	*	0.0055	-14.66	0.16	-90.88	<10E-06
haplo.base14	15	T	C	G	C	0.4428	NA	NA	NA	NA
Geno.11	16	C	A	C	C	0.1094	-16.12	3.86	-4.17	3.45E-05
Geno.65	16	T	G	C	C	0.3602	-5.19	2.44	-2.13	0.03336
Geno.rare15	16	*	*	*	*	0.0048	-14.78	0.09	-172.37	<10E-06
haplo.base15	16	C	G	C	C	0.5255	NA	NA	NA	NA
Geno.12	17	A	C	C	I	0.1086	-13.12	3.66	-3.58	0.00037
Geno.66	17	G	C	C	I	0.1210	4.10	3.46	1.18	0.23656
Geno.rare16	17	*	*	*	*	0.0058	-12.94	0.08	-161.31	<10E-06
haplo.base16	17	G	C	C	W	0.7646	NA	NA	NA	NA
Geno.46	29	G	C	A	T	0.1483	8.80	3.25	2.71	0.00700
Geno.56	29	G	C	G	G	0.0354	18.27	6.44	2.84	0.00471
Geno.rare28	29	*	*	*	*	0.0074	-4.63	0.36	-12.75	<10E-06
haplo.base28	29	G	C	G	T	0.8088	NA	NA	NA	NA
Geno.26	30	C	A	T	G	0.1522	7.41	3.17	2.34	0.01968
Geno.311	30	C	G	G	G	0.0388	12.99	5.81	2.24	0.02557
Geno.rare29	30	*	*	*	*	0.0024	48.33	0.03	1478.96	<10E-06
haplo.base29	30	C	G	T	G	0.8066	NA	NA	NA	NA
Geno.27	31	A	T	G	A	0.1519	9.03	3.17	2.85	0.00457
Geno.47	31	G	G	G	G	0.0363	17.96	6.13	2.93	0.00351
Geno.68	31	G	T	G	A	0.0349	6.75	6.29	1.07	0.28422
Geno.rare30	31	*	*	*	*	0.0033	-44.40	0.24	-184.85	<10E-06
haplo.base30	31	G	T	G	G	0.7737	NA	NA	NA	NA
Geno.28	32	G	G	G	A	0.0376	12.34	6.17	2.00	0.04586
Geno.48	32	T	G	A	G	0.1883	7.13	2.93	2.43	0.01529
Geno.rare31	32	*	*	*	*	0.0037	36.13	0.31	116.64	<10E-06
haplo.base31	32	T	G	G	A	0.7704	NA	NA	NA	NA
Geno.312	33	G	A	G	C	0.1850	11.78	3.20	3.68	0.00025
Geno.69	33	G	G	A	G	0.3723	9.14	2.61	3.50	0.00050
Geno.rare32	33	*	*	*	*	0.0070	13.80	0.03	487.26	<10E-06
haplo.base32	33	G	G	A	C	0.4358	NA	NA	NA	NA
Geno.13	34	A	G	C	C	0.1851	11.71	3.20	3.66	0.00028
Geno.610	34	G	A	G	C	0.3480	9.11	2.68	3.40	0.00072
Geno.75	34	G	A	G	G	0.0246	8.66	7.15	1.21	0.22644
Geno.rare33	34	*	*	*	*	0.0061	16.42	0.05	303.71	<10E-06
haplo.base33	34	G	A	C	C	0.4363	NA	NA	NA	NA
Geno.49	35	A	G	C	C	0.3457	8.75	2.66	3.29	0.00107
Geno.611	35	A	G	G	C	0.0239	7.87	7.26	1.08	0.27866
Geno.76	35	G	C	C	C	0.1550	10.92	3.39	3.22	0.00134
Geno.rare34	35	*	*	*	*	0.0081	9.03	0.16	55.45	<10E-06
haplo.base34	35	A	C	C	C	0.4674	NA	NA	NA	NA
Geno.314	40	A	T	G	C	0.4225	8.26	2.54	3.25	0.00120
Geno.412	40	A	T	G	G	0.1152	-6.88	3.71	-1.85	0.06432
Geno.rare39	40	*	*	*	*	0.0038	-8.13	0.07	-114.06	<10E-06

Cont. Table 33

haplo.base39	40	A	T	C	C	0.4584	NA	NA	NA	NA
Geno.315	41	T	C	C	C	0.3218	-5.88	3.17	-1.86	0.06353
Geno.413	41	T	C	C	G	0.1359	-11.56	3.80	-3.04	0.00249
Geno.83	41	T	G	C	G	0.0645	3.46	5.80	0.60	0.55073
Geno.91	41	T	G	G	C	0.0894	-14.42	4.54	-3.17	0.00158
Geno.10	41	T	G	G	G	0.0259	-15.84	8.35	-1.90	0.05835
Geno.rare40	41	*	*	*	*	0.0037	-15.60	0.17	-93.81	<10E-06
haplo.base40	41	T	G	C	C	0.3587	NA	NA	NA	NA
Geno.15	42	C	C	C	C	0.3241	-6.11	3.16	-1.93	0.05371
Geno.316	42	C	C	G	C	0.1304	-12.23	3.91	-3.13	0.00184
Geno.77	42	G	C	G	C	0.0661	3.75	5.75	0.65	0.51499
Geno.84	42	G	G	C	C	0.0912	-14.70	4.51	-3.26	0.00118
Geno.92	42	G	G	G	C	0.0256	-16.28	8.48	-1.92	0.05521
Geno.rare41	42	*	*	*	*	0.0055	1.95	0.28	7.05	4.95E-12
haplo.base41	42	G	C	C	C	0.3572	NA	NA	NA	NA
Geno.29	43	C	C	C	T	0.0130	17.22	11.08	1.55	0.12054
Geno.414	43	C	G	C	C	0.1930	-2.97	3.02	-0.98	0.32675
Geno.613	43	G	C	C	C	0.0886	-10.16	4.43	-2.29	0.02213
Geno.85	43	G	G	C	C	0.0249	-10.90	8.38	-1.30	0.19376
Geno.rare42	43	*	*	*	*	0.0137	-13.67	10.84	-1.26	0.20771
haplo.base42	43	C	C	C	C	0.6668	NA	NA	NA	NA
Geno.317	46	C	C	G	A	0.0362	-1.31	6.13	-0.21	0.83047
Geno.59	46	T	C	A	A	0.0226	3.78	7.79	0.49	0.62766
Geno.rare45	46	*	*	*	*	0.0025	67.19	0.04	1511.14	<10E-06
haplo.base45	46	C	C	A	A	0.9387	NA	NA	NA	NA
Geno.417	47	C	G	A	G	0.0362	-1.43	6.12	-0.23	0.81513
Geno.rare46	47	*	*	*	*	0.0041	47.71	0.05	901.97	<10E-06
haplo.base46	47	C	A	A	G	0.9597	NA	NA	NA	NA
Geno.16	54	A	G	C	G	0.0224	-20.88	7.53	-2.77	0.00576
Geno.620	54	G	G	T	G	0.4791	-3.14	2.28	-1.38	0.16831
Geno.rare53	54	*	*	*	*	0.0113	-0.45	0.51	-0.87	0.38446
haplo.base53	54	G	G	C	G	0.4872	NA	NA	NA	NA
Geno.422	60	G	G	A	G	0.0371	-0.47	6.16	-0.08	0.93870
Geno.517	60	G	G	G	G	0.4548	0.45	2.29	0.20	0.84486
Geno.rare58	60	*	*	*	*	0.0048	53.51	0.16	343.07	<10E-06
haplo.base59	60	C	G	G	G	0.5033	NA	NA	NA	NA
Geno.320	61	G	A	G	G	0.0372	-1.28	6.06	-0.21	0.83302
Geno.423	61	G	G	G	A	0.0363	-7.79	6.12	-1.27	0.20308
Geno.rare59	61	*	*	*	*	0.0048	52.71	0.09	598.53	<10E-06
haplo.base60	61	G	G	G	G	0.9217	NA	NA	NA	NA
Geno.18	62	A	G	G	A	0.0372	-0.52	6.16	-0.08	0.93272
Geno.212	62	G	G	A	A	0.0372	-5.86	6.15	-0.95	0.34095
Geno.321	62	G	G	G	A	0.4196	1.50	2.33	0.65	0.51914
Geno.rare60	62	*	*	*	*	0.0040	53.39	0.19	286.58	<10E-06
haplo.base61	62	G	G	G	T	0.5020	NA	NA	NA	NA
Geno.19	63	G	A	A	D	0.0374	-5.71	6.12	-0.93	0.35098
Geno.213	63	G	G	A	D	0.1823	-1.76	2.98	-0.59	0.55596

Cont. Table 33

Geno.322	63	G	G	A	W	0.2760	3.62	2.72	1.33	0.18266
Geno.rare61	63	*	*	*	*	0.0061	40.97	0.20	209.25	<10E-06
haplo.base62	63	G	G	T	D	0.4983	NA	NA	NA	NA

hap.freq: haplotype frequency; coef: coefficient; se: standard errors; t.stat: test statistic; p-val: haplotyep p-value.

Table 34. Haplotype-based association summary of significant windows with TC in NHWs

	TC									
	Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
Geno.3	1	A	T	C	C	0.2563	-10.78	2.98	-3.61	0.00033
Geno.4	1	A	T	C	T	0.0211	-0.04	7.67	-0.01	0.99575
Geno.5	1	A	T	G	C	0.1195	4.03	3.70	1.09	0.27585
Geno.7	1	T	G	G	C	0.0804	-22.45	4.80	-4.67	3.62E-06
Geno.8	1	T	T	C	C	0.0796	1.47	4.54	0.32	0.74659
Geno.rare	1	*	*	*	*	0.0046	95.77	0.16	604.97	<10E-06
haplo.base	1	A	G	G	C	0.4386	NA	NA	NA	NA
Geno.2	3	C	C	G	G	0.3374	-7.44	2.75	-2.71	0.00695
Geno.31	3	C	T	G	G	0.0211	-1.58	7.96	-0.20	0.84270
Geno.52	3	G	C	A	G	0.1149	2.78	3.93	0.71	0.48050
Geno.72	3	G	C	G	G	0.1220	-16.61	3.83	-4.34	1.67E-05
Geno.rare2	3	*	*	*	*	0.0019	-8.91	0.09	-99.94	<10E-06
haplo.base2	3	G	C	G	A	0.4027	NA	NA	NA	NA
Geno.32	4	C	A	G	T	0.1149	12.74	3.92	3.25	0.00123
Geno.53	4	C	G	A	T	0.4021	9.73	2.58	3.77	0.00018
Geno.9	4	T	G	G	T	0.0211	7.66	8.03	0.95	0.34050
Geno.rare3	4	*	*	*	*	0.0112	2.13	11.30	0.19	0.85094
haplo.base3	4	C	G	G	T	0.4507	NA	NA	NA	NA
Geno.33	5	A	G	T	G	0.1147	12.36	3.91	3.17	0.00163
Geno.61	5	G	A	T	G	0.4004	9.20	2.54	3.62	0.00032
Geno.rare4	5	*	*	*	*	0.0129	6.05	0.25	24.40	<10E-06
haplo.base4	5	G	G	T	G	0.4721	NA	NA	NA	NA
Geno.34	6	A	T	G	T	0.4000	6.75	2.45	2.76	0.0059
Geno.41	6	G	G	G	T	0.0112	0.80	0.15	5.51	5.31E-08
Geno.rare5	6	*	*	*	*	0.0024	30.16	0.00	8221.07	<10E-06
haplo.base5	6	G	T	G	T	0.5864	NA	NA	NA	NA
Geno.35	8	G	T	C	C	0.1493	3.84	3.29	1.16	0.24448
Geno.63	8	G	T	T	T	0.0776	-22.06	4.46	-4.95	9.68E-07
Geno.rare7	8	*	*	*	*	0.0054	59.95	0.08	705.34	<10E-06
haplo.base7	8	G	T	T	C	0.7677	NA	NA	NA	NA
Geno.36	9	T	C	C	T	0.1515	4.56	3.31	1.38	0.16872
Geno.73	9	T	T	T	T	0.0806	-18.87	4.33	-4.36	1.54E-05
Geno.rare8	9	*	*	*	*	0.0048	-37.56	0.07	-576.22	<10E-06
haplo.base8	9	T	T	C	T	0.7631	NA	NA	NA	NA
Geno.21	10	C	C	T	C	0.1523	4.68	3.30	1.42	0.15737
Geno.74	10	T	T	T	C	0.0806	-18.81	4.33	-4.34	1.66E-05
Geno.rare9	10	*	*	*	*	0.0048	-35.00	0.07	-534.40	<10E-06

Cont. Table 34

haplo.base9	10	T	C	T	C	0.7622	NA	NA	NA	NA
Geno.54	11	T	T	C	C	0.0806	-19.27	4.33	-4.46	9.95E-06
Geno.rare10	11	*	*	*	*	0.0129	-1.15	10.71	-0.11	0.91464
haplo.base10	11	C	T	C	C	0.9065	NA	NA	NA	NA
Geno.22	14	C	C	C	G	0.0811	0.23	4.49	0.05	0.95933
Geno.43	14	C	T	C	A	0.1094	-16.60	4.01	-4.14	3.94E-05
Geno.64	14	C	T	T	G	0.3556	-6.51	2.67	-2.44	0.01504
Geno.rare13	14	*	*	*	*	0.0095	15.17	0.33	46.30	<10E-06
haplo.base13	14	C	T	C	G	0.4444	NA	NA	NA	NA
Geno.23	15	C	C	G	C	0.0838	0.14	4.41	0.03	0.97417
Geno.44	15	T	C	A	C	0.1094	-17.19	4.02	-4.28	2.18E-05
Geno.81	15	T	T	G	C	0.3579	-6.35	2.64	-2.41	0.01636
Geno.rare14	15	*	*	*	*	0.0055	-24.20	0.17	-142.40	<10E-06
haplo.base14	15	T	C	G	C	0.4435	NA	NA	NA	NA
Geno.11	16	C	A	C	C	0.1087	-17.52	3.97	-4.42	1.17E-05
Geno.65	16	T	G	C	C	0.3602	-6.48	2.53	-2.57	0.01054
Geno.rare15	16	*	*	*	*	0.0049	-16.38	0.09	-192.48	<10E-06
haplo.base15	16	C	G	C	C	0.5263	NA	NA	NA	NA
Geno.12	17	A	C	C	I	0.1081	-14.22	3.83	-3.71	0.00022
Geno.66	17	G	C	C	I	0.1216	3.33	3.61	0.92	0.35675
Geno.rare16	17	*	*	*	*	0.0058	-11.10	0.08	-132.40	<10E-06
haplo.base16	17	G	C	C	W	0.7646	NA	NA	NA	NA
Geno.46	29	G	C	A	T	0.1515	6.46	3.32	1.95	0.05198
Geno.56	29	G	C	G	G	0.0387	14.61	6.10	2.40	0.01690
Geno.rare28	29	*	*	*	*	0.0042	24.64	0.07	345.55	<10E-06
haplo.base28	29	G	C	G	T	0.8057	NA	NA	NA	NA
Geno.26	30	C	A	T	G	0.1521	6.68	3.28	2.03	0.04235
Geno.311	30	C	G	G	G	0.0388	14.82	6.03	2.46	0.01430
Geno.rare29	30	*	*	*	*	0.0024	84.10	0.03	2478.60	<10E-06
haplo.base29	30	C	G	T	G	0.8067	NA	NA	NA	NA
Geno.27	31	A	T	G	A	0.1541	6.77	3.31	2.05	0.04109
Geno.47	31	G	G	G	G	0.0379	13.68	6.19	2.21	0.02751
Geno.68	31	G	T	G	A	0.0342	8.14	6.70	1.21	0.22501
Geno.rare30	31	*	*	*	*	0.0017	49.83	NA	NA	NA
haplo.base30	31	G	T	G	G	0.7722	NA	NA	NA	NA
Geno.28	32	G	G	G	A	0.0387	14.69	6.05	2.43	0.01550
Geno.48	32	T	G	A	G	0.1893	6.50	3.01	2.16	0.03130
Geno.rare31	32	*	*	*	*	0.0026	65.08	0.03	2546.45	<10E-06
haplo.base31	32	T	G	G	A	0.7694	NA	NA	NA	NA
Geno.312	33	G	A	G	C	0.1849	10.70	3.34	3.20	0.00144
Geno.69	33	G	G	A	G	0.3729	9.46	2.73	3.47	0.00056
Geno.rare32	33	*	*	*	*	0.0071	37.39	0.02	2008.39	<10E-06
haplo.base32	33	G	G	A	C	0.4352	NA	NA	NA	NA
Geno.13	34	A	G	C	C	0.1850	10.72	3.35	3.20	0.00142
Geno.610	34	G	A	G	C	0.3486	9.72	2.80	3.47	0.00056
Geno.75	34	G	A	G	G	0.0246	6.62	7.45	0.89	0.37435
Geno.rare33	34	*	*	*	*	0.0061	35.54	0.06	593.93	<10E-06

Cont. Table 34

haplo.base33	34	G	A	C	C	0.4357	NA	NA	NA	NA
Geno.49	35	A	G	C	C	0.3462	9.18	2.79	3.29	0.00106
Geno.611	35	A	G	G	C	0.0239	5.59	7.57	0.74	0.46084
Geno.76	35	G	C	C	C	0.1546	9.84	3.53	2.79	0.00547
Geno.rare34	35	*	*	*	*	0.0082	20.91	0.14	146.67	<10E-06
haplo.base34	35	A	C	C	C	0.4672	NA	NA	NA	NA
Geno.314	40	A	T	G	C	0.4232	8.18	2.66	3.08	0.00220
Geno.412	40	A	T	G	G	0.1148	-5.83	3.87	-1.51	0.13185
Geno.rare39	40	*	*	*	*	0.0038	-20.96	0.08	-274.35	<10E-06
haplo.base39	40	A	T	C	C	0.4583	NA	NA	NA	NA
Geno.315	41	T	C	C	C	0.3211	-7.56	3.33	-2.27	0.02337
Geno.413	41	T	C	C	G	0.1366	-9.68	3.97	-2.44	0.01497
Geno.83	41	T	G	C	G	0.0638	-0.58	6.34	-0.09	0.92727
Geno.91	41	T	G	G	C	0.0890	-14.54	4.79	-3.03	0.00252
Geno.10	41	T	G	G	G	0.0259	-12.67	8.86	-1.43	0.15319
Geno.rare40	41	*	*	*	*	0.0036	-28.99	0.19	-154.32	<10E-06
haplo.base40	41	T	G	C	C	0.3600	NA	NA	NA	NA
Geno.15	42	C	C	C	C	0.3232	-7.85	3.33	-2.36	0.01861
Geno.316	42	C	C	G	C	0.1312	-9.75	4.07	-2.39	0.01697
Geno.77	42	G	C	G	C	0.0652	-0.50	6.31	-0.08	0.93707
Geno.84	42	G	G	C	C	0.0907	-14.86	4.77	-3.12	0.00190
Geno.92	42	G	G	G	C	0.0256	-13.00	8.96	-1.45	0.14753
Geno.rare41	42	*	*	*	*	0.0054	-8.58	0.30	-28.83	<10E-06
haplo.base41	42	G	C	C	C	0.3587	NA	NA	NA	NA
Geno.317	46	C	C	G	A	0.0362	-4.71	6.37	-0.74	0.45918
Geno.59	46	T	C	A	A	0.0226	8.36	8.12	1.03	0.30381
Geno.rare45	46	*	*	*	*	0.0025	89.59	0.05	1945.73	<10E-06
haplo.base45	46	C	C	A	A	0.9387	NA	NA	NA	NA
Geno.417	47	C	G	A	G	0.0362	-5.06	6.37	-0.79	0.42772
Geno.rare46	47	*	*	*	*	0.0041	60.52	0.05	1100.73	<10E-06
haplo.base46	47	C	A	A	G	0.9597	NA	NA	NA	NA
Geno.510	48	G	A	G	C	0.0362	-5.27	6.41	-0.82	0.41096
Geno.rare47	48	*	*	*	*	0.0041	36.56	0.06	661.46	<10E-06
haplo.base47	48	A	A	G	C	0.9597	NA	NA	NA	NA
Geno.422	60	G	G	A	G	0.0371	-4.22	6.42	-0.66	0.51117
Geno.517	60	G	G	G	G	0.4548	-0.81	2.39	-0.34	0.73305
Geno.rare58	60	*	*	*	*	0.0048	58.46	0.16	359.65	<10E-06
haplo.base59	60	C	G	G	G	0.5032	NA	NA	NA	NA
Geno.320	61	G	A	G	G	0.0372	-4.16	6.32	-0.66	0.51082
Geno.423	61	G	G	G	A	0.0363	-3.62	6.40	-0.57	0.57191
Geno.rare59	61	*	*	*	*	0.0048	58.74	0.09	635.36	<10E-06
haplo.base60	61	G	G	G	G	0.9217	NA	NA	NA	NA
Geno.18	62	A	G	G	A	0.0372	-4.77	6.42	-0.74	0.45765
Geno.212	62	G	G	A	A	0.0372	-2.98	6.43	-0.46	0.64363
Geno.321	62	G	G	G	A	0.4195	-1.47	2.43	-0.60	0.54721
Geno.rare60	62	*	*	*	*	0.0040	56.97	0.19	292.45	<10E-06
haplo.base61	62	G	G	G	T	0.5020	NA	NA	NA	NA

Cont. Table 34

Geno.19	63	G	A	A	D	0.0374	-2.79	6.41	-0.43	0.66380
Geno.213	63	G	G	A	D	0.1823	-5.23	3.12	-1.68	0.09413
Geno.322	63	G	G	A	W	0.2759	0.92	2.84	0.32	0.74682
Geno.rare61	63	*	*	*	*	0.0061	45.74	0.21	223.11	<10E-06
haplo.base62	63	G	G	T	D	0.4983	NA	NA	NA	NA

hap.freq: haplotype frequency; coef: coefficient; se: standard errors; t.stat: test statistic; p-val: haplotyep p-value.

Table 35. Haplotype-based association summary of significant windows with ApoB in NHWs

	ApoB									
	Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
Geno.2	1	A	T	C	C	0.2534	0.24	0.58	0.41	0.67873
Geno.3	1	A	T	C	T	0.0221	0.92	1.41	0.65	0.51564
Geno.4	1	A	T	G	C	0.1313	2.00	0.69	2.91	0.00382
Geno.6	1	T	G	G	C	0.0748	-2.62	0.95	-2.75	0.00616
Geno.7	1	T	T	C	C	0.0781	1.36	0.86	1.58	0.11430
Geno.rare	1	*	*	*	*	0.0012	-20.89	6.37	-3.28	0.00113
haplo.base	1	A	G	G	C	0.4390	NA	NA	NA	NA
Geno.5	2	T	C	C	G	0.3288	1.04	0.49	2.13	0.03342
Geno.61	2	T	C	T	G	0.0214	1.56	1.45	1.07	0.28307
Geno.71	2	T	G	C	A	0.1258	2.47	0.70	3.55	0.00042
Geno.rare1	2	*	*	*	*	0.0104	-4.18	2.26	-1.85	0.06480
haplo.base1	2	G	G	C	G	0.5136	NA	NA	NA	NA
Geno.21	3	C	C	G	G	0.3301	0.18	0.51	0.36	0.72077
Geno.31	3	C	T	G	G	0.0222	0.46	1.42	0.32	0.74598
Geno.51	3	G	C	A	G	0.1270	1.65	0.70	2.34	0.01960
Geno.72	3	G	C	G	G	0.1212	-3.20	0.70	-4.53	7.49E-06
Geno.rare2	3	*	*	*	*	0.0025	-6.15	4.42	-1.39	0.16502
haplo.base2	3	G	C	G	A	0.3970	NA	NA	NA	NA
Geno.32	4	C	A	G	T	0.1274	2.36	0.73	3.26	0.00122
Geno.52	4	C	G	A	T	0.3962	0.71	0.49	1.46	0.14637
Geno.10	4	T	G	G	T	0.0221	1.39	1.45	0.96	0.33866
Geno.rare3	4	*	*	*	*	0.0104	0.06	2.23	0.03	0.97919
haplo.base3	4	C	G	G	T	0.4438	NA	NA	NA	NA
Geno.33	5	A	G	T	G	0.1269	2.26	0.72	3.13	0.00185
Geno.62	5	G	A	T	G	0.3951	0.59	0.49	1.22	0.22353
Geno.rare4	5	*	*	*	*	0.0115	1.49	2.10	0.71	0.47789
haplo.base4	5	G	G	T	G	0.4666	NA	NA	NA	NA
Geno.34	6	A	T	G	T	0.3949	0.12	0.46	0.25	0.80387
Geno.41	6	G	G	G	T	0.0104	-0.11	2.19	-0.05	0.95879
Geno.rare5	6	*	*	*	*	0.0023	11.46	4.57	2.51	0.01251
haplo.base5	6	G	T	G	T	0.5924	NA	NA	NA	NA
Geno.63	7	T	G	T	C	0.1582	2.04	0.61	3.31	0.00101
Geno.rare6	7	*	*	*	*	0.0127	2.37	1.97	1.20	0.22976
haplo.base6	7	T	G	T	T	0.8291	NA	NA	NA	NA
Geno.35	8	G	T	C	C	0.1606	1.52	0.58	2.63	0.00888

Cont. Table 35

Geno.64	8	G	T	T	T	0.0810	-5.37	0.76	-7.03	8.41E-12
Geno.rare7	8	*	*	*	*	0.0032	10.05	4.26	2.36	0.01883
haplo.base7	8	G	T	T	C	0.7552	NA	NA	NA	NA
Geno.36	9	T	C	C	T	0.1586	1.37	0.60	2.28	0.02327
Geno.73	9	T	T	T	T	0.0797	-5.53	0.81	-6.79	3.76E-11
Geno.rare8	9	*	*	*	*	0.0056	3.67	3.38	1.09	0.27814
haplo.base8	9	T	T	C	T	0.7560	NA	NA	NA	NA
Geno.22	10	C	C	T	C	0.1606	1.50	0.61	2.46	0.01427
Geno.74	10	T	T	T	C	0.0804	-5.41	0.84	-6.47	2.67E-10
Geno.rare9	10	*	*	*	*	0.0118	1.31	2.18	0.60	0.54871
haplo.base9	10	T	C	T	C	0.7471	NA	NA	NA	NA
Geno.37	11	C	T	C	C	0.0702	-0.15	0.81	-0.18	0.85709
Geno.8	11	T	T	C	T	0.0813	-5.59	0.76	-7.32	1.21E-12
Geno.rare10	11	*	*	*	*	0.0110	0.37	2.07	0.18	0.85654
haplo.base10	11	C	T	C	T	0.8375	NA	NA	NA	NA
Geno.1	13	C	C	C	G	0.0717	-0.59	0.85	-0.70	0.48383
Geno.23	13	C	T	C	A	0.1109	-4.07	0.73	-5.57	4.54E-08
Geno.42	13	C	T	T	G	0.3568	-0.49	0.48	-1.03	0.30417
Geno.rare12	13	*	*	*	*	0.0081	0.58	2.52	0.23	0.81910
haplo.base12	13	C	T	C	G	0.4526	NA	NA	NA	NA
Geno.24	14	C	C	G	C	0.0749	-0.45	0.83	-0.54	0.59038
Geno.38	14	T	C	A	C	0.1109	-4.09	0.73	-5.61	3.67E-08
Geno.75	14	T	T	G	C	0.3572	-0.49	0.48	-1.02	0.30781
Geno.rare13	14	*	*	*	*	0.0023	-3.82	4.44	-0.86	0.38954
haplo.base13	14	T	C	G	C	0.4547	NA	NA	NA	NA
Geno.11	15	C	A	C	C	0.1098	-4.05	0.72	-5.59	4.00E-08
Geno.65	15	T	G	C	C	0.3585	-0.45	0.46	-0.98	0.32812
Geno.rare14	15	*	*	*	*	0.0035	-3.19	3.64	-0.88	0.38004
haplo.base14	15	C	G	C	C	0.5283	NA	NA	NA	NA
Geno.12	16	A	C	C	I	0.1084	-3.63	0.69	-5.24	2.49E-07
Geno.66	16	G	C	C	I	0.1325	1.42	0.64	2.22	0.02712
Geno.rare15	16	*	*	*	*	0.0048	-2.00	3.16	-0.63	0.52723
haplo.base15	16	G	C	C	W	0.7543	NA	NA	NA	NA
Geno.26	19	I	G	A	G	0.2402	-0.77	0.52	-1.48	0.13858
Geno.rare18	19	*	*	*	*	0.0047	7.68	3.24	2.37	0.01838
haplo.base18	19	W	G	A	G	0.7551	NA	NA	NA	NA
Geno.rare19	20	*	*	*	*	0.0058	6.84	3.24	2.11	0.03538
haplo.base19	20	G	A	G	G	0.9942	NA	NA	NA	NA
Geno.311	27	C	G	C	A	0.1626	1.61	0.61	2.66	0.00813
Geno.rare26	27	*	*	*	*	0.0082	-2.29	2.80	-0.82	0.41387
haplo.base26	27	C	G	C	G	0.8291	NA	NA	NA	NA
Geno.44	28	G	C	A	T	0.1629	1.67	0.61	2.75	0.00623
Geno.55	28	G	C	G	G	0.0349	2.17	1.18	1.85	0.06524
Geno.rare27	28	*	*	*	*	0.0047	-0.72	3.76	-0.19	0.84788
haplo.base27	28	G	C	G	T	0.7975	NA	NA	NA	NA
Geno.27	29	C	A	T	A	0.1626	1.71	0.61	2.81	0.00519
Geno.45	29	C	G	G	G	0.0311	1.80	1.32	1.36	0.17327

Cont. Table 35

Geno.56	29	C	G	T	A	0.0339	1.74	1.28	1.36	0.17368
Geno.rare28	29	*	*	*	*	0.0050	6.58	4.47	1.47	0.14222
haplo.base28	29	C	G	T	G	0.7674	NA	NA	NA	NA
Geno.46	30	A	T	A	G	0.1638	1.63	0.61	2.67	0.00791
Geno.68	30	G	G	G	A	0.0311	1.97	1.35	1.46	0.14504
Geno.82	30	G	T	A	G	0.0340	1.83	1.29	1.42	0.15664
Geno.rare29	30	*	*	*	*	0.0063	4.40	3.90	1.13	0.26068
haplo.base29	30	G	T	G	A	0.7648	NA	NA	NA	NA
Geno.28	31	G	G	A	C	0.0348	2.94	1.19	2.47	0.01378
Geno.312	31	T	A	G	C	0.1978	2.67	0.62	4.31	2.06E-05
Geno.69	31	T	G	A	G	0.3566	1.64	0.52	3.18	0.00155
Geno.rare30	31	*	*	*	*	0.0063	0.48	3.06	0.16	0.87473
haplo.base30	31	T	G	A	C	0.4045	NA	NA	NA	NA
Geno.29	32	A	G	C	C	0.1976	2.53	0.62	4.07	5.68E-05
Geno.76	32	G	A	G	C	0.3343	1.43	0.53	2.72	0.00672
Geno.83	32	G	A	G	G	0.0224	1.43	1.43	1.00	0.31820
Geno.rare31	32	*	*	*	*	0.0065	0.27	3.08	0.09	0.93039
haplo.base31	32	G	A	C	C	0.4393	NA	NA	NA	NA
Geno.47	33	A	G	C	C	0.3325	1.25	0.53	2.35	0.01942
Geno.57	33	A	G	G	C	0.0224	1.20	1.44	0.83	0.40541
Geno.77	33	G	C	C	C	0.1696	2.08	0.65	3.19	0.00154
Geno.rare32	33	*	*	*	*	0.0071	1.35	3.06	0.44	0.66038
haplo.base32	33	A	C	C	C	0.4684	NA	NA	NA	NA
Geno.415	47	C	C	C	G	0.3667	0.31	0.47	0.65	0.51801
Geno.515	47	C	C	T	A	0.0193	-5.00	1.52	-3.28	0.00114
Geno.612	47	C	C	T	G	0.1148	1.44	0.71	2.02	0.04446
Geno.rare46	47	*	*	*	*	0.0038	-3.04	3.69	-0.82	0.41088
haplo.base46	47	C	T	C	G	0.4954	NA	NA	NA	NA
Geno.212	48	C	C	G	G	0.3678	0.29	0.47	0.61	0.54354
Geno.416	48	C	T	A	G	0.0185	-5.01	1.55	-3.23	0.00135
Geno.613	48	C	T	G	G	0.1148	1.45	0.71	2.02	0.04349
Geno.rare47	48	*	*	*	*	0.0119	-1.28	2.12	-0.60	0.54826
haplo.base47	48	T	C	G	G	0.4869	NA	NA	NA	NA
Geno.213	49	C	G	G	C	0.3798	0.09	0.48	0.18	0.85784
Geno.614	49	T	A	G	C	0.0185	-5.09	1.55	-3.27	0.00115
Geno.93	49	T	G	G	C	0.1148	1.37	0.72	1.90	0.05776
Geno.rare48	49	*	*	*	*	0.0119	-1.31	2.12	-0.62	0.53790
haplo.base48	49	C	G	G	T	0.4750	NA	NA	NA	NA
Geno.14	50	A	G	C	G	0.0214	-5.20	1.47	-3.54	0.00045
Geno.615	50	G	G	T	G	0.4740	-0.41	0.45	-0.92	0.35904
Geno.rare49	50	*	*	*	*	0.0116	-1.74	2.16	-0.81	0.41994
haplo.base49	50	G	G	C	G	0.4930	NA	NA	NA	NA

hap.freq: haplotype frequency; coef: coefficient; se: standard errors; t.stat: test statistic; p-val: haplotyep p-value.

Table 36. Haplotype-based association summary of significant windows with TG in NHWs

	TG									
	Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
Geno.3	1	A	T	C	C	0.2597	-0.093	0.030	-3.063	0.00229
Geno.4	1	A	T	C	T	0.0212	-0.125	0.077	-1.614	0.10696
Geno.5	1	A	T	G	C	0.1191	-0.021	0.037	-0.563	0.57379
Geno.7	1	T	G	G	C	0.0815	-0.047	0.048	-0.979	0.32783
Geno.8	1	T	T	C	C	0.0767	-0.074	0.046	-1.602	0.10978
Geno.rare	1	*	*	*	*	0.0018	0.680	0.387	1.755	0.07969
haplo.base	1	A	G	G	C	0.4400	NA	NA	NA	NA
Geno.51	2	T	C	C	G	0.3351	-0.079	0.025	-3.107	0.00198
Geno.6	2	T	C	T	G	0.0208	-0.119	0.078	-1.523	0.12829
Geno.71	2	T	G	C	A	0.1134	-0.008	0.038	-0.201	0.84085
Geno.rare1	2	*	*	*	*	0.0106	-0.091	0.115	-0.796	0.42648
haplo.base1	2	G	G	C	G	0.5201	NA	NA	NA	NA
Geno.2	3	C	C	G	G	0.3364	-0.083	0.027	-3.082	0.00215
Geno.31	3	C	T	G	G	0.0212	-0.130	0.078	-1.667	0.09597
Geno.52	3	G	C	A	G	0.1148	-0.019	0.038	-0.486	0.62712
Geno.72	3	G	C	G	G	0.1220	-0.047	0.038	-1.261	0.20779
Geno.rare2	3	*	*	*	*	0.0019	-0.439	0.275	-1.598	0.11047
haplo.base2	3	G	C	G	A	0.4037	NA	NA	NA	NA
Geno.33	5	A	G	T	G	0.1146	0.048	0.038	1.257	0.20924
Geno.61	5	G	A	T	G	0.4015	0.072	0.025	2.902	0.00384
Geno.rare4	5	*	*	*	*	0.0129	-0.003	0.102	-0.026	0.97936
haplo.base4	5	G	G	T	G	0.4710	NA	NA	NA	NA
Geno.67	23	G	G	G	A	0.3371	-0.075	0.024	-3.124	0.00187
Geno.rare22	23	*	*	*	*	0.0091	-0.165	0.122	-1.354	0.17626
haplo.base22	23	G	G	G	G	0.6538	NA	NA	NA	NA
Geno.55	24	G	G	A	G	0.3362	-0.075	0.024	-3.117	0.00191
Geno.rare23	24	*	*	*	*	0.0082	-0.175	0.135	-1.303	0.19293
haplo.base23	24	G	G	G	G	0.6555	NA	NA	NA	NA
Geno.45	25	G	A	G	C	0.3382	-0.078	0.024	-3.222	0.00134
Geno.rare24	25	*	*	*	*	0.0100	-0.058	0.122	-0.474	0.63557
haplo.base24	25	G	G	G	C	0.6518	NA	NA	NA	NA
Geno.39	26	A	G	C	G	0.3397	-0.078	0.024	-3.231	0.00130
Geno.rare25	26	*	*	*	*	0.0066	-0.012	0.161	-0.071	0.94310
haplo.base25	26	G	G	C	G	0.6537	NA	NA	NA	NA
Geno.312	33	G	A	G	C	0.1855	0.027	0.033	0.836	0.40320
Geno.69	33	G	G	A	G	0.3737	0.047	0.026	1.775	0.07645
Geno.rare32	33	*	*	*	*	0.0069	0.390	0.217	1.796	0.07293
haplo.base32	33	G	G	A	C	0.4339	NA	NA	NA	NA
Geno.417	47	C	G	A	G	0.0365	0.020	0.062	0.321	0.74844
Geno.rare46	47	*	*	*	*	0.0041	0.573	0.199	2.878	0.00414
haplo.base46	47	C	A	A	G	0.9594	NA	NA	NA	NA
Geno.510	48	G	A	G	C	0.0365	0.019	0.062	0.302	0.76284
Geno.rare47	48	*	*	*	*	0.0041	0.452	0.200	2.260	0.02417
haplo.base47	48	A	A	G	C	0.9594	NA	NA	NA	NA

Cont. Table 36

Geno.511	49	A	G	C	T	0.4935	0.019	0.023	0.825	0.40944
Geno.rare48	49	*	*	*	*	0.0041	0.465	0.201	2.320	0.02069
haplo.base48	49	A	G	C	C	0.5024	NA	NA	NA	NA

hap.freq: haplotype frequency; coef: coefficient; se: standard errors; t.stat: test statistic; p-val: haplotyep p-value.

Table 37. Haplotype-based association summary of significant windows with HDL-C in NHWs

	HDL-C									
	Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
Geno.37	12	T	C	C	C	0.0814	0.034	0.019	1.765	0.07798
Geno.rare11	12	*	*	*	*	0.0130	0.096	0.050	1.934	0.05354
haplo.base11	12	T	C	C	T	0.9057	NA	NA	NA	NA
Geno.1	13	C	C	C	C	0.0800	0.035	0.020	1.743	0.08184
Geno.42	13	C	C	T	T	0.3545	0.008	0.011	0.755	0.45065
Geno.rare12	13	*	*	*	*	0.0108	0.133	0.056	2.379	0.01768
haplo.base12	13	C	C	T	C	0.5547	NA	NA	NA	NA
Geno.24	19	I	G	A	G	0.2290	-0.021	0.013	-1.668	0.09583
Geno.rare18	19	*	*	*	*	0.0032	0.318	0.130	2.440	0.01497
haplo.base18	19	W	G	A	G	0.7677	NA	NA	NA	NA
Geno.rare19	20	*	*	*	*	0.0049	0.278	0.092	3.014	0.00268
haplo.base19	20	G	A	G	G	0.9951	NA	NA	NA	NA
Geno.416	43	C	C	T	C	0.0175	0.010	0.043	0.233	0.81592
Geno.612	43	G	C	C	C	0.2173	0.033	0.013	2.591	0.00980
Geno.rare42	43	*	*	*	*	0.0101	-0.106	0.062	-1.702	0.08927
haplo.base42	43	C	C	C	C	0.7551	NA	NA	NA	NA
Geno.513	49	G	C	C	C	0.3625	0.001	0.012	0.045	0.96388
Geno.614	49	G	C	C	T	0.1390	0.020	0.016	1.280	0.20088
Geno.rare48	49	*	*	*	*	0.0024	-0.317	0.131	-2.424	0.01563
haplo.base48	49	G	C	T	C	0.4961	NA	NA	NA	NA
Geno.318	57	T	G	C	G	0.0212	0.073	0.041	1.811	0.07062
Geno.517	57	T	G	G	G	0.3370	0.001	0.012	0.105	0.91679
Geno.79	57	T	T	G	G	0.1597	0.024	0.015	1.532	0.12595
Geno.rare56	57	*	*	*	*	0.0024	-0.342	0.131	-2.616	0.00910
haplo.base56	57	T	T	C	G	0.4796	NA	NA	NA	NA

hap.freq: haplotype frequency; coef: coefficient; se: standard errors; t.stat: test statistic; p-val: haplotyep p-value.

Table 38. Haplotype-based association summary of significant windows with ApoA1 in NHWs

	ApoA1									
	Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
Geno.25	18	C	I	G	A	0.2396	-0.79	2.62	-0.30	0.76340
Geno.rare17	18	*	*	*	*	0.0035	49.06	0.04	1119.99	<10E-06
haplo.base17	18	C	W	G	A	0.7569	NA	NA	NA	NA
Geno.26	19	I	G	A	G	0.2408	-0.02	2.62	-0.01	0.99278
Geno.rare18	19	*	*	*	*	0.0046	44.78	0.06	761.17	<10E-06
haplo.base18	19	W	G	A	G	0.7546	NA	NA	NA	NA
Geno.rare19	20	*	*	*	*	0.0058	30.69	0.01	2087.61	<10E-06
haplo.base19	20	G	A	G	G	0.9942	NA	NA	NA	NA
Geno.321	52	C	G	G	C	0.0207	-11.21	7.92	-1.42	0.15749
Geno.418	52	C	G	G	G	0.3413	-0.77	2.52	-0.31	0.76016
Geno.617	52	C	G	T	G	0.1506	-1.13	3.27	-0.34	0.73060
Geno.rare51	52	*	*	*	*	0.0061	41.27	0.22	184.54	<10E-06
haplo.base51	52	T	G	T	C	0.4813	NA	NA	NA	NA

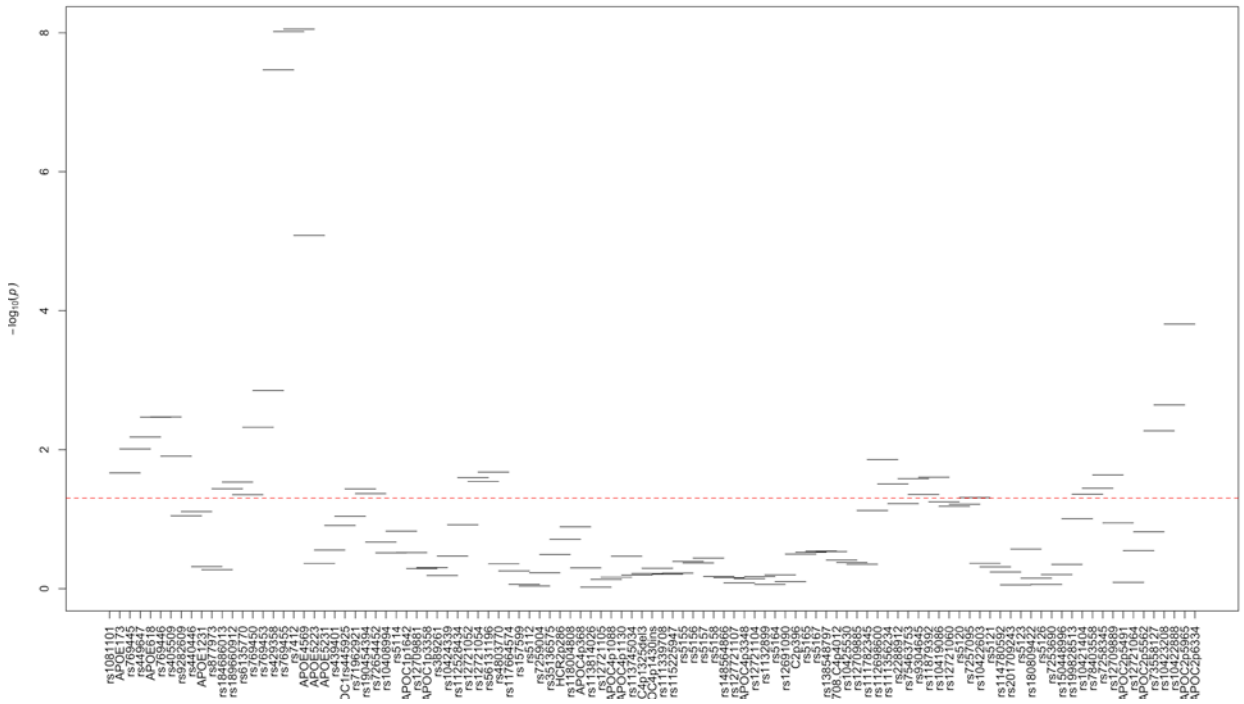
hap.freq: haplotype frequency; coef: coefficient; se: standard errors; t.stat: test statistic; p-val: haplotyep p-value.

3.6.3.2 African Blacks

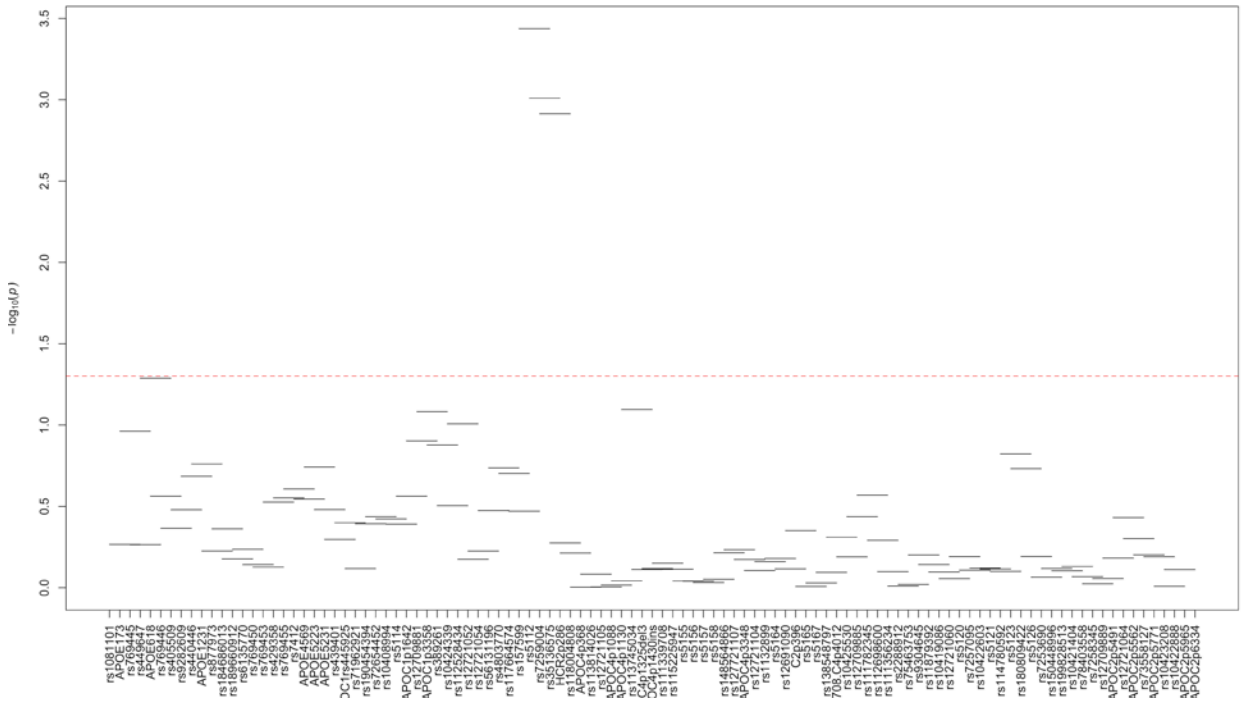
Tables 39-46 summarized the haplotype-based association analysis in Blacks and **Figure 24** represents the plots of haplotype 4-SNP windows p-value with lipid traits. Multiple windows showed significant global p-values with LDL-C and TC as it has been seen in NHWs, but the effect on apoB was much smaller in Blacks as compared to NHWs. The top significant associated windows with LDL-C and TC were mapped to the *APOE2/E4* alleles. The significant signals with LDL-C and TC were derived from common/uncommon variants (MAF>1%) with significant single effect except one region mapped to windows 95, 96, and 97 where none of the variants included in those windows had significant effect in the single locus analysis. Most of the significant haplotype windows with HDL-C, TG, and apoA1 contained SNPs that also yielded significant association in the single-locus association analysis. However, three windows, 41, 42, and 43, that showed significant haplotype global p-values with HDL-C and apoA1, did not

contain any SNP that was significant in the single-locus analysis. Two of the variants included in these three windows, rs7259004 and *HCR2*p188/rs35136575, were associated with HDL-C and apoA1 in NHWs, indicating their potential involvement in HDL metabolism in both racial groups.

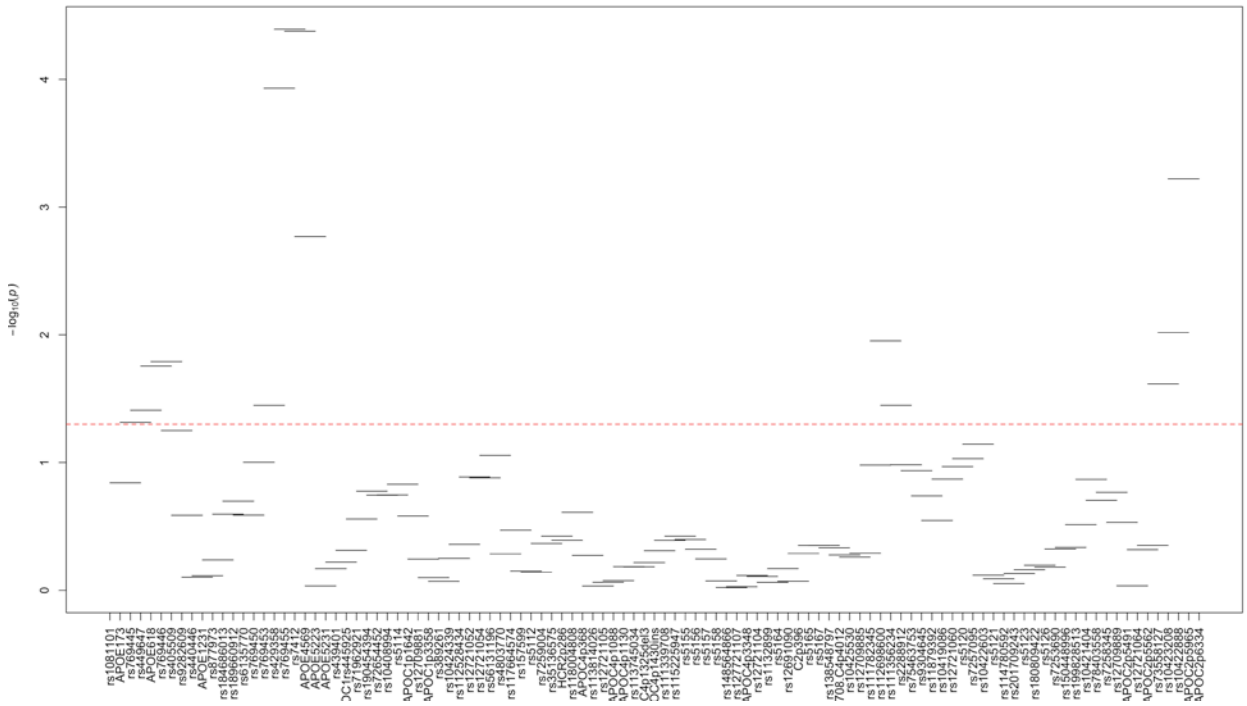
a) LDL-C



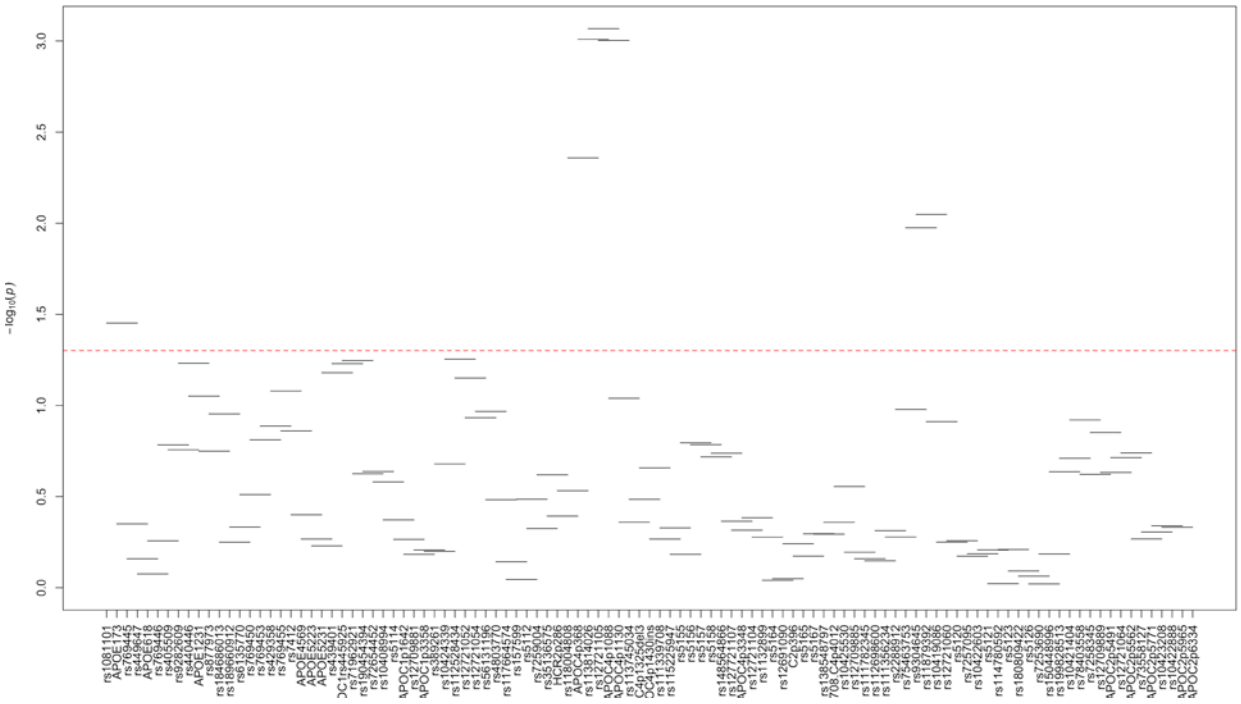
b) HDL-C



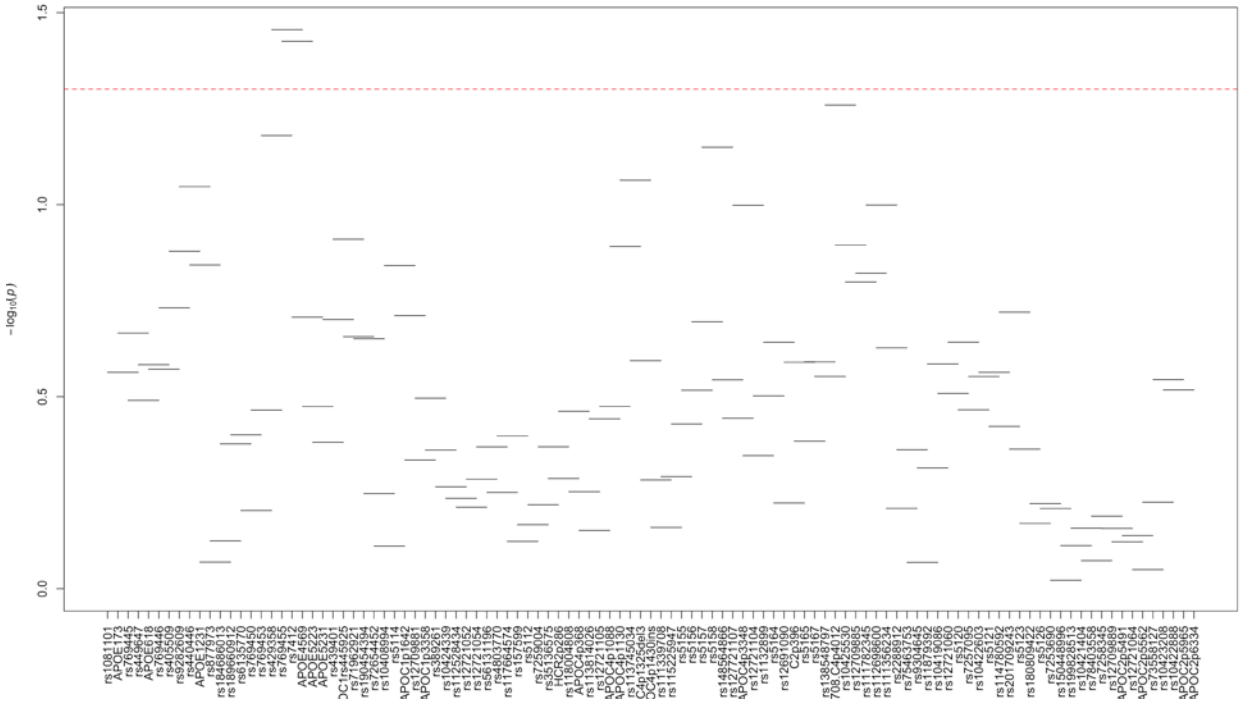
c) TC



d) TG



e) ApoB



f) ApoA1

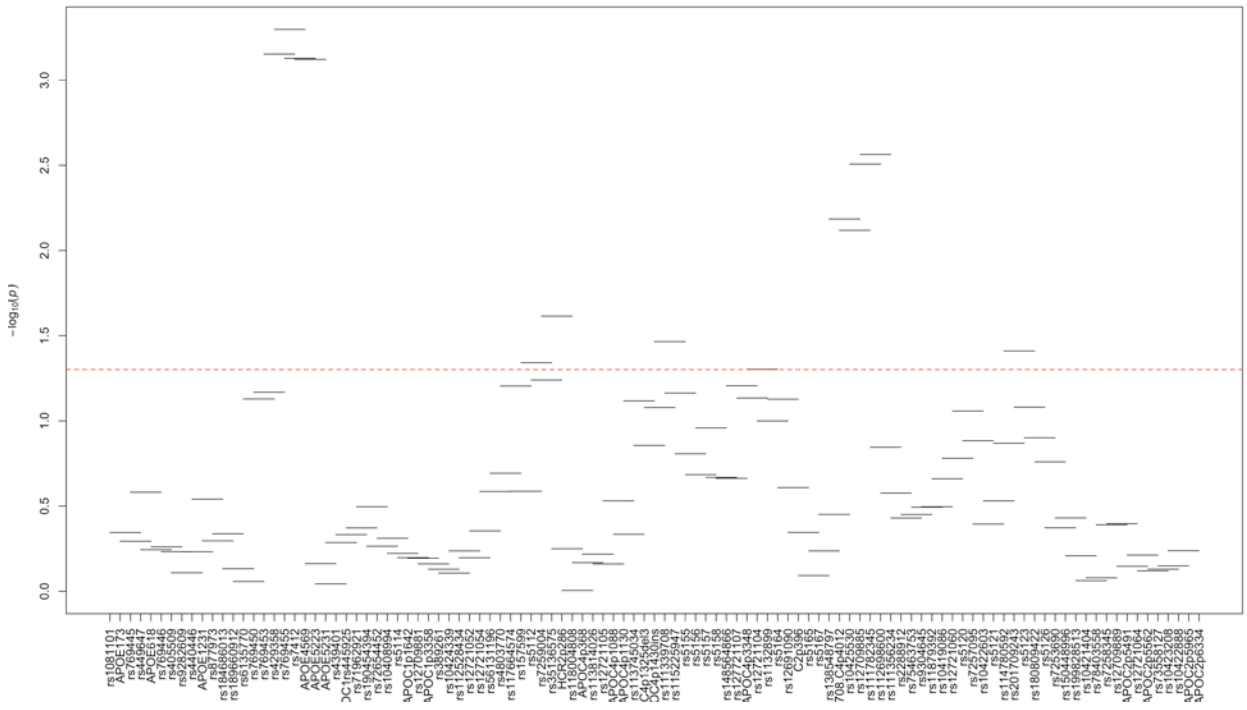


Figure 24. Haplotype p-value plots with lipid traits in Blacks

The X-axis has the genotyped markers that included in each window and the Y-axis has the –log (global p-value), the red line represent the significance threshold of the global haplotype p-value, each line is corresponding to one window, all line underneath the red line means non significant global p-value and vice versa.

Table 39. Haplotype-based association results with LDL-C, TC, and ApoB in Blacks

HAPLOTYPE WINDOWS						LDL-C[a]			TC[a]			ApoB[a]		
wind	w.snp	Function	RegulomeDB score	Genotype	MAF	Beta	Single-p	hap_P	Beta	single-p	hap_P	Beta	single-p	hap_P
1	APOE73/rs1081101	5'flanking	4	CC/CT/TT	0.0611	-0.62	0.11098	0.02165	-0.2	0.32826	0.14422	0.65	0.54877	0.27317
1	APOE173	5'flanking	3a	AA/GA	0.002	-1.14	0.59789	NA	0.41	0.71509	NA	3.2	0.59226	NA
1	APOE308/rs769445	5'flanking	4	CC/TC	0.0072	-0.37	0.75764	NA	-0.06	0.92177	NA	1.87	0.55135	NA
1	APOE560/rs449647	5'flanking	5	AA/AT/TT	0.3663	0.58	0.00307	NA	0.25	0.01773	NA	0.92	0.09509	NA
2	APOE173	5'flanking	3a	AA/GA	0.002	-1.14	0.59789	0.00975	0.41	0.71509	0.04834	3.2	0.59226	0.21585
2	APOE308/rs769445	5'flanking	4	CC/TC	0.0072	-0.37	0.75764	NA	-0.06	0.92177	NA	1.87	0.55135	NA
2	APOE560/rs449647	5'flanking	5	AA/AT/TT	0.3663	0.58	0.00307	NA	0.25	0.01773	NA	0.92	0.09509	NA
2	APOE618	5'flanking	4	GC/GG	0.0006	-2.85	0.44324	NA	-3.62	0.0634	NA	4.15	0.68762	NA
3	APOE308/rs769445	5'flanking	4	CC/TC	0.0072	-0.37	0.75764	0.00658	-0.06	0.92177	0.03895	1.87	0.55135	0.32323
3	APOE560/rs449647	5'flanking	5	AA/AT/TT	0.3663	0.58	0.00307	NA	0.25	0.01773	NA	0.92	0.09509	NA
3	APOE618	5'flanking	4	GC/GG	0.0006	-2.85	0.44324	NA	-3.62	0.0634	NA	4.15	0.68762	NA
3	APOE624/rs769446	5'flanking	3a	TC/TT	0.0077	-2.86	0.02138	NA	-1.25	0.04403	NA	-4.19	0.20373	NA
4	APOE560/rs449647	5'flanking	5	AA/AT/TT	0.3663	0.58	0.00307	0.00341	0.25	0.01773	0.01752	0.92	0.09509	0.26109
4	APOE618	5'flanking	4	GC/GG	0.0006	-2.85	0.44324	NA	-3.62	0.0634	NA	4.15	0.68762	NA
4	APOE624/rs769446	5'flanking	3a	TC/TT	0.0077	-2.86	0.02138	NA	-1.25	0.04403	NA	-4.19	0.20373	NA
4	APOE832/rs405509	5'flanking	1f	GG/GT/TT	0.2561	0.6	0.00436	NA	0.22	0.05286	NA	0.66	0.26113	NA
5	APOE618	5'flanking	4	GC/GG	0.0006	-2.85	0.44324	0.00338	-3.62	0.0634	0.01618	4.15	0.68762	0.26816
5	APOE624/rs769446	5'flanking	3a	TC/TT	0.0077	-2.86	0.02138	NA	-1.25	0.04403	NA	-4.19	0.20373	NA
5	APOE832/rs405509	5'flanking	1f	GG/GT/TT	0.2561	0.6	0.00436	NA	0.22	0.05286	NA	0.66	0.26113	NA
5	APOE1109/rs9282609	Splice site	4	CC/TC/TT	0.0415	0.05	0.91835	NA	0.12	0.63205	NA	1.38	0.27683	NA
6	APOE624/rs769446	5'flanking	3a	TC/TT	0.0077	-2.86	0.02138	0.01244	-1.25	0.04403	0.05618	-4.19	0.20373	0.18559
6	APOE832/rs405509	5'flanking	1f	GG/GT/TT	0.2561	0.6	0.00436	NA	0.22	0.05286	NA	0.66	0.26113	NA
6	APOE1109/rs9282609	Splice site	4	CC/TC/TT	0.0415	0.05	0.91835	NA	0.12	0.63205	NA	1.38	0.27683	NA
6	APOE1163/rs440446	intron1	4	CC/CG/GG	0.1004	0.44	0.17914	NA	0.12	0.47483	NA	2.3	0.01093	NA
7	APOE832/rs405509	5'flanking	1f	GG/GT/TT	0.2561	0.6	0.00436	0.08954	0.22	0.05286	0.25817	0.66	0.26113	0.13222
7	APOE1109/rs9282609	Splice site	4	CC/TC/TT	0.0415	0.05	0.91835	NA	0.12	0.63205	NA	1.38	0.27683	NA

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7	APOE1163/rs440446	intron1	4	CC/CG/GG	0.1004	0.44	0.17914	NA	0.12	0.47483	NA	2.3	0.01093	NA
7	APOE1231	intron1	2b	GA/GG	0.0125	-0.71	0.41393	NA	-0.46	0.3315	NA	-1.71	0.47484	NA
8	APOE1109/rs9282609	Splice site	4	CC/TC/TT	0.0415	0.05	0.91835	0.0781	0.12	0.63205	0.79076	1.38	0.27683	0.0897
8	APOE1163/rs440446	intron1	4	CC/CG/GG	0.1004	0.44	0.17914	NA	0.12	0.47483	NA	2.3	0.01093	NA
8	APOE1231	intron1	2b	GA/GG	0.0125	-0.71	0.41393	NA	-0.46	0.3315	NA	-1.71	0.47484	NA
8	APOE1279/rs877973	intron1	4	AA/CA/CC	0.0597	-0.15	0.72081	NA	0.04	0.85443	NA	-0.45	0.68467	NA
9	APOE1163/rs440446	intron1	4	CC/CG/GG	0.1004	0.44	0.17914	0.48376	0.12	0.47483	0.77016	2.3	0.01093	0.1435
9	APOE1231	intron1	2b	GA/GG	0.0125	-0.71	0.41393	NA	-0.46	0.3315	NA	-1.71	0.47484	NA
9	APOE1279/rs877973	intron1	4	AA/CA/CC	0.0597	-0.15	0.72081	NA	0.04	0.85443	NA	-0.45	0.68467	NA
9	APOE1539/rs184686013	intron1	4	AA/AG/GG	0.0086	-1.03	0.28621	NA	-0.33	0.51724	NA	0.23	0.93296	NA
10	APOE1231	intron1	2b	GA/GG	0.0125	-0.71	0.41393	0.53353	-0.46	0.3315	0.57901	-1.71	0.47484	0.85223
10	APOE1279/rs877973	intron1	4	AA/CA/CC	0.0597	-0.15	0.72081	NA	0.04	0.85443	NA	-0.45	0.68467	NA
10	APOE1539/rs184686013	intron1	4	AA/AG/GG	0.0086	-1.03	0.28621	NA	-0.33	0.51724	NA	0.23	0.93296	NA
10	APOE2072/rs189660912	intron 2	4	GA/GG	0.0079	-0.5	0.64333	NA	-0.4	0.47964	NA	0.7	0.81486	NA
11	APOE1279/rs877973	intron1	4	AA/CA/CC	0.0597	-0.15	0.72081	0.0365	0.04	0.85443	0.25311	-0.45	0.68467	0.75077
11	APOE1539/rs184686013	intron1	4	AA/AG/GG	0.0086	-1.03	0.28621	NA	-0.33	0.51724	NA	0.23	0.93296	NA
11	APOE2072/rs189660912	intron 2	4	GA/GG	0.0079	-0.5	0.64333	NA	-0.4	0.47964	NA	0.7	0.81486	NA
11	APOE2269/rs6135770	intron 2	5	GA/GG	0.0169	-2.05	0.00643	NA	-0.69	0.07713	NA	-2.56	0.22005	NA
12	APOE1539/rs184686013	intron1	4	AA/AG/GG	0.0086	-1.03	0.28621	0.02941	-0.33	0.51724	0.20075	0.23	0.93296	0.41949
12	APOE2072/rs189660912	intron 2	4	GA/GG	0.0079	-0.5	0.64333	NA	-0.4	0.47964	NA	0.7	0.81486	NA
12	APOE2269/rs6135770	intron 2	5	GA/GG	0.0169	-2.05	0.00643	NA	-0.69	0.07713	NA	-2.56	0.22005	NA
12	APOE2440/rs769450	intron 2	5	AA/AG/GG	0.387	0.2	0.34094	NA	0.11	0.30813	NA	-0.5	0.37248	NA
13	APOE2072/rs189660912	intron 2	4	GA/GG	0.0079	-0.5	0.64333	0.04441	-0.4	0.47964	0.25754	0.7	0.81486	0.3972
13	APOE2269/rs6135770	intron 2	5	GA/GG	0.0169	-2.05	0.00643	NA	-0.69	0.07713	NA	-2.56	0.22005	NA
13	APOE2440/rs769450	intron 2	5	AA/AG/GG	0.387	0.2	0.34094	NA	0.11	0.30813	NA	-0.5	0.37248	NA
13	APOE3673/rs769453	intron 3	5	CC/GC	0.0066	-0.37	0.76494	NA	-0.07	0.90541	NA	2.02	0.5386	NA
14	APOE2269/rs6135770	intron 2	5	GA/GG	0.0169	-2.05	0.00643	0.00475	-0.69	0.07713	0.09962	-2.56	0.22005	0.62589
14	APOE2440/rs769450	intron 2	5	AA/AG/GG	0.387	0.2	0.34094	NA	0.11	0.30813	NA	-0.5	0.37248	NA
14	APOE3673/rs769453	intron 3	5	CC/GC	0.0066	-0.37	0.76494	NA	-0.07	0.90541	NA	2.02	0.5386	NA

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14	APOE3937/rs429358	exon 4	5	CC/CT/TT	0.2656	0.46	0.03172	NA	0.17	0.13228	NA	0.05	0.9371	NA
15	APOE2440/rs769450	intron 2	5	AA/AG/GG	0.387	0.2	0.34094	0.00141	0.11	0.30813	0.03556	-0.5	0.37248	0.34287
15	APOE3673/rs769453	intron 3	5	CC/GC	0.0066	-0.37	0.76494	NA	-0.07	0.90541	NA	2.02	0.5386	NA
15	APOE3937/rs429358	exon 4	5	CC/CT/TT	0.2656	0.46	0.03172	NA	0.17	0.13228	NA	0.05	0.9371	NA
15	APOE4036/rs769455	exon 4	5	CC/TC/TT	0.02	-2.23	0.00095	NA	-0.87	0.01293	NA	-3.45	0.06644	NA
16	APOE3673/rs769453	intron 3	5	CC/GC	0.0066	-0.37	0.76494	3.41E-08	-0.07	0.90541	0.00012	2.02	0.5386	0.06604
16	APOE3937/rs429358	exon 4	5	CC/CT/TT	0.2656	0.46	0.03172	NA	0.17	0.13228	NA	0.05	0.9371	NA
16	APOE4036/rs769455	exon 4	5	CC/TC/TT	0.02	-2.23	0.00095	NA	-0.87	0.01293	NA	-3.45	0.06644	NA
16	APOE4075/rs7412	exon 4	5	AA/GA/GG	0.0605	-2.05	5.35E-07	NA	-0.82	0.00012	NA	-2.35	0.03564	NA
17	APOE3937/rs429358	exon 4	5	CC/CT/TT	0.2656	0.46	0.03172	9.58E-09	0.17	0.13228	0.00004	0.05	0.9371	0.03501
17	APOE4036/rs769455	exon 4	5	CC/TC/TT	0.02	-2.23	0.00095	NA	-0.87	0.01293	NA	-3.45	0.06644	NA
17	APOE4075/rs7412	exon 4	5	AA/GA/GG	0.0605	-2.05	5.35E-07	NA	-0.82	0.00012	NA	-2.35	0.03564	NA
17	APOE4569	3'UTR	5	GG/GT	0.0007	8.87	0.01732	NA	5.12	0.00895	NA	14.25	0.1684	NA
18	APOE4036/rs769455	exon 4	5	CC/TC/TT	0.02	-2.23	0.00095	8.86E-09	-0.87	0.01293	0.00004	-3.45	0.06644	0.03755
18	APOE4075/rs7412	exon 4	5	AA/GA/GG	0.0605	-2.05	5.35E-07	NA	-0.82	0.00012	NA	-2.35	0.03564	NA
18	APOE4569	3'UTR	5	GG/GT	0.0007	8.87	0.01732	NA	5.12	0.00895	NA	14.25	0.1684	NA
18	APOE5223	3'flanking	2b	CC/CG	0.0051	-2.25	0.08744	NA	-0.94	0.1738	NA	-2.54	0.51655	NA
19	APOE4075/rs7412	exon 4	5	AA/GA/GG	0.0605	-2.05	5.35E-07	8.23E-06	-0.82	0.00012	0.0017	-2.35	0.03564	0.19616
19	APOE4569	3'UTR	5	GG/GT	0.0007	8.87	0.01732	NA	5.12	0.00895	NA	14.25	0.1684	NA
19	APOE5223	3'flanking	2b	CC/CG	0.0051	-2.25	0.08744	NA	-0.94	0.1738	NA	-2.54	0.51655	NA
19	APOE5231	3'flanking	2b	GG/GT/TT	0.027	-0.1	0.85869	NA	-0.03	0.92075	NA	-0.82	0.60359	NA
20	APOE4569	3'UTR	5	GG/GT	0.0007	8.87	0.01732	0.43401	5.12	0.00895	0.92313	14.25	0.1684	0.33533
20	APOE5223	3'flanking	2b	CC/CG	0.0051	-2.25	0.08744	NA	-0.94	0.1738	NA	-2.54	0.51655	NA
20	APOE5231	3'flanking	2b	GG/GT/TT	0.027	-0.1	0.85869	NA	-0.03	0.92075	NA	-0.82	0.60359	NA
20	rs439401	intragenic	1b	CC/CT/TT	0.1092	0.39	0.19327	NA	0.07	0.66212	NA	1.42	0.0862	NA
21	APOE5223	3'flanking	2b	CC/CG	0.0051	-2.25	0.08744	0.27982	-0.94	0.1738	0.67578	-2.54	0.51655	0.4156
21	APOE5231	3'flanking	2b	GG/GT/TT	0.027	-0.1	0.85869	NA	-0.03	0.92075	NA	-0.82	0.60359	NA
21	rs439401	intragenic	1b	CC/CT/TT	0.1092	0.39	0.19327	NA	0.07	0.66212	NA	1.42	0.0862	NA
21	rs445925	intragenic	No Data	AA/GA/GG	0.299	-0.01	0.95085	NA	-0.01	0.89831	NA	-0.31	0.59161	NA

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22	APOE5231	3'flanking	2b	GG/GT/TT	0.027	-0.1	0.85869	0.12356	-0.03	0.92075	0.60182	-0.82	0.60359	0.19909
22	rs439401	intragenic	1b	CC/CT/TT	0.1092	0.39	0.19327	NA	0.07	0.66212	NA	1.42	0.0862	NA
22	rs445925	intragenic	No Data	AA/GA/GG	0.299	-0.01	0.95085	NA	-0.01	0.89831	NA	-0.31	0.59161	NA
22	APOC1p720ins4/rs71962921	5'flanking	4	II/WI/WW	0.2737	-0.57	0.00839	NA	-0.2	0.07407	NA	-1.1	0.06438	NA
23	rs439401	intragenic	1b	CC/CT/TT	0.1092	0.39	0.19327	0.09082	0.07	0.66212	0.48628	1.42	0.0862	0.12299
23	rs445925	intragenic	No Data	AA/GA/GG	0.299	-0.01	0.95085	NA	-0.01	0.89831	NA	-0.31	0.59161	NA
23	APOC1p720ins4/rs71962921	5'flanking	4	II/WI/WW	0.2737	-0.57	0.00839	NA	-0.2	0.07407	NA	-1.1	0.06438	NA
23	APOC1p894/rs190454394	5'flanking	4	CC/CT	0.002	3.7	0.08521	NA	1.71	0.13168	NA	8.19	0.17048	NA
24	rs445925	intragenic	No Data	AA/GA/GG	0.299	-0.01	0.95085	0.03672	-0.01	0.89831	0.27701	-0.31	0.59161	0.22067
24	APOC1p720ins4/rs71962921	5'flanking	4	II/WI/WW	0.2737	-0.57	0.00839	NA	-0.2	0.07407	NA	-1.1	0.06438	NA
24	APOC1p894/rs190454394	5'flanking	4	CC/CT	0.002	3.7	0.08521	NA	1.71	0.13168	NA	8.19	0.17048	NA
24	APOC1p1166/rs72654452	intron1	2b	CC/CT/TT	0.0308	0.49	0.3678	NA	0.31	0.27827	NA	0.98	0.51091	NA
25	APOC1p720ins4/rs71962921	5'flanking	4	II/WI/WW	0.2737	-0.57	0.00839	0.04284	-0.2	0.07407	0.16734	-1.1	0.06438	0.22334
25	APOC1p894/rs190454394	5'flanking	4	CC/CT	0.002	3.7	0.08521	NA	1.71	0.13168	NA	8.19	0.17048	NA
25	APOC1p1166/rs72654452	intron1	2b	CC/CT/TT	0.0308	0.49	0.3678	NA	0.31	0.27827	NA	0.98	0.51091	NA
25	APOC1p1331/rs10408994	intron2	4	AG/GG	0.0666	0.62	0.12376	NA	0.34	0.1116	NA	-0.83	0.46727	NA
26	APOC1p894/rs190454394	5'flanking	4	CC/CT	0.002	3.7	0.08521	0.21391	1.71	0.13168	0.17969	8.19	0.17048	0.56497
26	APOC1p1166/rs72654452	intron1	2b	CC/CT/TT	0.0308	0.49	0.3678	NA	0.31	0.27827	NA	0.98	0.51091	NA
26	APOC1p1331/rs10408994	intron2	4	AG/GG	0.0666	0.62	0.12376	NA	0.34	0.1116	NA	-0.83	0.46727	NA
26	APOC1p1526/rs5114	intron2	4	CC/CT/TT	0.0579	-0.05	0.90533	NA	0.12	0.58756	NA	-0.22	0.84865	NA
27	APOC1p1166/rs72654452	intron1	2b	CC/CT/TT	0.0308	0.49	0.3678	0.30552	0.31	0.27827	0.179	0.98	0.51091	0.77431
27	APOC1p1331/rs10408994	intron2	4	AG/GG	0.0666	0.62	0.12376	NA	0.34	0.1116	NA	-0.83	0.46727	NA
27	APOC1p1526/rs5114	intron2	4	CC/CT/TT	0.0579	-0.05	0.90533	NA	0.12	0.58756	NA	-0.22	0.84865	NA
27	APOC1p1642	intron2	4	CC/CT	0.0103	-1.05	0.26484	NA	-0.64	0.21318	NA	-1.86	0.47702	NA
28	APOC1p1331/rs10408994	intron2	4	AG/GG	0.0666	0.62	0.12376	0.14874	0.34	0.1116	0.14809	-0.83	0.46727	0.14402
28	APOC1p1526/rs5114	intron2	4	CC/CT/TT	0.0579	-0.05	0.90533	NA	0.12	0.58756	NA	-0.22	0.84865	NA
28	APOC1p1642	intron2	4	CC/CT	0.0103	-1.05	0.26484	NA	-0.64	0.21318	NA	-1.86	0.47702	NA
28	APOC1p1684/rs12709881	intron2	4	AA/GA/GG	0.0973	-0.51	0.11788	NA	-0.16	0.36396	NA	-1.48	0.09465	NA
29	APOC1p1526/rs5114	intron2	4	CC/CT/TT	0.0579	-0.05	0.90533	0.304	0.12	0.58756	0.26146	-0.22	0.84865	0.19431

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29	APOC1p1642	intron2	4	CC/CT	0.0103	-1.05	0.26484	NA	-0.64	0.21318	NA	-1.86	0.47702	NA
29	APOC1p1684/rs12709881	intron2	4	AA/GA/GG	0.0973	-0.51	0.11788	NA	-0.16	0.36396	NA	-1.48	0.09465	NA
29	APOC1p3358	intron3	No Data	AA/GA	0.0021	-0.25	0.9068	NA	0.34	0.76322	NA	-3.96	0.50955	NA
30	APOC1p1642	intron2	4	CC/CT	0.0103	-1.05	0.26484	0.51472	-0.64	0.21318	0.57007	-1.86	0.47702	0.46237
30	APOC1p1684/rs12709881	intron2	4	AA/GA/GG	0.0973	-0.51	0.11788	NA	-0.16	0.36396	NA	-1.48	0.09465	NA
30	APOC1p3358	intron3	No Data	AA/GA	0.0021	-0.25	0.9068	NA	0.34	0.76322	NA	-3.96	0.50955	NA
30	APOC1p3423/rs389261	intron3	No Data	AA/GA/GG	0.331	0.19	0.35557	NA	0.12	0.29576	NA	-0.04	0.94719	NA
31	APOC1p1684/rs12709881	intron2	4	AA/GA/GG	0.0973	-0.51	0.11788	0.49945	-0.16	0.36396	0.79551	-1.48	0.09465	0.31902
31	APOC1p3358	intron3	No Data	AA/GA	0.0021	-0.25	0.9068	NA	0.34	0.76322	NA	-3.96	0.50955	NA
31	APOC1p3423/rs389261	intron3	No Data	AA/GA/GG	0.331	0.19	0.35557	NA	0.12	0.29576	NA	-0.04	0.94719	NA
31	APOC1p3573/rs10424339	intron3	No Data	AA/GA/GG	0.1396	-0.02	0.93742	NA	0.07	0.63708	NA	-0.71	0.36467	NA
32	APOC1p3358	intron3	No Data	AA/GA	0.0021	-0.25	0.9068	0.64592	0.34	0.76322	0.85041	-3.96	0.50955	0.43518
32	APOC1p3423/rs389261	intron3	No Data	AA/GA/GG	0.331	0.19	0.35557	NA	0.12	0.29576	NA	-0.04	0.94719	NA
32	APOC1p3573/rs10424339	intron3	No Data	AA/GA/GG	0.1396	-0.02	0.93742	NA	0.07	0.63708	NA	-0.71	0.36467	NA
32	APOC1p5006/rs112528434	intron3	No Data	GG/GT/TT	0.085	-0.38	0.28869	NA	-0.1	0.60525	NA	-1.22	0.2099	NA
33	APOC1p3423/rs389261	intron3	No Data	AA/GA/GG	0.331	0.19	0.35557	0.33982	0.12	0.29576	0.56257	-0.04	0.94719	0.54287
33	APOC1p3573/rs10424339	intron3	No Data	AA/GA/GG	0.1396	-0.02	0.93742	NA	0.07	0.63708	NA	-0.71	0.36467	NA
33	APOC1p5006/rs112528434	intron3	No Data	GG/GT/TT	0.085	-0.38	0.28869	NA	-0.1	0.60525	NA	-1.22	0.2099	NA
33	APOC1p5053/rs12721052	intron3	No Data	DD/WD/WW	0.22	0.3	0.19047	NA	0.13	0.27278	NA	0.66	0.29256	NA
34	APOC1p3573/rs10424339	intron3	No Data	AA/GA/GG	0.1396	-0.02	0.93742	0.12074	0.07	0.63708	0.43673	-0.71	0.36467	0.58189
34	APOC1p5006/rs112528434	intron3	No Data	GG/GT/TT	0.085	-0.38	0.28869	NA	-0.1	0.60525	NA	-1.22	0.2099	NA
34	APOC1p5053/rs12721052	intron3	No Data	DD/WD/WW	0.22	0.3	0.19047	NA	0.13	0.27278	NA	0.66	0.29256	NA
34	APOC1p5667/rs12721054	3'UTR	6	AA/GA/GG	0.1446	-0.77	0.00631	NA	-0.3	0.04743	NA	-1.01	0.18808	NA
35	APOC1p5006/rs112528434	intron3	No Data	GG/GT/TT	0.085	-0.38	0.28869	0.02523	-0.1	0.60525	0.12946	-1.22	0.2099	0.61316
35	APOC1p5053/rs12721052	intron3	No Data	DD/WD/WW	0.22	0.3	0.19047	NA	0.13	0.27278	NA	0.66	0.29256	NA
35	APOC1p5667/rs12721054	3'UTR	6	AA/GA/GG	0.1446	-0.77	0.00631	NA	-0.3	0.04743	NA	-1.01	0.18808	NA
35	APOC1p5926/rs56131196	3'flanking	No Data	AA/AG/GG	0.1745	-0.22	0.39246	NA	-0.05	0.72955	NA	-0.7	0.33774	NA
36	APOC1p5053/rs12721052	intron3	No Data	DD/WD/WW	0.22	0.3	0.19047	0.02869	0.13	0.27278	0.13147	0.66	0.29256	0.51852
36	APOC1p5667/rs12721054	3'UTR	6	AA/GA/GG	0.1446	-0.77	0.00631	NA	-0.3	0.04743	NA	-1.01	0.18808	NA

Cont. Table 39

36	APOC1p5926/rs56131196	3'flanking	No Data	AA/AG/GG	0.1745	-0.22	0.39246	NA	-0.05	0.72955	NA	-0.7	0.33774	NA
36	rs4803770	HCR-1	5	CC/GC/GG	0.2695	0.38	0.08103	NA	0.18	0.11016	NA	0.9	0.13554	NA
37	APOC1p5667/rs12721054	3'UTR	6	AA/GA/GG	0.1446	-0.77	0.00631	0.02105	-0.3	0.04743	0.08779	-1.01	0.18808	0.42696
37	APOC1p5926/rs56131196	3'flanking	No Data	AA/AG/GG	0.1745	-0.22	0.39246	NA	-0.05	0.72955	NA	-0.7	0.33774	NA
37	rs4803770	HCR-1	5	CC/GC/GG	0.2695	0.38	0.08103	NA	0.18	0.11016	NA	0.9	0.13554	NA
37	HCR1p424/rs117664574	HCR-1	4	AG/GG	0.0073	-0.58	0.6076	NA	0.12	0.83438	NA	2.07	0.5106	NA
38	APOC1p5926/rs56131196	3'flanking	No Data	AA/AG/GG	0.1745	-0.22	0.39246	0.4397	-0.05	0.72955	0.5191	-0.7	0.33774	0.56102
38	rs4803770	HCR-1	5	CC/GC/GG	0.2695	0.38	0.08103	NA	0.18	0.11016	NA	0.9	0.13554	NA
38	HCR1p424/rs117664574	HCR-1	4	AG/GG	0.0073	-0.58	0.6076	NA	0.12	0.83438	NA	2.07	0.5106	NA
38	HCR1p575/rs157599	HCR-1	3a	AA/AG/GG	0.3595	0.17	0.40674	NA	0.08	0.46903	NA	0.27	0.64249	NA
39	rs4803770	HCR-1	5	CC/GC/GG	0.2695	0.38	0.08103	0.55556	0.18	0.11016	0.33791	0.9	0.13554	0.40008
39	HCR1p424/rs117664574	HCR-1	4	AG/GG	0.0073	-0.58	0.6076	NA	0.12	0.83438	NA	2.07	0.5106	NA
39	HCR1p575/rs157599	HCR-1	3a	AA/AG/GG	0.3595	0.17	0.40674	NA	0.08	0.46903	NA	0.27	0.64249	NA
39	rs5112	APC1P1	4	CC/GC/GG	0.4797	0.1	0.60734	NA	0.16	0.10913	NA	0.54	0.31703	NA
40	HCR1p424/rs117664574	HCR-1	4	AG/GG	0.0073	-0.58	0.6076	0.86661	0.12	0.83438	0.70627	2.07	0.5106	0.75338
40	HCR1p575/rs157599	HCR-1	3a	AA/AG/GG	0.3595	0.17	0.40674	NA	0.08	0.46903	NA	0.27	0.64249	NA
40	rs5112	APC1P1	4	CC/GC/GG	0.4797	0.1	0.60734	NA	0.16	0.10913	NA	0.54	0.31703	NA
40	rs7259004	APC1P1	6	CC/CG/GG	0.302	-0.02	0.90614	NA	0.09	0.39758	NA	0.37	0.51449	NA
41	HCR1p575/rs157599	HCR-1	3a	AA/AG/GG	0.3595	0.17	0.40674	0.91652	0.08	0.46903	0.72208	0.27	0.64249	0.6815
41	rs5112	APC1P1	4	CC/GC/GG	0.4797	0.1	0.60734	NA	0.16	0.10913	NA	0.54	0.31703	NA
41	rs7259004	APC1P1	6	CC/CG/GG	0.302	-0.02	0.90614	NA	0.09	0.39758	NA	0.37	0.51449	NA
41	HCR2p188/rs35136575	HCR-2	2a	CC/GC/GG	0.1546	-0.16	0.53272	NA	0.01	0.9184	NA	-0.61	0.4015	NA
42	rs5112	APC1P1	4	CC/GC/GG	0.4797	0.1	0.60734	0.59044	0.16	0.10913	0.42978	0.54	0.31703	0.60429
42	rs7259004	APC1P1	6	CC/CG/GG	0.302	-0.02	0.90614	NA	0.09	0.39758	NA	0.37	0.51449	NA
42	HCR2p188/rs35136575	HCR-2	2a	CC/GC/GG	0.1546	-0.16	0.53272	NA	0.01	0.9184	NA	-0.61	0.4015	NA
42	HCR2p286	HCR-2	2a	AA/AG/GG	0.0457	0.79	0.07851	NA	0.31	0.18468	NA	1.37	0.27692	NA
43	rs7259004	APC1P1	6	CC/CG/GG	0.302	-0.02	0.90614	0.32356	0.09	0.39758	0.37754	0.37	0.51449	0.42678
43	HCR2p188/rs35136575	HCR-2	2a	CC/GC/GG	0.1546	-0.16	0.53272	NA	0.01	0.9184	NA	-0.61	0.4015	NA
43	HCR2p286	HCR-2	2a	AA/AG/GG	0.0457	0.79	0.07851	NA	0.31	0.18468	NA	1.37	0.27692	NA

Cont. Table 39

43	HCR2p523/rs118004808	HCR-2	2b	CC/TC	0.0026	2.74	0.14181	NA	1.17	0.23621	NA	6.71	0.19588	NA
44	HCR2p188/rs35136575	HCR-2	2a	CC/GC/GG	0.1546	-0.16	0.53272	0.1954	0.01	0.9184	0.40593	-0.61	0.4015	0.51614
44	HCR2p286	HCR-2	2a	AA/AG/GG	0.0457	0.79	0.07851	NA	0.31	0.18468	NA	1.37	0.27692	NA
44	HCR2p523/rs118004808	HCR-2	2b	CC/TC	0.0026	2.74	0.14181	NA	1.17	0.23621	NA	6.71	0.19588	NA
44	APOC4p368	5′ flanking	6	TC/TT	0.0019	1.04	0.6283	NA	0.71	0.52903	NA	-1.39	0.81479	NA
45	HCR2p286	HCR-2	2a	AA/AG/GG	0.0457	0.79	0.07851	0.12917	0.31	0.18468	0.24482	1.37	0.27692	0.34524
45	HCR2p523/rs118004808	HCR-2	2b	CC/TC	0.0026	2.74	0.14181	NA	1.17	0.23621	NA	6.71	0.19588	NA
45	APOC4p368	5′ flanking	6	TC/TT	0.0019	1.04	0.6283	NA	0.71	0.52903	NA	-1.39	0.81479	NA
45	APOC4p637/rs113814026	5′ flanking	No Data	GG/GT/TT	0.0452	-0.23	0.61266	NA	-0.13	0.58316	NA	1.34	0.29549	NA
46	HCR2p523/rs118004808	HCR-2	2b	CC/TC	0.0026	2.74	0.14181	0.50368	1.17	0.23621	0.53391	6.71	0.19588	0.55865
46	APOC4p368	5′ flanking	6	TC/TT	0.0019	1.04	0.6283	NA	0.71	0.52903	NA	-1.39	0.81479	NA
46	APOC4p637/rs113814026	5′ flanking	No Data	GG/GT/TT	0.0452	-0.23	0.61266	NA	-0.13	0.58316	NA	1.34	0.29549	NA
46	APOC4p757/rs12721105	5′ flanking	5	GG/GT/TT	0.0376	0.14	0.77797	NA	0.13	0.61917	NA	0.45	0.7436	NA
47	APOC4p368	5′ flanking	6	TC/TT	0.0019	1.04	0.6283	0.95138	0.71	0.52903	0.92464	-1.39	0.81479	0.70523
47	APOC4p637/rs113814026	5′ flanking	No Data	GG/GT/TT	0.0452	-0.23	0.61266	NA	-0.13	0.58316	NA	1.34	0.29549	NA
47	APOC4p757/rs12721105	5′ flanking	5	GG/GT/TT	0.0376	0.14	0.77797	NA	0.13	0.61917	NA	0.45	0.7436	NA
47	APOC4p1088	intron1	2b	GT/TT	0.0013	-2.69	0.30478	NA	-1.51	0.27674	NA	-2.07	0.7775	NA
48	APOC4p637/rs113814026	5′ flanking	No Data	GG/GT/TT	0.0452	-0.23	0.61266	0.73798	-0.13	0.58316	0.8653	1.34	0.29549	0.36088
48	APOC4p757/rs12721105	5′ flanking	5	GG/GT/TT	0.0376	0.14	0.77797	NA	0.13	0.61917	NA	0.45	0.7436	NA
48	APOC4p1088	intron1	2b	GT/TT	0.0013	-2.69	0.30478	NA	-1.51	0.27674	NA	-2.07	0.7775	NA
48	APOC4p1130	intron1	5	CT/TT	0.0007	-0.71	0.84908	NA	1.5	0.44346	NA	-21.03	0.04207	NA
49	APOC4p757/rs12721105	5′ flanking	5	GG/GT/TT	0.0376	0.14	0.77797	0.68677	0.13	0.61917	0.83976	0.45	0.7436	0.33508
49	APOC4p1088	intron1	2b	GT/TT	0.0013	-2.69	0.30478	NA	-1.51	0.27674	NA	-2.07	0.7775	NA
49	APOC4p1130	intron1	5	CT/TT	0.0007	-0.71	0.84908	NA	1.5	0.44346	NA	-21.03	0.04207	NA
49	APOC4p1192/rs113745034	intron1	4	GA/GG	0.0124	-0.63	0.48231	NA	-0.31	0.50557	NA	2.83	0.26681	NA
50	APOC4p1088	intron1	2b	GT/TT	0.0013	-2.69	0.30478	0.3418	-1.51	0.27674	0.65242	-2.07	0.7775	0.12845
50	APOC4p1130	intron1	5	CT/TT	0.0007	-0.71	0.84908	NA	1.5	0.44346	NA	-21.03	0.04207	NA
50	APOC4p1192/rs113745034	intron1	4	GA/GG	0.0124	-0.63	0.48231	NA	-0.31	0.50557	NA	2.83	0.26681	NA
50	APOC4p1325del3	intron1	4	WD/WW	0.0245	0.7	0.2711	NA	0.28	0.40992	NA	1.71	0.33255	NA

Cont. Table 39

51	APOC4p1130	intron1	5	CT/TT	0.0007	-0.71	0.84908	0.63734	1.5	0.44346	0.65455	-21.03	0.04207	0.08634
51	APOC4p1192/rs113745034	intron1	4	GA/GG	0.0124	-0.63	0.48231	NA	-0.31	0.50557	NA	2.83	0.26681	NA
51	APOC4p1325del3	intron1	4	WD/WW	0.0245	0.7	0.2711	NA	0.28	0.40992	NA	1.71	0.33255	NA
51	APOC4p1430ins	intron1	5	II/WI/WW	0.0341	0.32	0.5609	NA	0.35	0.22899	NA	1.43	0.35841	NA
52	APOC4p1192/rs113745034	intron1	4	GA/GG	0.0124	-0.63	0.48231	0.60585	-0.31	0.50557	0.60688	2.83	0.26681	0.25455
52	APOC4p1325del3	intron1	4	WD/WW	0.0245	0.7	0.2711	NA	0.28	0.40992	NA	1.71	0.33255	NA
52	APOC4p1430ins	intron1	5	II/WI/WW	0.0341	0.32	0.5609	NA	0.35	0.22899	NA	1.43	0.35841	NA
52	APOC4p2099/rs111339708	intron1	No Data	GG/GT	0.0141	-0.83	0.30264	NA	-0.42	0.33673	NA	1.19	0.59549	NA
53	APOC4p1325del3	intron1	4	WD/WW	0.0245	0.7	0.2711	0.5103	0.28	0.40992	0.48905	1.71	0.33255	0.52124
53	APOC4p1430ins	intron1	5	II/WI/WW	0.0341	0.32	0.5609	NA	0.35	0.22899	NA	1.43	0.35841	NA
53	APOC4p2099/rs111339708	intron1	No Data	GG/GT	0.0141	-0.83	0.30264	NA	-0.42	0.33673	NA	1.19	0.59549	NA
53	APOC4p2467/rs115225947	intron1	5	GA/GG	0.0141	0.68	0.40563	NA	0.3	0.49226	NA	-0.42	0.85407	NA
54	APOC4p1430ins	intron1	5	II/WI/WW	0.0341	0.32	0.5609	0.61806	0.35	0.22899	0.40631	1.43	0.35841	0.69268
54	APOC4p2099/rs111339708	intron1	No Data	GG/GT	0.0141	-0.83	0.30264	NA	-0.42	0.33673	NA	1.19	0.59549	NA
54	APOC4p2467/rs115225947	intron1	5	GA/GG	0.0141	0.68	0.40563	NA	0.3	0.49226	NA	-0.42	0.85407	NA
54	APOC4p2559/rs5155	intron1	4	CC/CT/TT	0.0986	-0.27	0.40279	NA	-0.22	0.20901	NA	-0.98	0.27438	NA
55	APOC4p2099/rs111339708	intron1	No Data	GG/GT	0.0141	-0.83	0.30264	0.59808	-0.42	0.33673	0.37761	1.19	0.59549	0.51034
55	APOC4p2467/rs115225947	intron1	5	GA/GG	0.0141	0.68	0.40563	NA	0.3	0.49226	NA	-0.42	0.85407	NA
55	APOC4p2559/rs5155	intron1	4	CC/CT/TT	0.0986	-0.27	0.40279	NA	-0.22	0.20901	NA	-0.98	0.27438	NA
55	APOC4p2607/rs5156	intron1	4	AG/GG	0.0129	-1.04	0.23497	NA	-0.49	0.2981	NA	1.6	0.50775	NA
56	APOC4p2467/rs115225947	intron1	5	GA/GG	0.0141	0.68	0.40563	0.40521	0.3	0.49226	0.40068	-0.42	0.85407	0.37254
56	APOC4p2559/rs5155	intron1	4	CC/CT/TT	0.0986	-0.27	0.40279	NA	-0.22	0.20901	NA	-0.98	0.27438	NA
56	APOC4p2607/rs5156	intron1	4	AG/GG	0.0129	-1.04	0.23497	NA	-0.49	0.2981	NA	1.6	0.50775	NA
56	APOC4p2623/rs5157	intron1	4	CC/CT/TT	0.1723	0.28	0.27026	NA	0.13	0.32874	NA	1.43	0.04428	NA
57	APOC4p2559/rs5155	intron1	4	CC/CT/TT	0.0986	-0.27	0.40279	0.42585	-0.22	0.20901	0.4764	-0.98	0.27438	0.30408
57	APOC4p2607/rs5156	intron1	4	AG/GG	0.0129	-1.04	0.23497	NA	-0.49	0.2981	NA	1.6	0.50775	NA
57	APOC4p2623/rs5157	intron1	4	CC/CT/TT	0.1723	0.28	0.27026	NA	0.13	0.32874	NA	1.43	0.04428	NA
57	APOC4p2640/rs5158	intron1	2b	CC/CT	0.0213	0.55	0.41401	NA	0.01	0.97117	NA	1.44	0.44596	NA
58	APOC4p2607/rs5156	intron1	4	AG/GG	0.0129	-1.04	0.23497	0.36303	-0.49	0.2981	0.56782	1.6	0.50775	0.20187

Cont. Table 39

58	APOC4p2623/rs5157	intron1	4	CC/CT/TT	0.1723	0.28	0.27026	NA	0.13	0.32874	NA	1.43	0.04428	NA
58	APOC4p2640/rs5158	intron1	2b	CC/CT	0.0213	0.55	0.41401	NA	0.01	0.97117	NA	1.44	0.44596	NA
58	APOC4p2678/rs148564866	intron1	2b	GC/GG	0.0086	-0.61	0.55495	NA	-0.31	0.58397	NA	0.87	0.76308	NA
59	APOC4p2623/rs5157	intron1	4	CC/CT/TT	0.1723	0.28	0.27026	0.66648	0.13	0.32874	0.84546	1.43	0.04428	0.07085
59	APOC4p2640/rs5158	intron1	2b	CC/CT	0.0213	0.55	0.41401	NA	0.01	0.97117	NA	1.44	0.44596	NA
59	APOC4p2678/rs148564866	intron1	2b	GC/GG	0.0086	-0.61	0.55495	NA	-0.31	0.58397	NA	0.87	0.76308	NA
59	APOC4p2767/rs127721107	intron1	4	GG/GT	0.0254	0.35	0.57878	NA	0.16	0.62791	NA	3.15	0.07284	NA
60	APOC4p2640/rs5158	intron1	2b	CC/CT	0.0213	0.55	0.41401	0.69787	0.01	0.97117	0.94946	1.44	0.44596	0.28586
60	APOC4p2678/rs148564866	intron1	2b	GC/GG	0.0086	-0.61	0.55495	NA	-0.31	0.58397	NA	0.87	0.76308	NA
60	APOC4p2767/rs127721107	intron1	4	GG/GT	0.0254	0.35	0.57878	NA	0.16	0.62791	NA	3.15	0.07284	NA
60	APOC4p3348	intron1	5	AG/GG	0.0007	-2.86	0.44034	NA	0.74	0.70666	NA	-9.98	0.33555	NA
61	APOC4p2678/rs148564866	intron1	2b	GC/GG	0.0086	-0.61	0.55495	0.827	-0.31	0.58397	0.93681	0.87	0.76308	0.35963
61	APOC4p2767/rs127721107	intron1	4	GG/GT	0.0254	0.35	0.57878	NA	0.16	0.62791	NA	3.15	0.07284	NA
61	APOC4p3348	intron1	5	AG/GG	0.0007	-2.86	0.44034	NA	0.74	0.70666	NA	-9.98	0.33555	NA
61	APOC2p75APOC4p3380/rs12721104	C4-intron1	5	AA/GA/GG	0.1368	0.02	0.93583	NA	-0.01	0.92441	NA	-0.07	0.92847	NA
62	APOC4p2767/rs127721107	intron1	4	GG/GT	0.0254	0.35	0.57878	0.72016	0.16	0.62791	0.76596	3.15	0.07284	0.10037
62	APOC4p3348	intron1	5	AG/GG	0.0007	-2.86	0.44034	NA	0.74	0.70666	NA	-9.98	0.33555	NA
62	APOC2p75C4p3380/rs12721104	C4-intron1	5	AA/GA/GG	0.1368	0.02	0.93583	NA	-0.01	0.92441	NA	-0.07	0.92847	NA
62	APOC2p194C4p3498/rs1132899	C4-exon2	5	CC/CT/TT	0.2368	0.21	0.36149	NA	0.11	0.35464	NA	0.95	0.13191	NA
63	APOC4p3348	intron1	5	AG/GG	0.0007	-2.86	0.44034	0.66798	0.74	0.70666	0.77939	-9.98	0.33555	0.45032
63	APOC2p75C4p3380/rs12721104	C4-intron1	5	AA/GA/GG	0.1368	0.02	0.93583	NA	-0.01	0.92441	NA	-0.07	0.92847	NA
63	APOC2p194C4p3498/rs1132899	C4-exon2	5	CC/CT/TT	0.2368	0.21	0.36149	NA	0.11	0.35464	NA	0.95	0.13191	NA
63	APOC2p228/rs5164	C4-exon2	5	AG/GA/GG	0.0066	-0.78	0.51255	NA	-0.43	0.49532	NA	2.49	0.4501	NA
64	APOC2p75C4p3380/rs12721104	C4-intron1	5	AA/GA/GG	0.1368	0.02	0.93583	0.86909	-0.01	0.92441	0.86658	-0.07	0.92847	0.31477
64	APOC2p194C4p3498/rs1132899	C4-exon2	5	CC/CT/TT	0.2368	0.21	0.36149	NA	0.11	0.35464	NA	0.95	0.13191	NA
64	APOC2p228/rs5164	C4-exon2	5	AG/GA/GG	0.0066	-0.78	0.51255	NA	-0.43	0.49532	NA	2.49	0.4501	NA
64	APOC2p288C4p3592/rs12691090	C4-exon2	5	CC/CT	0.0272	-0.02	0.97528	NA	0.02	0.94191	NA	1.96	0.24561	NA
65	APOC2p194C4p3498/rs1132899	C4-exon2	5	CC/CT/TT	0.2368	0.21	0.36149	0.63255	0.11	0.35464	0.67514	0.95	0.13191	0.22814
65	APOC2p228/rs5164	C4-exon2	5	AG/GA/GG	0.0066	-0.78	0.51255	NA	-0.43	0.49532	NA	2.49	0.4501	NA

Cont. Table 39

65	APOC2p288C4p3592/rs12691090	C4-exon2	5	CC/CT	0.0272	-0.02	0.97528	NA	0.02	0.94191	NA	1.96	0.24561	NA
65	APOC2p396C4p3700	C4-intron2	5	GA/GG	0.0007	-4.47	0.23235	NA	-1.4	0.48018	NA	-9.04	0.38386	NA
66	APOC2p228/rs5164	C4-exon2	5	AG/GA/GG	0.0066	-0.78	0.51255	0.79407	-0.43	0.49532	0.84915	2.49	0.4501	0.59814
66	APOC2p288C4p3592/rs12691090	C4-exon2	5	CC/CT	0.0272	-0.02	0.97528	NA	0.02	0.94191	NA	1.96	0.24561	NA
66	APOC2p396C4p3700	C4-intron2	5	GA/GG	0.0007	-4.47	0.23235	NA	-1.4	0.48018	NA	-9.04	0.38386	NA
66	APOC2p488C4p3792/rs5165	C4-intron2	5	GA/GG	0.0146	0.13	0.87346	NA	-0.07	0.86634	NA	-0.83	0.71058	NA
67	APOC2p288C4p3592/rs12691090	C4-exon2	5	CC/CT	0.0272	-0.02	0.97528	0.3186	0.02	0.94191	0.51413	1.96	0.24561	0.25723
67	APOC2p396C4p3700	C4-intron2	5	GA/GG	0.0007	-4.47	0.23235	NA	-1.4	0.48018	NA	-9.04	0.38386	NA
67	APOC2p488C4p3792/rs5165	C4-intron2	5	GA/GG	0.0146	0.13	0.87346	NA	-0.07	0.86634	NA	-0.83	0.71058	NA
67	APOC2p623C4p3927/rs5167	C4-exon3	5	GG/GT/TT	0.4594	-0.37	0.05268	NA	-0.16	0.10575	NA	-0.54	0.31017	NA
68	APOC2p396C4p3700	C4-intron2	5	GA/GG	0.0007	-4.47	0.23235	0.29963	-1.4	0.48018	0.44481	-9.04	0.38386	0.41284
68	APOC2p488C4p3792/rs5165	C4-intron2	5	GA/GG	0.0146	0.13	0.87346	NA	-0.07	0.86634	NA	-0.83	0.71058	NA
68	APOC2p623C4p3927/rs5167	C4-exon3	5	GG/GT/TT	0.4594	-0.37	0.05268	NA	-0.16	0.10575	NA	-0.54	0.31017	NA
68	APOC2p665C4p3969/rs138548797	C4-exon3	No Data	AA/CA	0.0086	0.18	0.86495	NA	-0.004	0.99377	NA	4.09	0.15807	NA
69	APOC2p488C4p3792/rs5165	C4-intron2	5	GA/GG	0.0146	0.13	0.87346	0.28969	-0.07	0.86634	0.44485	-0.83	0.71058	0.25662
69	APOC2p623C4p3927/rs5167	C4-exon3	5	GG/GT/TT	0.4594	-0.37	0.05268	NA	-0.16	0.10575	NA	-0.54	0.31017	NA
69	APOC2p665C4p3969/rs138548797	C4-exon3	No Data	AA/CA	0.0086	0.18	0.86495	NA	-0.004	0.99377	NA	4.09	0.15807	NA
69	APOC2p708C4p4012	C4-exon3	6	GA/GG	0.0007	-1.33	0.72116	NA	-1.34	0.49361	NA	6.46	0.53306	NA
70	APOC2p623C4p3927/rs5167	C4-exon3	5	GG/GT/TT	0.4594	-0.37	0.05268	0.29355	-0.16	0.10575	0.46468	-0.54	0.31017	0.27985
70	APOC2p665C4p3969/rs138548797	C4-exon3	No Data	AA/CA	0.0086	0.18	0.86495	NA	-0.004	0.99377	NA	4.09	0.15807	NA
70	APOC2p708C4p4012	C4-exon3	6	GA/GG	0.0007	-1.33	0.72116	NA	-1.34	0.49361	NA	6.46	0.53306	NA
70	APOC2p853C4p4157/rs10425530	C4-3' UTR	6	AA/GA/GG	0.11	-0.2	0.53149	NA	-0.06	0.70512	NA	-0.53	0.5399	NA
71	APOC2p665C4p3969/rs138548797	C4-exon3	No Data	AA/CA	0.0086	0.18	0.86495	0.38779	-0.004	0.99377	0.52916	4.09	0.15807	0.05501
71	APOC2p708C4p4012	C4-exon3	6	GA/GG	0.0007	-1.33	0.72116	NA	-1.34	0.49361	NA	6.46	0.53306	NA
71	APOC2p853C4p4157/rs10425530	C4-3' UTR	6	AA/GA/GG	0.11	-0.2	0.53149	NA	-0.06	0.70512	NA	-0.53	0.5399	NA
71	APOC2p1042C4p4346/rs12709885	C4-3'FR/C2-5'FR	5	AA/TA/TT	0.0178	-1.25	0.08548	NA	-0.55	0.15479	NA	-4.39	0.02431	NA
72	APOC2p708C4p4012	C4-exon3	6	GA/GG	0.0007	-1.33	0.72116	0.41917	-1.34	0.49361	0.54987	6.46	0.53306	0.12738
72	APOC2p853C4p4157/rs10425530	C4-3' UTR	6	AA/GA/GG	0.11	-0.2	0.53149	NA	-0.06	0.70512	NA	-0.53	0.5399	NA
72	APOC2p1042C4p4346/rs12709885	C4-3'FR/C2-5'FR	5	AA/TA/TT	0.0178	-1.25	0.08548	NA	-0.55	0.15479	NA	-4.39	0.02431	NA

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72	APOC2p1187C4p4491/rs111782345	C4-3'FR/C2-5'FR	5	AG/GG	0.0178	0.21	0.77726	NA	0.17	0.67391	NA	3.17	0.13276	NA
73	APOC2p853C4p4157/rs10425530	C4-3' UTR	6	AA/GA/GG	0.11	-0.2	0.53149	0.44704	-0.06	0.70512	0.51182	-0.53	0.5399	0.15897
73	APOC2p1042C4p4346/rs12709885	C4-3'FR/C2-5'FR	5	AA/TA/TT	0.0178	-1.25	0.08548	NA	-0.55	0.15479	NA	-4.39	0.02431	NA
73	APOC2p1187C4p4491/rs111782345	C4-3'FR/C2-5'FR	5	AG/GG	0.0178	0.21	0.77726	NA	0.17	0.67391	NA	3.17	0.13276	NA
73	APOC2p1229C4p4533/rs112698600	C4-3'FR/C2-5'FR	2b	CC/CT	0.014	-0.17	0.83981	NA	0.04	0.93279	NA	2.78	0.23927	NA
74	APOC2p1042C4p4346/rs12709885	C4-3'FR/C2-5'FR	5	AA/TA/TT	0.0178	-1.25	0.08548	0.07529	-0.55	0.15479	0.1048	-4.39	0.02431	0.15071
74	APOC2p1187C4p4491/rs111782345	C4-3'FR/C2-5'FR	5	AG/GG	0.0178	0.21	0.77726	NA	0.17	0.67391	NA	3.17	0.13276	NA
74	APOC2p1229C4p4533/rs112698600	C4-3'FR/C2-5'FR	2b	CC/CT	0.014	-0.17	0.83981	NA	0.04	0.93279	NA	2.78	0.23927	NA
74	APOC2p1275C4p4579/rs111356234	C4-3'FR/C2-5'FR	4	GA/GG	0.0352	-0.95	0.07519	NA	-0.48	0.09537	NA	-0.23	0.87888	NA
75	APOC2p1187C4p4491/rs111782345	C4-3'FR/C2-5'FR	5	AG/GG	0.0178	0.21	0.77726	0.01391	0.17	0.67391	0.01114	3.17	0.13276	0.10023
75	APOC2p1229C4p4533/rs112698600	C4-3'FR/C2-5'FR	2b	CC/CT	0.014	-0.17	0.83981	NA	0.04	0.93279	NA	2.78	0.23927	NA
75	APOC2p1275C4p4579/rs111356234	C4-3'FR/C2-5'FR	4	GA/GG	0.0352	-0.95	0.07519	NA	-0.48	0.09537	NA	-0.23	0.87888	NA
75	APOC2p1357C4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	CC/GC/GG	0.2581	0.51	0.02019	NA	0.28	0.01532	NA	1.37	0.02344	NA
76	APOC2p1229C4p4533/rs112698600	C4-3'FR/C2-5'FR	2b	CC/CT	0.014	-0.17	0.83981	0.03127	0.04	0.93279	0.03556	2.78	0.23927	0.23594
76	APOC2p1275C4p4579/rs111356234	C4-3'FR/C2-5'FR	4	GA/GG	0.0352	-0.95	0.07519	NA	-0.48	0.09537	NA	-0.23	0.87888	NA
76	APOC2p1357C4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	CC/GC/GG	0.2581	0.51	0.02019	NA	0.28	0.01532	NA	1.37	0.02344	NA
76	APOC2p1540C4p4844/rs75463753	C2-intron1	4	AA/GA/GG	0.1079	0.8	0.01138	NA	0.42	0.01106	NA	1.08	0.21814	NA
77	APOC2p1275C4p4579/rs111356234	C4-3'FR/C2-5'FR	4	GA/GG	0.0352	-0.95	0.07519	0.05978	-0.48	0.09537	0.10413	-0.23	0.87888	0.61764
77	APOC2p1357C4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	CC/GC/GG	0.2581	0.51	0.02019	NA	0.28	0.01532	NA	1.37	0.02344	NA
77	APOC2p1540C4p4844/rs75463753	C2-intron1	4	AA/GA/GG	0.1079	0.8	0.01138	NA	0.42	0.01106	NA	1.08	0.21814	NA
77	APOC2p2486/rs9304645	intron1	4	AA/GA/GG	0.3655	-0.54	0.00842	NA	-0.2	0.07368	NA	-0.21	0.7176	NA
78	APOC2p1357C4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	CC/GC/GG	0.2581	0.51	0.02019	0.02612	0.28	0.01532	0.11574	1.37	0.02344	0.43439
78	APOC2p1540C4p4844/rs75463753	C2-intron1	4	AA/GA/GG	0.1079	0.8	0.01138	NA	0.42	0.01106	NA	1.08	0.21814	NA
78	APOC2p2486/rs9304645	intron1	4	AA/GA/GG	0.3655	-0.54	0.00842	NA	-0.2	0.07368	NA	-0.21	0.7176	NA
78	APOC2p2935/rs11879392	intron1	2b	CC/GC	0.0135	0.87	0.31703	NA	0.27	0.53988	NA	0.44	0.85516	NA
79	APOC2p1540C4p4844/rs75463753	C2-intron1	4	AA/GA/GG	0.1079	0.8	0.01138	0.04403	0.42	0.01106	0.18207	1.08	0.21814	0.85396
79	APOC2p2486/rs9304645	intron1	4	AA/GA/GG	0.3655	-0.54	0.00842	NA	-0.2	0.07368	NA	-0.21	0.7176	NA
79	APOC2p2935/rs11879392	intron1	2b	CC/GC	0.0135	0.87	0.31703	NA	0.27	0.53988	NA	0.44	0.85516	NA
79	APOC2p3010/rs10419086	intron1	6	AA/AG/GG	0.1253	0.03	0.92147	NA	-0.05	0.74391	NA	-0.91	0.2581	NA

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80	APOC2p2486/rs9304645	intron1	4	AA/GA/GG	0.3655	-0.54	0.00842	0.0249	-0.2	0.07368	0.28434	-0.21	0.7176	0.48475
80	APOC2p2935/rs11879392	intron1	2b	CC/GC	0.0135	0.87	0.31703	NA	0.27	0.53988	NA	0.44	0.85516	NA
80	APOC2p3010/rs10419086	intron1	6	AA/AG/GG	0.1253	0.03	0.92147	NA	-0.05	0.74391	NA	-0.91	0.2581	NA
80	APOC2p3692/rs12721060	intron1	No Data	GT/TT	0.0172	-0.19	0.8123	NA	-0.04	0.92973	NA	2.28	0.31473	NA
81	APOC2p2935/rs11879392	intron1	2b	CC/GC	0.0135	0.87	0.31703	0.05641	0.27	0.53988	0.13454	0.44	0.85516	0.26005
81	APOC2p3010/rs10419086	intron1	6	AA/AG/GG	0.1253	0.03	0.92147	NA	-0.05	0.74391	NA	-0.91	0.2581	NA
81	APOC2p3692/rs12721060	intron1	No Data	GT/TT	0.0172	-0.19	0.8123	NA	-0.04	0.92973	NA	2.28	0.31473	NA
81	APOC2p3778/rs5120	intron1	4	AA/AT/TT	0.1845	0.6	0.01577	NA	0.33	0.01287	NA	1.11	0.10763	NA
82	APOC2p3010/rs10419086	intron1	6	AA/AG/GG	0.1253	0.03	0.92147	0.06512	-0.05	0.74391	0.10754	-0.91	0.2581	0.31029
82	APOC2p3692/rs12721060	intron1	No Data	GT/TT	0.0172	-0.19	0.8123	NA	-0.04	0.92973	NA	2.28	0.31473	NA
82	APOC2p3778/rs5120	intron1	4	AA/AT/TT	0.1845	0.6	0.01577	NA	0.33	0.01287	NA	1.11	0.10763	NA
82	APOC2p3805/rs7257095	intron1	2a	CC/CG/GG	0.1649	0.35	0.18831	NA	0.13	0.35514	NA	0.72	0.33716	NA
83	APOC2p3692/rs12721060	intron1	No Data	GT/TT	0.0172	-0.19	0.8123	0.06095	-0.04	0.92973	0.09301	2.28	0.31473	0.22803
83	APOC2p3778/rs5120	intron1	4	AA/AT/TT	0.1845	0.6	0.01577	NA	0.33	0.01287	NA	1.11	0.10763	NA
83	APOC2p3805/rs7257095	intron1	2a	CC/CG/GG	0.1649	0.35	0.18831	NA	0.13	0.35514	NA	0.72	0.33716	NA
83	APOC2p3814/rs10422603	intron1	2b	GG/GT/TT	0.3008	-0.3	0.1716	NA	-0.08	0.47136	NA	-0.1	0.87424	NA
84	APOC2p3778/rs5120	intron1	4	AA/AT/TT	0.1845	0.6	0.01577	0.04904	0.33	0.01287	0.07184	1.11	0.10763	0.34215
84	APOC2p3805/rs7257095	intron1	2a	CC/CG/GG	0.1649	0.35	0.18831	NA	0.13	0.35514	NA	0.72	0.33716	NA
84	APOC2p3814/rs10422603	intron1	2b	GG/GT/TT	0.3008	-0.3	0.1716	NA	-0.08	0.47136	NA	-0.1	0.87424	NA
84	APOC2p3892/rs5121	exon2	5	CC/TC/TT	0.0358	-0.21	0.69569	NA	-0.11	0.69795	NA	-0.03	0.98356	NA
85	APOC2p3805/rs7257095	intron1	2a	CC/CG/GG	0.1649	0.35	0.18831	0.43254	0.13	0.35514	0.7624	0.72	0.33716	0.28002
85	APOC2p3814/rs10422603	intron1	2b	GG/GT/TT	0.3008	-0.3	0.1716	NA	-0.08	0.47136	NA	-0.1	0.87424	NA
85	APOC2p3892/rs5121	exon2	5	CC/TC/TT	0.0358	-0.21	0.69569	NA	-0.11	0.69795	NA	-0.03	0.98356	NA
85	APOC2p4086/rs114780592	intron2	4	GA/GG	0.0278	-0.04	0.95091	NA	-0.02	0.95061	NA	3.05	0.0669	NA
86	APOC2p3814/rs10422603	intron1	2b	GG/GT/TT	0.3008	-0.3	0.1716	0.48676	-0.08	0.47136	0.81254	-0.1	0.87424	0.27317
86	APOC2p3892/rs5121	exon2	5	CC/TC/TT	0.0358	-0.21	0.69569	NA	-0.11	0.69795	NA	-0.03	0.98356	NA
86	APOC2p4086/rs114780592	intron2	4	GA/GG	0.0278	-0.04	0.95091	NA	-0.02	0.95061	NA	3.05	0.0669	NA
86	APOC2p4118/rs201709243	exon3	4	GA/GG	0.0007	-6.14	0.10156	NA	0.52	0.79263	NA	-2.87	0.7826	NA
87	APOC2p3892/rs5121	exon2	5	CC/TC/TT	0.0358	-0.21	0.69569	0.57578	-0.11	0.69795	0.88586	-0.03	0.98356	0.37786

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87	APOC2p4086/rs114780592	intron2	4	GA/GG	0.0278	-0.04	0.95091	NA	-0.02	0.95061	NA	3.05	0.0669	NA
87	APOC2p4118/rs201709243	exon3	4	GA/GG	0.0007	-6.14	0.10156	NA	0.52	0.79263	NA	-2.87	0.7826	NA
87	APOC2p4319/rs5123	intron3	No Data	AA/GA/GG	0.0592	0.19	0.62684	NA	0.15	0.47956	NA	-0.25	0.82293	NA
88	APOC2p4086/rs114780592	intron2	4	GA/GG	0.0278	-0.04	0.95091	0.88184	-0.02	0.95061	0.73983	3.05	0.0669	0.19049
88	APOC2p4118/rs201709243	exon3	4	GA/GG	0.0007	-6.14	0.10156	NA	0.52	0.79263	NA	-2.87	0.7826	NA
88	APOC2p4319/rs5123	intron3	No Data	AA/GA/GG	0.0592	0.19	0.62684	NA	0.15	0.47956	NA	-0.25	0.82293	NA
88	APOC2p4513/rs180809422	intron3	5	AA/AC/CC	0.0135	0.46	0.57155	NA	0.34	0.438	NA	2.64	0.26202	NA
89	APOC2p4118/rs201709243	exon3	4	GA/GG	0.0007	-6.14	0.10156	0.26909	0.52	0.79263	0.68884	-2.87	0.7826	0.43281
89	APOC2p4319/rs5123	intron3	No Data	AA/GA/GG	0.0592	0.19	0.62684	NA	0.15	0.47956	NA	-0.25	0.82293	NA
89	APOC2p4513/rs180809422	intron3	5	AA/AC/CC	0.0135	0.46	0.57155	NA	0.34	0.438	NA	2.64	0.26202	NA
89	APOC2p4587/rs5126	exon4	5	AA/CA/CC	0.0499	-0.14	0.75702	NA	-0.07	0.77098	NA	1.71	0.18011	NA
90	APOC2p4319/rs5123	intron3	No Data	AA/GA/GG	0.0592	0.19	0.62684	0.70993	0.15	0.47956	0.63651	-0.25	0.82293	0.67584
90	APOC2p4513/rs180809422	intron3	5	AA/AC/CC	0.0135	0.46	0.57155	NA	0.34	0.438	NA	2.64	0.26202	NA
90	APOC2p4587/rs5126	exon4	5	AA/CA/CC	0.0499	-0.14	0.75702	NA	-0.07	0.77098	NA	1.71	0.18011	NA
90	APOC2p4754/rs7253690	exon4	5	AA/GA/GG	0.0606	0.26	0.50883	NA	0.25	0.22124	NA	0.19	0.85817	NA
91	APOC2p4513/rs180809422	intron3	5	AA/AC/CC	0.0135	0.46	0.57155	0.86975	0.34	0.438	0.6579	2.64	0.26202	0.60027
91	APOC2p4587/rs5126	exon4	5	AA/CA/CC	0.0499	-0.14	0.75702	NA	-0.07	0.77098	NA	1.71	0.18011	NA
91	APOC2p4754/rs7253690	exon4	5	AA/GA/GG	0.0606	0.26	0.50883	NA	0.25	0.22124	NA	0.19	0.85817	NA
91	APOC2p4853/rs150448996	3'flamking	No Data	DD/WD/WW	0.2736	0.1	0.65443	NA	-0.02	0.84447	NA	-0.05	0.93724	NA
92	APOC2p4587/rs5126	exon4	5	AA/CA/CC	0.0499	-0.14	0.75702	0.6262	-0.07	0.77098	0.47478	1.71	0.18011	0.61816
92	APOC2p4754/rs7253690	exon4	5	AA/GA/GG	0.0606	0.26	0.50883	NA	0.25	0.22124	NA	0.19	0.85817	NA
92	APOC2p4853/rs150448996	3'flamking	No Data	DD/WD/WW	0.2736	0.1	0.65443	NA	-0.02	0.84447	NA	-0.05	0.93724	NA
92	APOC2p4973/rs199828513	3'flamking	No Data	WI/WW	0.0082	-1.49	0.17137	NA	-0.79	0.16638	NA	3.46	0.24889	NA
93	APOC2p4754/rs7253690	exon4	5	AA/GA/GG	0.0606	0.26	0.50883	0.44971	0.25	0.22124	0.46142	0.19	0.85817	0.95026
93	APOC2p4853/rs150448996	3'flamking	No Data	DD/WD/WW	0.2736	0.1	0.65443	NA	-0.02	0.84447	NA	-0.05	0.93724	NA
93	APOC2p4973/rs199828513	3'flamking	No Data	WI/WW	0.0082	-1.49	0.17137	NA	-0.79	0.16638	NA	3.46	0.24889	NA
93	APOC2p5004/rs10421404	3'flanking	No Data	CC/CT/TT	0.2908	-0.34	0.11492	NA	-0.11	0.33714	NA	-0.04	0.94186	NA
94	APOC2p4853/rs150448996	3'flamking	No Data	DD/WD/WW	0.2736	0.1	0.65443	0.09847	-0.02	0.84447	0.30622	-0.05	0.93724	0.77226
94	APOC2p4973/rs199828513	3'flamking	No Data	WI/WW	0.0082	-1.49	0.17137	NA	-0.79	0.16638	NA	3.46	0.24889	NA

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94	APOC2p5004/rs10421404	3'flanking	No Data	CC/CT/TT	0.2908	-0.34	0.11492	NA	-0.11	0.33714	NA	-0.04	0.94186	NA
94	APOC2p5018/rs78403558	3'flanking	5	DD/WD/WW	0.0352	0.77	0.1368	NA	0.3	0.27612	NA	1.27	0.37773	NA
95	APOC2p4973/rs199828513	3'flamking	No Data	WI/WW	0.0082	-1.49	0.17137	0.04372	-0.79	0.16638	0.13522	3.46	0.24889	0.69567
95	APOC2p5004/rs10421404	3'flanking	No Data	CC/CT/TT	0.2908	-0.34	0.11492	NA	-0.11	0.33714	NA	-0.04	0.94186	NA
95	APOC2p5018/rs78403558	3'flanking	5	DD/WD/WW	0.0352	0.77	0.1368	NA	0.3	0.27612	NA	1.27	0.37773	NA
95	APOC2p5310/rs7258345	3'flanking	No Data	GG/GT/TT	0.3067	0.37	0.10176	NA	0.17	0.14969	NA	0.29	0.63627	NA
96	APOC2p5004/rs10421404	3'flanking	No Data	CC/CT/TT	0.2908	-0.34	0.11492	0.03596	-0.11	0.33714	0.19789	-0.04	0.94186	0.84515
96	APOC2p5018/rs78403558	3'flanking	5	DD/WD/WW	0.0352	0.77	0.1368	NA	0.3	0.27612	NA	1.27	0.37773	NA
96	APOC2p5310/rs7258345	3'flanking	No Data	GG/GT/TT	0.3067	0.37	0.10176	NA	0.17	0.14969	NA	0.29	0.63627	NA
96	APOC2p5398/rs12709889	3'flanking	6	AA/GA/GG	0.2587	0.19	0.38929	NA	0.02	0.84406	NA	0.16	0.79862	NA
97	APOC2p5018/rs78403558	3'flanking	5	DD/WD/WW	0.0352	0.77	0.1368	0.02314	0.3	0.27612	0.17091	1.27	0.37773	0.64727
97	APOC2p5310/rs7258345	3'flanking	No Data	GG/GT/TT	0.3067	0.37	0.10176	NA	0.17	0.14969	NA	0.29	0.63627	NA
97	APOC2p5398/rs12709889	3'flanking	6	AA/GA/GG	0.2587	0.19	0.38929	NA	0.02	0.84406	NA	0.16	0.79862	NA
97	APOC2p5491	3'flanking	6	CC/TC	0.0007	7.19	0.05297	NA	4.21	0.03146	NA	-8.06	0.43745	NA
98	APOC2p5310/rs7258345	3'flanking	No Data	GG/GT/TT	0.3067	0.37	0.10176	0.11359	0.17	0.14969	0.294	0.29	0.63627	0.69666
98	APOC2p5398/rs12709889	3'flanking	6	AA/GA/GG	0.2587	0.19	0.38929	NA	0.02	0.84406	NA	0.16	0.79862	NA
98	APOC2p5491	3'flanking	6	CC/TC	0.0007	7.19	0.05297	NA	4.21	0.03146	NA	-8.06	0.43745	NA
98	APOC2p5512/rs12721064	3'flanking	6	CC/CT	0.0083	-1.02	0.3246	NA	-0.1	0.86343	NA	-2.23	0.43911	NA
99	APOC2p5398/rs12709889	3'flanking	6	AA/GA/GG	0.2587	0.19	0.38929	0.81337	0.02	0.84406	0.92059	0.16	0.79862	0.75514
99	APOC2p5491	3'flanking	6	CC/TC	0.0007	7.19	0.05297	NA	4.21	0.03146	NA	-8.06	0.43745	NA
99	APOC2p5512/rs12721064	3'flanking	6	CC/CT	0.0083	-1.02	0.3246	NA	-0.1	0.86343	NA	-2.23	0.43911	NA
99	APOC2p5562	3'flanking	No Data	CG/GG	0.0175	-0.41	0.60115	NA	-0.21	0.59488	NA	-0.92	0.67145	NA
100	APOC2p5491	3'flanking	6	CC/TC	0.0007	7.19	0.05297	0.28478	4.21	0.03146	0.48016	-8.06	0.43745	0.727
100	APOC2p5512/rs12721064	3'flanking	6	CC/CT	0.0083	-1.02	0.3246	NA	-0.1	0.86343	NA	-2.23	0.43911	NA
100	APOC2p5562	3'flanking	No Data	CG/GG	0.0175	-0.41	0.60115	NA	-0.21	0.59488	NA	-0.92	0.67145	NA
100	APOC2p5586/rs73558127	3'flanking	No Data	GG/GT/TT	0.1001	-0.58	0.07133	NA	-0.23	0.17781	NA	0.13	0.88663	NA
101	APOC2p5512/rs12721064	3'flanking	6	CC/CT	0.0083	-1.02	0.3246	0.15191	-0.1	0.86343	0.44452	-2.23	0.43911	0.89229
101	APOC2p5562	3'flanking	No Data	CG/GG	0.0175	-0.41	0.60115	NA	-0.21	0.59488	NA	-0.92	0.67145	NA
101	APOC2p5586/rs73558127	3'flanking	No Data	GG/GT/TT	0.1001	-0.58	0.07133	NA	-0.23	0.17781	NA	0.13	0.88663	NA

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101	APOC2p5815/rs10423208	3'flanking	5	AA/GA/GG	0.3164	0.42	0.04737	NA	0.18	0.11697	NA	0.34	0.55855	NA
102	APOC2p5562	3'flanking	No Data	CG/GG	0.0175	-0.41	0.60115	0.00536	-0.21	0.59488	0.02416	-0.92	0.67145	0.59526
102	APOC2p5586/rs73558127	3'flanking	No Data	GG/GT/TT	0.1001	-0.58	0.07133	NA	-0.23	0.17781	NA	0.13	0.88663	NA
102	APOC2p5815/rs10423208	3'flanking	5	AA/GA/GG	0.3164	0.42	0.04737	NA	0.18	0.11697	NA	0.34	0.55855	NA
102	APOC2p5922/rs10422888	3'flanking	5	AA/AG/GG	0.0784	0.98	0.00786	NA	0.48	0.01291	NA	1.47	0.14838	NA
103	APOC2p5586/rs73558127	3'flanking	No Data	GG/GT/TT	0.1001	-0.58	0.07133	0.00228	-0.23	0.17781	0.00959	0.13	0.88663	0.28549
103	APOC2p5815/rs10423208	3'flanking	5	AA/GA/GG	0.3164	0.42	0.04737	NA	0.18	0.11697	NA	0.34	0.55855	NA
103	APOC2p5922/rs10422888	3'flanking	5	AA/AG/GG	0.0784	0.98	0.00786	NA	0.48	0.01291	NA	1.47	0.14838	NA
103	APOC2p5965	3'flanking	5	GA/GG	0.0013	2.76	0.29503	NA	1.58	0.25416	NA	-10.45	0.15456	NA
104	APOC2p5815/rs10423208	3'flanking	5	AA/GA/GG	0.3164	0.42	0.04737	0.00016	0.18	0.11697	0.0006	0.34	0.55855	0.30334
104	APOC2p5922/rs10422888	3'flanking	5	AA/AG/GG	0.0784	0.98	0.00786	NA	0.48	0.01291	NA	1.47	0.14838	NA
104	APOC2p5965	3'flanking	5	GA/GG	0.0013	2.76	0.29503	NA	1.58	0.25416	NA	-10.45	0.15456	NA
104	APOC2p6334	3'flanking	No Data	GA/GG	0.0096	1.76	0.06779	NA	0.94	0.06281	NA	3.15	0.2415	NA

wind: 4-SNPs haplotype window; w.snps: SNPs that were included in each window; p-value: single-locus p-value; hap-P: haplotype global p-value; [a] Cox-Box transformed data.

Table 40. Haplotype-based association results with HDL-C, TG, and ApoA1 in Blacks

WINDOWS						HDL-C[a]			TG[a]			ApoA1[a]		
wind	w.snp	Function	RegulomeDB score	Genotype	MAF	Beta	single-p	hap_P	Beta	single-p	hap_P	Beta	single-p	hap_P
1	APOE73/rs1081101	5'flanking	4	CC/CT/TT	0.0611	0.3	0.42732	0.54158	0.04	0.00927	0.03529	-0.003	0.99719	0.45239
1	APOE173	5'flanking	3a	AA/GA	0.00197	-2.1	0.32058	NA	0.04	0.70282	NA	6.86	0.19127	NA
1	APOE308/rs769445	5'flanking	4	CC/TC	0.00721	-1.06	0.34278	NA	0.06	0.20649	NA	3.21	0.2461	NA
1	APOE560/rs449647	5'flanking	5	AA/AT/TT	0.36627	-0.18	0.35635	NA	-0.001	0.84824	NA	-0.49	0.31886	NA
2	APOE173	5'flanking	3a	AA/GA	0.00197	-2.1	0.32058	0.10899	0.04	0.70282	0.44666	6.86	0.19127	0.50993
2	APOE308/rs769445	5'flanking	4	CC/TC	0.00721	-1.06	0.34278	NA	0.06	0.20649	NA	3.21	0.2461	NA
2	APOE560/rs449647	5'flanking	5	AA/AT/TT	0.36627	-0.18	0.35635	NA	-0.001	0.84824	NA	-0.49	0.31886	NA
2	APOE618	5'flanking	4	GC/GG	0.00064	-12.25	0.00079	NA	0.02	0.85598	NA	-18.42	0.04342	NA
3	APOE308/rs769445	5'flanking	4	CC/TC	0.00721	-1.06	0.34278	0.54334	0.06	0.20649	0.69378	3.21	0.2461	0.26279
3	APOE560/rs449647	5'flanking	5	AA/AT/TT	0.36627	-0.18	0.35635	NA	-0.001	0.84824	NA	-0.49	0.31886	NA
3	APOE618	5'flanking	4	GC/GG	0.00064	-12.25	0.00079	NA	0.02	0.85598	NA	-18.42	0.04342	NA
3	APOE624/rs769446	5'flanking	3a	TC/TT	0.00766	0.65	0.56874	NA	0.004	0.90959	NA	3.55	0.20204	NA
4	APOE560/rs449647	5'flanking	5	AA/AT/TT	0.36627	-0.18	0.35635	0.05152	-0.001	0.84824	0.83955	-0.49	0.31886	0.57085
4	APOE618	5'flanking	4	GC/GG	0.00064	-12.25	0.00079	NA	0.02	0.85598	NA	-18.42	0.04342	NA
4	APOE624/rs769446	5'flanking	3a	TC/TT	0.00766	0.65	0.56874	NA	0.004	0.90959	NA	3.55	0.20204	NA
4	APOE832/rs405509	5'flanking	1f	GG/GT/TT	0.25611	-0.19	0.36119	NA	0.002	0.74568	NA	-0.67	0.19928	NA
5	APOE618	5'flanking	4	GC/GG	0.00064	-12.25	0.00079	0.27407	0.02	0.85598	0.55355	-18.42	0.04342	0.5495
5	APOE624/rs769446	5'flanking	3a	TC/TT	0.00766	0.65	0.56874	NA	0.004	0.90959	NA	3.55	0.20204	NA
5	APOE832/rs405509	5'flanking	1f	GG/GT/TT	0.25611	-0.19	0.36119	NA	0.002	0.74568	NA	-0.67	0.19928	NA
5	APOE1109/rs9282609	Splice site	4	CC/TC/TT	0.0415	0.61	0.17876	NA	0.02	0.18141	NA	0.24	0.83418	NA
6	APOE624/rs769446	5'flanking	3a	TC/TT	0.00766	0.65	0.56874	0.43137	0.004	0.90959	0.16448	3.55	0.20204	0.58623
6	APOE832/rs405509	5'flanking	1f	GG/GT/TT	0.25611	-0.19	0.36119	NA	0.002	0.74568	NA	-0.67	0.19928	NA
6	APOE1109/rs9282609	Splice site	4	CC/TC/TT	0.0415	0.61	0.17876	NA	0.02	0.18141	NA	0.24	0.83418	NA
6	APOE1163/rs440446	intron1	4	CC/CG/GG	0.10042	-0.54	0.09464	NA	0.02	0.05369	NA	-0.44	0.58046	NA
7	APOE832/rs405509	5'flanking	1f	GG/GT/TT	0.25611	-0.19	0.36119	0.33192	0.002	0.74568	0.17516	-0.67	0.19928	0.78005
7	APOE1109/rs9282609	Splice site	4	CC/TC/TT	0.0415	0.61	0.17876	NA	0.02	0.18141	NA	0.24	0.83418	NA

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7	APOE1163/rs440446	intron1	4	CC/CG/GG	0.10042	-0.54	0.09464	NA	0.02	0.05369	NA	-0.44	0.58046	NA
7	APOE1231	intron1	2b	GA/GG	0.01247	-0.27	0.755	NA	-0.03	0.34414	NA	-1.12	0.59594	NA
8	APOE1109/rs9282609	Splice site	4	CC/TC/TT	0.0415	0.61	0.17876	0.20634	0.02	0.18141	0.05866	0.24	0.83418	0.5871
8	APOE1163/rs440446	intron1	4	CC/CG/GG	0.10042	-0.54	0.09464	NA	0.02	0.05369	NA	-0.44	0.58046	NA
8	APOE1231	intron1	2b	GA/GG	0.01247	-0.27	0.755	NA	-0.03	0.34414	NA	-1.12	0.59594	NA
8	APOE1279/rs877973	intron1	4	AA/CA/CC	0.05971	0.51	0.19812	NA	-0.03	0.05132	NA	1.06	0.27597	NA
9	APOE1163/rs440446	intron1	4	CC/CG/GG	0.10042	-0.54	0.09464	0.1736	0.02	0.05369	0.08886	-0.44	0.58046	0.28818
9	APOE1231	intron1	2b	GA/GG	0.01247	-0.27	0.755	NA	-0.03	0.34414	NA	-1.12	0.59594	NA
9	APOE1279/rs877973	intron1	4	AA/CA/CC	0.05971	0.51	0.19812	NA	-0.03	0.05132	NA	1.06	0.27597	NA
9	APOE1539/rs184686013	intron1	4	AA/AG/GG	0.00856	1.35	0.15682	NA	0.002	0.95463	NA	4.24	0.0738	NA
10	APOE1231	intron1	2b	GA/GG	0.01247	-0.27	0.755	0.5938	-0.03	0.34414	0.17822	-1.12	0.59594	0.5068
10	APOE1279/rs877973	intron1	4	AA/CA/CC	0.05971	0.51	0.19812	NA	-0.03	0.05132	NA	1.06	0.27597	NA
10	APOE1539/rs184686013	intron1	4	AA/AG/GG	0.00856	1.35	0.15682	NA	0.002	0.95463	NA	4.24	0.0738	NA
10	APOE2072/rs189660912	intron 2	4	GA/GG	0.00789	-0.4	0.70658	NA	0.01	0.82286	NA	-1.35	0.61188	NA
11	APOE1279/rs877973	intron1	4	AA/CA/CC	0.05971	0.51	0.19812	0.43466	-0.03	0.05132	0.11116	1.06	0.27597	0.46006
11	APOE1539/rs184686013	intron1	4	AA/AG/GG	0.00856	1.35	0.15682	NA	0.002	0.95463	NA	4.24	0.0738	NA
11	APOE2072/rs189660912	intron 2	4	GA/GG	0.00789	-0.4	0.70658	NA	0.01	0.82286	NA	-1.35	0.61188	NA
11	APOE2269/rs6135770	intron 2	5	GA/GG	0.01691	0.77	0.29121	NA	0.04	0.1489	NA	1.09	0.55027	NA
12	APOE1539/rs184686013	intron1	4	AA/AG/GG	0.00856	1.35	0.15682	0.66542	0.002	0.95463	0.5628	4.24	0.0738	0.73887
12	APOE2072/rs189660912	intron 2	4	GA/GG	0.00789	-0.4	0.70658	NA	0.01	0.82286	NA	-1.35	0.61188	NA
12	APOE2269/rs6135770	intron 2	5	GA/GG	0.01691	0.77	0.29121	NA	0.04	0.1489	NA	1.09	0.55027	NA
12	APOE2440/rs769450	intron 2	5	AA/AG/GG	0.38696	-0.02	0.93935	NA	0.002	0.7396	NA	-0.17	0.73856	NA
13	APOE2072/rs189660912	intron 2	4	GA/GG	0.00789	-0.4	0.70658	0.57996	0.01	0.82286	0.46495	-1.35	0.61188	0.87705
13	APOE2269/rs6135770	intron 2	5	GA/GG	0.01691	0.77	0.29121	NA	0.04	0.1489	NA	1.09	0.55027	NA
13	APOE2440/rs769450	intron 2	5	AA/AG/GG	0.38696	-0.02	0.93935	NA	0.002	0.7396	NA	-0.17	0.73856	NA
13	APOE3673/rs769453	intron 3	5	CC/GC	0.00657	-1.1	0.34567	NA	0.04	0.42419	NA	3.93	0.17574	NA
14	APOE2269/rs6135770	intron 2	5	GA/GG	0.01691	0.77	0.29121	0.72016	0.04	0.1489	0.3086	1.09	0.55027	0.07438
14	APOE2440/rs769450	intron 2	5	AA/AG/GG	0.38696	-0.02	0.93935	NA	0.002	0.7396	NA	-0.17	0.73856	NA
14	APOE3673/rs769453	intron 3	5	CC/GC	0.00657	-1.1	0.34567	NA	0.04	0.42419	NA	3.93	0.17574	NA

Cont. Table 40

14	APOE3937/rs429358	exon 4	5	CC/CT/TT	0.26558	-0.14	0.50743	NA	-0.01	0.30755	NA	-1	0.05924	NA
15	APOE2440/rs769450	intron 2	5	AA/AG/GG	0.38696	-0.02	0.93935	0.74715	0.002	0.7396	0.15443	-0.17	0.73856	0.06787
15	APOE3673/rs769453	intron 3	5	CC/GC	0.00657	-1.1	0.34567	NA	0.04	0.42419	NA	3.93	0.17574	NA
15	APOE3937/rs429358	exon 4	5	CC/CT/TT	0.26558	-0.14	0.50743	NA	-0.01	0.30755	NA	-1	0.05924	NA
15	APOE4036/rs769455	exon 4	5	CC/TC/TT	0.02	-0.46	0.48274	NA	0.06	0.03718	NA	-0.71	0.66412	NA
16	APOE3673/rs769453	intron 3	5	CC/GC	0.00657	-1.1	0.34567	0.29748	0.04	0.42419	0.12966	3.93	0.17574	0.0007
16	APOE3937/rs429358	exon 4	5	CC/CT/TT	0.26558	-0.14	0.50743	NA	-0.01	0.30755	NA	-1	0.05924	NA
16	APOE4036/rs769455	exon 4	5	CC/TC/TT	0.02	-0.46	0.48274	NA	0.06	0.03718	NA	-0.71	0.66412	NA
16	APOE4075/rs7412	exon 4	5	AA/GA/GG	0.06049	0.75	0.06615	NA	-0.02	0.23759	NA	3.85	0.00008	NA
17	APOE3937/rs429358	exon 4	5	CC/CT/TT	0.26558	-0.14	0.50743	0.28056	-0.01	0.30755	0.08336	-1	0.05924	0.0005
17	APOE4036/rs769455	exon 4	5	CC/TC/TT	0.02	-0.46	0.48274	NA	0.06	0.03718	NA	-0.71	0.66412	NA
17	APOE4075/rs7412	exon 4	5	AA/GA/GG	0.06049	0.75	0.06615	NA	-0.02	0.23759	NA	3.85	0.00008	NA
17	APOE4569	3'UTR	5	GG/GT	0.00066	5.29	0.14968	NA	0.07	0.59764	NA	15.53	0.08835	NA
18	APOE4036/rs769455	exon 4	5	CC/TC/TT	0.02	-0.46	0.48274	0.24697	0.06	0.03718	0.13785	-0.71	0.66412	0.00074
18	APOE4075/rs7412	exon 4	5	AA/GA/GG	0.06049	0.75	0.06615	NA	-0.02	0.23759	NA	3.85	0.00008	NA
18	APOE4569	3'UTR	5	GG/GT	0.00066	5.29	0.14968	NA	0.07	0.59764	NA	15.53	0.08835	NA
18	APOE5223	3'flanking	2b	CC/CG	0.00508	0.39	0.763	NA	0.01	0.90777	NA	1.29	0.70886	NA
19	APOE4075/rs7412	exon 4	5	AA/GA/GG	0.06049	0.75	0.06615	0.28508	-0.02	0.23759	0.39788	3.85	0.00008	0.00076
19	APOE4569	3'UTR	5	GG/GT	0.00066	5.29	0.14968	NA	0.07	0.59764	NA	15.53	0.08835	NA
19	APOE5223	3'flanking	2b	CC/CG	0.00508	0.39	0.763	NA	0.01	0.90777	NA	1.29	0.70886	NA
19	APOE5231	3'flanking	2b	GG/GT/TT	0.02697	-0.18	0.76449	NA	-0.02	0.28357	NA	-0.03	0.98493	NA
20	APOE4569	3'UTR	5	GG/GT	0.00066	5.29	0.14968	0.18127	0.07	0.59764	0.54136	15.53	0.08835	0.688
20	APOE5223	3'flanking	2b	CC/CG	0.00508	0.39	0.763	NA	0.01	0.90777	NA	1.29	0.70886	NA
20	APOE5231	3'flanking	2b	GG/GT/TT	0.02697	-0.18	0.76449	NA	-0.02	0.28357	NA	-0.03	0.98493	NA
20	rs439401	intragenic	1b	CC/CT/TT	0.10925	-0.6	0.04448	NA	0.01	0.3401	NA	-0.5	0.50161	NA
21	APOE5223	3'flanking	2b	CC/CG	0.00508	0.39	0.763	0.33128	0.01	0.90777	0.58925	1.29	0.70886	0.90501
21	APOE5231	3'flanking	2b	GG/GT/TT	0.02697	-0.18	0.76449	NA	-0.02	0.28357	NA	-0.03	0.98493	NA
21	rs439401	intragenic	1b	CC/CT/TT	0.10925	-0.6	0.04448	NA	0.01	0.3401	NA	-0.5	0.50161	NA
21	rs445925	intragenic	No Data	AA/GA/GG	0.29896	0.1	0.64004	NA	-0.01	0.37485	NA	0.36	0.48026	NA

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22	APOE5231	3'flanking	2b	GG/GT/TT	0.02697	-0.18	0.76449	0.50534	-0.02	0.28357	0.06604	-0.03	0.98493	0.51882
22	rs439401	intragenic	1b	CC/CT/TT	0.10925	-0.6	0.04448	NA	0.01	0.3401	NA	-0.5	0.50161	NA
22	rs445925	intragenic	No Data	AA/GA/GG	0.29896	0.1	0.64004	NA	-0.01	0.37485	NA	0.36	0.48026	NA
22	APOC1p720ins4/rs71962921	5'flanking	4	II/WI/WW	0.2737	0.27	0.20872	NA	-0.01	0.11371	NA	1.03	0.04836	NA
23	rs439401	intragenic	1b	CC/CT/TT	0.10925	-0.6	0.04448	0.39897	0.01	0.3401	0.059	-0.5	0.50161	0.46512
23	rs445925	intragenic	No Data	AA/GA/GG	0.29896	0.1	0.64004	NA	-0.01	0.37485	NA	0.36	0.48026	NA
23	APOC1p720ins4/rs71962921	5'flanking	4	II/WI/WW	0.2737	0.27	0.20872	NA	-0.01	0.11371	NA	1.03	0.04836	NA
23	APOC1p894/rs190454394	5'flanking	4	CC/CT	0.00198	0.74	0.72955	NA	0.02	0.79072	NA	0.4	0.93927	NA
24	APOC1rs445925	intragenic	No Data	AA/GA/GG	0.29896	0.1	0.64004	0.76357	-0.01	0.37485	0.05661	0.36	0.48026	0.42518
24	APOC1p720ins4/rs71962921	5'flanking	4	II/WI/WW	0.2737	0.27	0.20872	NA	-0.01	0.11371	NA	1.03	0.04836	NA
24	APOC1p894/rs190454394	5'flanking	4	CC/CT	0.00198	0.74	0.72955	NA	0.02	0.79072	NA	0.4	0.93927	NA
24	APOC1p1166/rs72654452	intron1	2b	CC/CT/TT	0.03077	-0.61	0.25404	NA	0.03	0.16303	NA	-1.09	0.40589	NA
25	APOC1p720ins4/rs71962921	5'flanking	4	II/WI/WW	0.2737	0.27	0.20872	0.40482	-0.01	0.11371	0.23671	1.03	0.04836	0.31929
25	APOC1p894/rs190454394	5'flanking	4	CC/CT	0.00198	0.74	0.72955	NA	0.02	0.79072	NA	0.4	0.93927	NA
25	APOC1p1166/rs72654452	intron1	2b	CC/CT/TT	0.03077	-0.61	0.25404	NA	0.03	0.16303	NA	-1.09	0.40589	NA
25	APOC1p1331/rs10408994	intron2	4	AG/GG	0.06658	0.35	0.38621	NA	0.02	0.28616	NA	-0.66	0.50656	NA
26	APOC1p894/rs190454394	5'flanking	4	CC/CT	0.00198	0.74	0.72955	0.36566	0.02	0.79072	0.23032	0.4	0.93927	0.54481
26	APOC1p1166/rs72654452	intron1	2b	CC/CT/TT	0.03077	-0.61	0.25404	NA	0.03	0.16303	NA	-1.09	0.40589	NA
26	APOC1p1331/rs10408994	intron2	4	AG/GG	0.06658	0.35	0.38621	NA	0.02	0.28616	NA	-0.66	0.50656	NA
26	APOC1p1526/rs5114	intron2	4	CC/CT/TT	0.05792	0.55	0.1745	NA	-0.02	0.11175	NA	1.38	0.165	NA
27	APOC1p1166/rs72654452	intron1	2b	CC/CT/TT	0.03077	-0.61	0.25404	0.37708	0.03	0.16303	0.26295	-1.09	0.40589	0.48858
27	APOC1p1331/rs10408994	intron2	4	AG/GG	0.06658	0.35	0.38621	NA	0.02	0.28616	NA	-0.66	0.50656	NA
27	APOC1p1526/rs5114	intron2	4	CC/CT/TT	0.05792	0.55	0.1745	NA	-0.02	0.11175	NA	1.38	0.165	NA
27	APOC1p1642	intron2	4	CC/CT	0.01027	-0.59	0.53986	NA	-0.02	0.58314	NA	-1.9	0.4104	NA
28	APOC1p1331/rs10408994	intron2	4	AG/GG	0.06658	0.35	0.38621	0.40668	0.02	0.28616	0.42419	-0.66	0.50656	0.60006
28	APOC1p1526/rs5114	intron2	4	CC/CT/TT	0.05792	0.55	0.1745	NA	-0.02	0.11175	NA	1.38	0.165	NA
28	APOC1p1642	intron2	4	CC/CT	0.01027	-0.59	0.53986	NA	-0.02	0.58314	NA	-1.9	0.4104	NA
28	APOC1p1684/rs12709881	intron2	4	AA/GA/GG	0.09729	0.4	0.20729	NA	-0.02	0.15409	NA	0.73	0.34454	NA
29	APOC1p1526/rs5114	intron2	4	CC/CT/TT	0.05792	0.55	0.1745	0.27406	-0.02	0.11175	0.54353	1.38	0.165	0.63514

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29	APOC1p1642	intron2	4	CC/CT	0.01027	-0.59	0.53986	NA	-0.02	0.58314	NA	-1.9	0.4104	NA
29	APOC1p1684/rs12709881	intron2	4	AA/GA/GG	0.09729	0.4	0.20729	NA	-0.02	0.15409	NA	0.73	0.34454	NA
29	APOC1p3358	intron3	No Data	AA/GA	0.00208	3.44	0.10895	NA	0.002	0.97274	NA	-2.34	0.6601	NA
30	APOC1p1642	intron2	4	CC/CT	0.01027	-0.59	0.53986	0.12516	-0.02	0.58314	0.6562	-1.9	0.4104	0.6398
30	APOC1p1684/rs12709881	intron2	4	AA/GA/GG	0.09729	0.4	0.20729	NA	-0.02	0.15409	NA	0.73	0.34454	NA
30	APOC1p3358	intron3	No Data	AA/GA	0.00208	3.44	0.10895	NA	0.002	0.97274	NA	-2.34	0.6601	NA
30	APOC1p3423/rs389261	intron3	No Data	AA/GA/GG	0.33104	0.24	0.26136	NA	-0.001	0.81164	NA	-0.36	0.48713	NA
31	APOC1p1684/rs12709881	intron2	4	AA/GA/GG	0.09729	0.4	0.20729	0.08271	-0.02	0.15409	0.62061	0.73	0.34454	0.6907
31	APOC1p3358	intron3	No Data	AA/GA	0.00208	3.44	0.10895	NA	0.002	0.97274	NA	-2.34	0.6601	NA
31	APOC1p3423/rs389261	intron3	No Data	AA/GA/GG	0.33104	0.24	0.26136	NA	-0.001	0.81164	NA	-0.36	0.48713	NA
31	APOC1p3573/rs10424339	intron3	No Data	AA/GA/GG	0.1396	0.55	0.0455	NA	0.001	0.90959	NA	0.4	0.55931	NA
32	APOC1p3358	intron3	No Data	AA/GA	0.00208	3.44	0.10895	0.13261	0.002	0.97274	0.63103	-2.34	0.6601	0.74383
32	APOC1p3423/rs389261	intron3	No Data	AA/GA/GG	0.33104	0.24	0.26136	NA	-0.001	0.81164	NA	-0.36	0.48713	NA
32	APOC1p3573/rs10424339	intron3	No Data	AA/GA/GG	0.1396	0.55	0.0455	NA	0.001	0.90959	NA	0.4	0.55931	NA
32	APOC1p5006/rs112528434	intron3	No Data	GG/GT/TT	0.085	0.32	0.3879	NA	-0.02	0.17321	NA	0.67	0.44123	NA
33	APOC1p3423/rs389261	intron3	No Data	AA/GA/GG	0.33104	0.24	0.26136	0.31249	-0.001	0.81164	0.20941	-0.36	0.48713	0.78355
33	APOC1p3573/rs10424339	intron3	No Data	AA/GA/GG	0.1396	0.55	0.0455	NA	0.001	0.90959	NA	0.4	0.55931	NA
33	APOC1p5006/rs112528434	intron3	No Data	GG/GT/TT	0.085	0.32	0.3879	NA	-0.02	0.17321	NA	0.67	0.44123	NA
33	APOC1p5053/rs12721052	intron3	No Data	DD/WD/WW	0.22	-0.31	0.16174	NA	0.003	0.65241	NA	-0.42	0.4506	NA
34	APOC1p3573/rs10424339	intron3	No Data	AA/GA/GG	0.1396	0.55	0.0455	0.09833	0.001	0.90959	0.05564	0.4	0.55931	0.58076
34	APOC1p5006/rs112528434	intron3	No Data	GG/GT/TT	0.085	0.32	0.3879	NA	-0.02	0.17321	NA	0.67	0.44123	NA
34	APOC1p5053/rs12721052	intron3	No Data	DD/WD/WW	0.22	-0.31	0.16174	NA	0.003	0.65241	NA	-0.42	0.4506	NA
34	APOC1p5667/rs12721054	3'UTR	6	AA/GA/GG	0.14459	0.23	0.42209	NA	-0.03	0.00699	NA	1.01	0.14096	NA
35	APOC1p5006/rs112528434	intron3	No Data	GG/GT/TT	0.085	0.32	0.3879	0.66834	-0.02	0.17321	0.07071	0.67	0.44123	0.63652
35	APOC1p5053/rs12721052	intron3	No Data	DD/WD/WW	0.22	-0.31	0.16174	NA	0.003	0.65241	NA	-0.42	0.4506	NA
35	APOC1p5667/rs12721054	3'UTR	6	AA/GA/GG	0.14459	0.23	0.42209	NA	-0.03	0.00699	NA	1.01	0.14096	NA
35	APOC1p5926/rs56131196	3'flanking	No Data	AA/AG/GG	0.17453	0.31	0.22541	NA	-0.02	0.04423	NA	0.87	0.17334	NA
36	APOC1p5053/rs12721052	intron3	No Data	DD/WD/WW	0.22	-0.31	0.16174	0.59414	0.003	0.65241	0.11658	-0.42	0.4506	0.4423
36	APOC1p5667/rs12721054	3'UTR	6	AA/GA/GG	0.14459	0.23	0.42209	NA	-0.03	0.00699	NA	1.01	0.14096	NA

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36	APOC1p5926/rs56131196	3'flanking	No Data	AA/AG/GG	0.17453	0.31	0.22541	NA	-0.02	0.04423	NA	0.87	0.17334	NA
36	rs4803770	HCR-1	5	CC/GC/GG	0.26954	-0.27	0.21475	NA	0.005	0.5732	NA	-0.53	0.32036	NA
37	APOC1p5667/rs12721054	3'UTR	6	AA/GA/GG	0.14459	0.23	0.42209	0.33569	-0.03	0.00699	0.10784	1.01	0.14096	0.26008
37	APOC1p5926/rs56131196	3'flanking	No Data	AA/AG/GG	0.17453	0.31	0.22541	NA	-0.02	0.04423	NA	0.87	0.17334	NA
37	rs4803770	HCR-1	5	CC/GC/GG	0.26954	-0.27	0.21475	NA	0.005	0.5732	NA	-0.53	0.32036	NA
37	HCR1p424/rs117664574	HCR-1	4	AG/GG	0.00726	2.06	0.06453	NA	0.02	0.55251	NA	5.74	0.04801	NA
38	APOC1p5926/rs56131196	3'flanking	No Data	AA/AG/GG	0.17453	0.31	0.22541	0.18352	-0.02	0.04423	0.32895	0.87	0.17334	0.20305
38	rs4803770	HCR-1	5	CC/GC/GG	0.26954	-0.27	0.21475	NA	0.005	0.5732	NA	-0.53	0.32036	NA
38	HCR1p424/rs117664574	HCR-1	4	AG/GG	0.00726	2.06	0.06453	NA	0.02	0.55251	NA	5.74	0.04801	NA
38	HCR1p575/rs157599	HCR-1	3a	AA/AG/GG	0.35949	0.19	0.36879	NA	-0.004	0.61322	NA	-0.63	0.22016	NA
39	rs4803770	HCR-1	5	CC/GC/GG	0.26954	-0.27	0.21475	0.19821	0.005	0.5732	0.71998	-0.53	0.32036	0.06248
39	HCR1p424/rs117664574	HCR-1	4	AG/GG	0.00726	2.06	0.06453	NA	0.02	0.55251	NA	5.74	0.04801	NA
39	HCR1p575/rs157599	HCR-1	3a	AA/AG/GG	0.35949	0.19	0.36879	NA	-0.004	0.61322	NA	-0.63	0.22016	NA
39	rs5112	APC1P1	4	CC/GC/GG	0.47975	0.25	0.18503	NA	0.01	0.18177	NA	0.8	0.0924	NA
40	HCR1p424/rs117664574	HCR-1	4	AG/GG	0.00726	2.06	0.06453	0.33872	0.02	0.55251	0.90041	5.74	0.04801	0.25936
40	HCR1p575/rs157599	HCR-1	3a	AA/AG/GG	0.35949	0.19	0.36879	NA	-0.004	0.61322	NA	-0.63	0.22016	NA
40	rs5112	APC1P1	4	CC/GC/GG	0.47975	0.25	0.18503	NA	0.01	0.18177	NA	0.8	0.0924	NA
40	rs7259004	APC1P1	6	CC/CG/GG	0.30201	0.29	0.15235	NA	0.01	0.43279	NA	0.83	0.10102	NA
41	HCR1p575/rs157599	HCR-1	3a	AA/AG/GG	0.35949	0.19	0.36879	0.00037	-0.004	0.61322	0.32698	-0.63	0.22016	0.04554
41	rs5112	APC1P1	4	CC/GC/GG	0.47975	0.25	0.18503	NA	0.01	0.18177	NA	0.8	0.0924	NA
41	rs7259004	APC1P1	6	CC/CG/GG	0.30201	0.29	0.15235	NA	0.01	0.43279	NA	0.83	0.10102	NA
41	HCR2p188/rs35136575	HCR-2	2a	CC/GC/GG	0.15462	0.3	0.23716	NA	0	0.604	NA	0.85	0.18117	NA
42	rs5112	APC1P1	4	CC/GC/GG	0.47975	0.25	0.18503	0.00098	0.01	0.18177	0.47329	0.8	0.0924	0.05761
42	rs7259004	APC1P1	6	CC/CG/GG	0.30201	0.29	0.15235	NA	0.01	0.43279	NA	0.83	0.10102	NA
42	HCR2p188/rs35136575	HCR-2	2a	CC/GC/GG	0.15462	0.3	0.23716	NA	0.005	0.604	NA	0.85	0.18117	NA
42	HCR2p286	HCR-2	2a	AA/AG/GG	0.0457	-0.7	0.11626	NA	0.03	0.1292	NA	-0.59	0.59403	NA
43	rs7259004	APC1P1	6	CC/CG/GG	0.30201	0.29	0.15235	0.00122	0.01	0.43279	0.23994	0.83	0.10102	0.02426
43	HCR2p188/rs35136575	HCR-2	2a	CC/GC/GG	0.15462	0.3	0.23716	NA	0.005	0.604	NA	0.85	0.18117	NA
43	HCR2p286	HCR-2	2a	AA/AG/GG	0.0457	-0.7	0.11626	NA	0.03	0.1292	NA	-0.59	0.59403	NA

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43	HCR2p523/rs118004808	HCR-2	2b	CC/TC	0.00263	0.02	0.99167	NA	0.03	0.62894	NA	-0.21	0.96328	NA
44	HCR2p188/rs35136575	HCR-2	2a	CC/GC/GG	0.15462	0.3	0.23716	0.53105	0.005	0.604	0.40465	0.85	0.18117	0.56339
44	HCR2p286	HCR-2	2a	AA/AG/GG	0.0457	-0.7	0.11626	NA	0.03	0.1292	NA	-0.59	0.59403	NA
44	HCR2p523/rs118004808	HCR-2	2b	CC/TC	0.00263	0.02	0.99167	NA	0.03	0.62894	NA	-0.21	0.96328	NA
44	APOC4p368	5′ flanking	6	TC/TT	0.00194	0.33	0.87548	NA	0.09	0.26413	NA	-0.69	0.8967	NA
45	HCR2p286	HCR-2	2a	AA/AG/GG	0.0457	-0.7	0.11626	0.61331	0.03	0.1292	0.29318	-0.59	0.59403	0.9891
45	HCR2p523/rs118004808	HCR-2	2b	CC/TC	0.00263	0.02	0.99167	NA	0.03	0.62894	NA	-0.21	0.96328	NA
45	APOC4p368	5′ flanking	6	TC/TT	0.00194	0.33	0.87548	NA	0.09	0.26413	NA	-0.69	0.8967	NA
45	APOC4p637/rs113814026	5′ flanking	No Data	GG/GT/TT	0.04516	0.1	0.82864	NA	-0.01	0.4457	NA	0.14	0.90262	NA
46	HCR2p523/rs118004808	HCR-2	2b	CC/TC	0.00263	0.02	0.99167	0.99283	0.03	0.62894	0.00438	-0.21	0.96328	0.67928
46	APOC4p368	5′ flanking	6	TC/TT	0.00194	0.33	0.87548	NA	0.09	0.26413	NA	-0.69	0.8967	NA
46	APOC4p637/rs113814026	5′ flanking	No Data	GG/GT/TT	0.04516	0.1	0.82864	NA	-0.01	0.4457	NA	0.14	0.90262	NA
46	APOC4p757/rs12721105	5′ flanking	5	GG/GT/TT	0.03763	-0.19	0.69377	NA	0.06	0.00052	NA	-1.4	0.23935	NA
47	APOC4p368	5′ flanking	6	TC/TT	0.00194	0.33	0.87548	0.82562	0.09	0.26413	0.00098	-0.69	0.8967	0.60638
47	APOC4p637/rs113814026	5′ flanking	No Data	GG/GT/TT	0.04516	0.1	0.82864	NA	-0.01	0.4457	NA	0.14	0.90262	NA
47	APOC4p757/rs12721105	5′ flanking	5	GG/GT/TT	0.03763	-0.19	0.69377	NA	0.06	0.00052	NA	-1.4	0.23935	NA
47	APOC4p1088	intron1	2b	GT/TT	0.00133	-4.26	0.10128	NA	0.18	0.06327	NA	-4.8	0.45794	NA
48	APOC4p637/rs113814026	5′ flanking	No Data	GG/GT/TT	0.04516	0.1	0.82864	0.99009	-0.01	0.4457	0.00086	0.14	0.90262	0.69116
48	APOC4p757/rs12721105	5′ flanking	5	GG/GT/TT	0.03763	-0.19	0.69377	NA	0.06	0.00052	NA	-1.4	0.23935	NA
48	APOC4p1088	intron1	2b	GT/TT	0.00133	-4.26	0.10128	NA	0.18	0.06327	NA	-4.8	0.45794	NA
48	APOC4p1130	intron1	5	CT/TT	0.00066	9.46	0.00979	NA	0.1	0.48004	NA	14.38	0.11483	NA
49	APOC4p757/rs12721105	5′ flanking	5	GG/GT/TT	0.03763	-0.19	0.69377	0.96485	0.06	0.00052	0.00099	-1.4	0.23935	0.29465
49	APOC4p1088	intron1	2b	GT/TT	0.00133	-4.26	0.10128	NA	0.18	0.06327	NA	-4.8	0.45794	NA
49	APOC4p1130	intron1	5	CT/TT	0.00066	9.46	0.00979	NA	0.1	0.48004	NA	14.38	0.11483	NA
49	APOC4p1192/rs113745034	intron1	4	GA/GG	0.01238	0.35	0.69302	NA	-0.01	0.8015	NA	3.44	0.12841	NA
50	APOC4p1088	intron1	2b	GT/TT	0.00133	-4.26	0.10128	0.90718	0.18	0.06327	0.09132	-4.8	0.45794	0.46302
50	APOC4p1130	intron1	5	CT/TT	0.00066	9.46	0.00979	NA	0.1	0.48004	NA	14.38	0.11483	NA
50	APOC4p1192/rs113745034	intron1	4	GA/GG	0.01238	0.35	0.69302	NA	-0.01	0.8015	NA	3.44	0.12841	NA
50	APOC4p1325del3	intron1	4	WD/WW	0.02447	0.3	0.63292	NA	-0.04	0.09089	NA	-0.31	0.84012	NA

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51	APOC4p1130	intron1	5	CT/TT	0.00066	9.46	0.00979	0.08027	0.1	0.48004	0.43671	14.38	0.11483	0.07629
51	APOC4p1192/rs113745034	intron1	4	GA/GG	0.01238	0.35	0.69302	NA	-0.01	0.8015	NA	3.44	0.12841	NA
51	APOC4p1325del3	intron1	4	WD/WW	0.02447	0.3	0.63292	NA	-0.04	0.09089	NA	-0.31	0.84012	NA
51	APOC4p1430ins	intron1	5	II/WI/WW	0.03411	0.69	0.22691	NA	-0.01	0.64588	NA	2.68	0.05543	NA
52	APOC4p1192/rs113745034	intron1	4	GA/GG	0.01238	0.35	0.69302	0.77257	-0.01	0.8015	0.32748	3.44	0.12841	0.13951
52	APOC4p1325del3	intron1	4	WD/WW	0.02447	0.3	0.63292	NA	-0.04	0.09089	NA	-0.31	0.84012	NA
52	APOC4p1430ins	intron1	5	II/WI/WW	0.03411	0.69	0.22691	NA	-0.01	0.64588	NA	2.68	0.05543	NA
52	APOC4p2099/rs111339708	intron1	No Data	GG/GT	0.01414	0.35	0.6678	NA	-0.03	0.27451	NA	3.04	0.13403	NA
53	APOC4p1325del3	intron1	4	WD/WW	0.02447	0.3	0.63292	0.76353	-0.04	0.09089	0.22013	-0.31	0.84012	0.0836
53	APOC4p1430ins	intron1	5	II/WI/WW	0.03411	0.69	0.22691	NA	-0.01	0.64588	NA	2.68	0.05543	NA
53	APOC4p2099/rs111339708	intron1	No Data	GG/GT	0.01414	0.35	0.6678	NA	-0.03	0.27451	NA	3.04	0.13403	NA
53	APOC4p2467/rs115225947	intron1	5	GA/GG	0.01414	0.03	0.96646	NA	-0.03	0.37943	NA	-2.52	0.2125	NA
54	APOC4p1430ins	intron1	5	II/WI/WW	0.03411	0.69	0.22691	0.70625	-0.01	0.64588	0.54162	2.68	0.05543	0.03425
54	APOC4p2099/rs111339708	intron1	No Data	GG/GT	0.01414	0.35	0.6678	NA	-0.03	0.27451	NA	3.04	0.13403	NA
54	APOC4p2467/rs115225947	intron1	5	GA/GG	0.01414	0.03	0.96646	NA	-0.03	0.37943	NA	-2.52	0.2125	NA
54	APOC4p2559/rs5155	intron1	4	CC/CT/TT	0.09858	-0.2	0.53148	NA	-0.01	0.49082	NA	-1.47	0.06609	NA
55	APOC4p2099/rs111339708	intron1	No Data	GG/GT	0.01414	0.35	0.6678	0.7705	-0.03	0.27451	0.46951	3.04	0.13403	0.06868
55	APOC4p2467/rs115225947	intron1	5	GA/GG	0.01414	0.03	0.96646	NA	-0.03	0.37943	NA	-2.52	0.2125	NA
55	APOC4p2559/rs5155	intron1	4	CC/CT/TT	0.09858	-0.2	0.53148	NA	-0.01	0.49082	NA	-1.47	0.06609	NA
55	APOC4p2607/rs5156	intron1	4	AG/GG	0.01293	0.43	0.62963	NA	-0.03	0.37912	NA	3.6	0.10172	NA
56	APOC4p2467/rs115225947	intron1	5	GA/GG	0.01414	0.03	0.96646	0.90903	-0.03	0.37943	0.65639	-2.52	0.2125	0.15584
56	APOC4p2559/rs5155	intron1	4	CC/CT/TT	0.09858	-0.2	0.53148	NA	-0.01	0.49082	NA	-1.47	0.06609	NA
56	APOC4p2607/rs5156	intron1	4	AG/GG	0.01293	0.43	0.62963	NA	-0.03	0.37912	NA	3.6	0.10172	NA
56	APOC4p2623/rs5157	intron1	4	CC/CT/TT	0.17232	-0.14	0.59553	NA	0.0006	0.94809	NA	0.78	0.21466	NA
57	APOC4p2559/rs5155	intron1	4	CC/CT/TT	0.09858	-0.2	0.53148	0.91285	-0.01	0.49082	0.16019	-1.47	0.06609	0.20674
57	APOC4p2607/rs5156	intron1	4	AG/GG	0.01293	0.43	0.62963	NA	-0.03	0.37912	NA	3.6	0.10172	NA
57	APOC4p2623/rs5157	intron1	4	CC/CT/TT	0.17232	-0.14	0.59553	NA	0.0006	0.94809	NA	0.78	0.21466	NA
57	APOC4p2640/rs5158	intron1	2b	CC/CT	0.02129	-0.29	0.66191	NA	-0.05	0.03532	NA	-1.12	0.4997	NA
58	APOC4p2607/rs5156	intron1	4	AG/GG	0.01293	0.43	0.62963	0.93012	-0.03	0.37912	0.16394	3.6	0.10172	0.10981

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58	APOC4p2623/rs5157	intron1	4	CC/CT/TT	0.17232	-0.14	0.59553	NA	0.0006	0.94809	NA	0.78	0.21466	NA
58	APOC4p2640/rs5158	intron1	2b	CC/CT	0.02129	-0.29	0.66191	NA	-0.05	0.03532	NA	-1.12	0.4997	NA
58	APOC4p2678/rs148564866	intron1	2b	GC/GG	0.00863	0.07	0.94518	NA	0.04	0.28796	NA	2.67	0.29564	NA
59	APOC4p2623/rs5157	intron1	4	CC/CT/TT	0.17232	-0.14	0.59553	0.88648	0.0006	0.94809	0.1914	0.78	0.21466	0.21469
59	APOC4p2640/rs5158	intron1	2b	CC/CT	0.02129	-0.29	0.66191	NA	-0.05	0.03532	NA	-1.12	0.4997	NA
59	APOC4p2678/rs148564866	intron1	2b	GC/GG	0.00863	0.07	0.94518	NA	0.04	0.28796	NA	2.67	0.29564	NA
59	APOC4p2767/rs127721107	intron1	4	GG/GT	0.02537	0.56	0.37292	NA	-0.01	0.75986	NA	2.17	0.1601	NA
60	APOC4p2640/rs5158	intron1	2b	CC/CT	0.02129	-0.29	0.66191	0.61063	-0.05	0.03532	0.18293	-1.12	0.4997	0.21732
60	APOC4p2678/rs148564866	intron1	2b	GC/GG	0.00863	0.07	0.94518	NA	0.04	0.28796	NA	2.67	0.29564	NA
60	APOC4p2767/rs127721107	intron1	4	GG/GT	0.02537	0.56	0.37292	NA	-0.01	0.75986	NA	2.17	0.1601	NA
60	APOC4p3348	intron1	5	AG/GG	0.00066	11.56	0.00153	NA	-0.23	0.09471	NA	14.52	0.11008	NA
61	APOC4p2678/rs148564866	intron1	2b	GC/GG	0.00863	0.07	0.94518	0.58303	0.04	0.28796	0.43139	2.67	0.29564	0.06222
61	APOC4p2767/rs127721107	intron1	4	GG/GT	0.02537	0.56	0.37292	NA	-0.01	0.75986	NA	2.17	0.1601	NA
61	APOC4p3348	intron1	5	AG/GG	0.00066	11.56	0.00153	NA	-0.23	0.09471	NA	14.52	0.11008	NA
61	APOC2p75C4p3380/rs12721104	C4-intron1	5	AA/GA/GG	0.13684	-0.11	0.69346	NA	0.01	0.16334	NA	-1.25	0.06839	NA
62	APOC4p2767/rs127721107	intron1	4	GG/GT	0.02537	0.56	0.37292	0.67057	-0.01	0.75986	0.48353	2.17	0.1601	0.07338
62	APOC4p3348	intron1	5	AG/GG	0.00066	11.56	0.00153	NA	-0.23	0.09471	NA	14.52	0.11008	NA
62	APOC2p75C4p3380/rs12721104	C4-intron1	5	AA/GA/GG	0.13684	-0.11	0.69346	NA	0.01	0.16334	NA	-1.25	0.06839	NA
62	APOC2p194C4p3498/rs1132899	C4-exon2	5	CC/CT/TT	0.23681	-0.14	0.53341	NA	-0.001	0.87833	NA	0.88	0.11098	NA
63	APOC4p3348	intron1	5	AG/GG	0.00066	11.56	0.00153	0.78469	-0.23	0.09471	0.41289	14.52	0.11008	0.0498
63	APOC2p75C4p3380/rs12721104	C4-intron1	5	AA/GA/GG	0.13684	-0.11	0.69346	NA	0.01	0.16334	NA	-1.25	0.06839	NA
63	APOC2p194C4p3498/rs1132899	C4-exon2	5	CC/CT/TT	0.23681	-0.14	0.53341	NA	-0.001	0.87833	NA	0.88	0.11098	NA
63	APOC2p228/rs5164	C4-exon2	5	AG/GA/GG	0.00663	-0.72	0.54187	NA	0.04	0.41379	NA	3.31	0.25501	NA
64	APOC2p75C4p3380/rs12721104	C4-intron1	5	AA/GA/GG	0.13684	-0.11	0.69346	0.69081	0.01	0.16334	0.5277	-1.25	0.06839	0.10008
64	APOC2p194C4p3498/rs1132899	C4-exon2	5	CC/CT/TT	0.23681	-0.14	0.53341	NA	-0.001	0.87833	NA	0.88	0.11098	NA
64	APOC2p228/rs5164	C4-exon2	5	AG/GA/GG	0.00663	-0.72	0.54187	NA	0.04	0.41379	NA	3.31	0.25501	NA
64	APOC2p288C4p3592/rs12691090	C4-exon2	5	CC/CT	0.02722	0.75	0.21469	NA	-0.01	0.72615	NA	2	0.17721	NA
65	APOC2p194C4p3498/rs1132899	C4-exon2	5	CC/CT/TT	0.23681	-0.14	0.53341	0.6609	-0.001	0.87833	0.90956	0.88	0.11098	0.07457
65	APOC2p228/rs5164	C4-exon2	5	AG/GA/GG	0.00663	-0.72	0.54187	NA	0.04	0.41379	NA	3.31	0.25501	NA

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65	APOC2p288C4p3592/rs12691090	C4-exon2	5	CC/CT	0.02722	0.75	0.21469	NA	-0.01	0.72615	NA	2	0.17721	NA
65	APOC2p396C4p3700	C4-intron2	5	GA/GG	0.00068	5.9	0.11176	NA	-0.14	0.31613	NA	11.51	0.21156	NA
66	APOC2p228/rs5164	C4-exon2	5	AG/GA/GG	0.00663	-0.72	0.54187	0.76619	0.04	0.41379	0.89102	3.31	0.25501	0.24679
66	APOC2p288C4p3592/rs12691090	C4-exon2	5	CC/CT	0.02722	0.75	0.21469	NA	-0.01	0.72615	NA	2	0.17721	NA
66	APOC2p396C4p3700	C4-intron2	5	GA/GG	0.00068	5.9	0.11176	NA	-0.14	0.31613	NA	11.51	0.21156	NA
66	APOC2p488C4p3792/rs5165	C4-intron2	5	GA/GG	0.01465	-0.04	0.96019	NA	-0.02	0.40589	NA	-1.54	0.43321	NA
67	APOC2p288C4p3592/rs12691090	C4-exon2	5	CC/CT	0.02722	0.75	0.21469	0.44559	-0.01	0.72615	0.57369	2	0.17721	0.45181
67	APOC2p396C4p3700	C4-intron2	5	GA/GG	0.00068	5.9	0.11176	NA	-0.14	0.31613	NA	11.51	0.21156	NA
67	APOC2p488C4p3792/rs5165	C4-intron2	5	GA/GG	0.01465	-0.04	0.96019	NA	-0.02	0.40589	NA	-1.54	0.43321	NA
67	APOC2p623C4p3927/rs5167	C4-exon3	5	GG/GT/TT	0.45935	0.05	0.77107	NA	0.01	0.34212	NA	0.19	0.6794	NA
68	APOC2p396C4p3700	C4-intron2	5	GA/GG	0.00068	5.9	0.11176	0.98309	-0.14	0.31613	0.67109	11.51	0.21156	0.80964
68	APOC2p488C4p3792/rs5165	C4-intron2	5	GA/GG	0.01465	-0.04	0.96019	NA	-0.02	0.40589	NA	-1.54	0.43321	NA
68	APOC2p623C4p3927/rs5167	C4-exon3	5	GG/GT/TT	0.45935	0.05	0.77107	NA	0.01	0.34212	NA	0.19	0.6794	NA
68	APOC2p665C4p3969/rs138548797	C4-exon3	No Data	AA/CA	0.0086	-0.06	0.94985	NA	0.02	0.66857	NA	-2.07	0.41707	NA
69	APOC2p488C4p3792/rs5165	C4-intron2	5	GA/GG	0.01465	-0.04	0.96019	0.9349	-0.02	0.40589	0.50575	-1.54	0.43321	0.5806
69	APOC2p623C4p3927/rs5167	C4-exon3	5	GG/GT/TT	0.45935	0.05	0.77107	NA	0.01	0.34212	NA	0.19	0.6794	NA
69	APOC2p665C4p3969/rs138548797	C4-exon3	No Data	AA/CA	0.0086	-0.06	0.94985	NA	0.02	0.66857	NA	-2.07	0.41707	NA
69	APOC2p708C4p4012	C4-exon3	6	GA/GG	0.00066	-7.15	0.05187	NA	0.29	0.0381	NA	-9.42	0.30174	NA
70	APOC2p623C4p3927/rs5167	C4-exon3	5	GG/GT/TT	0.45935	0.05	0.77107	0.80536	0.01	0.34212	0.50769	0.19	0.6794	0.35483
70	APOC2p665C4p3969/rs138548797	C4-exon3	No Data	AA/CA	0.0086	-0.06	0.94985	NA	0.02	0.66857	NA	-2.07	0.41707	NA
70	APOC2p708C4p4012	C4-exon3	6	GA/GG	0.00066	-7.15	0.05187	NA	0.29	0.0381	NA	-9.42	0.30174	NA
70	APOC2p853C4p4157/rs10425530	C4-3' UTR	6	AA/GA/GG	0.11003	0.24	0.43314	NA	-0.004	0.75183	NA	1.17	0.12757	NA
71	APOC2p665C4p3969/rs138548797	C4-exon3	No Data	AA/CA	0.0086	-0.06	0.94985	0.48905	0.02	0.66857	0.43709	-2.07	0.41707	0.00654
71	APOC2p708C4p4012	C4-exon3	6	GA/GG	0.00066	-7.15	0.05187	NA	0.29	0.0381	NA	-9.42	0.30174	NA
71	APOC2p853C4p4157/rs10425530	C4-3' UTR	6	AA/GA/GG	0.11003	0.24	0.43314	NA	-0.004	0.75183	NA	1.17	0.12757	NA
71	APOC2p1042C4p4346/rs12709885	C4-3'FR/C2-5'FR	5	AA/TA/TT	0.01781	1.1	0.13505	NA	-0.04	0.18665	NA	5.95	0.00071	NA
72	APOC2p708C4p4012	C4-exon3	6	GA/GG	0.00066	-7.15	0.05187	0.64651	0.29	0.0381	0.27827	-9.42	0.30174	0.00761
72	APOC2p853C4p4157/rs10425530	C4-3' UTR	6	AA/GA/GG	0.11003	0.24	0.43314	NA	-0.004	0.75183	NA	1.17	0.12757	NA
72	APOC2p1042C4p4346/rs12709885	C4-3'FR/C2-5'FR	5	AA/TA/TT	0.01781	1.1	0.13505	NA	-0.04	0.18665	NA	5.95	0.00071	NA

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72	APOC2p1187C4p4491/rs111782345	C4-3'FR/C2-5'FR	5	AG/GG	0.01781	0.58	0.44007	NA	-0.01	0.63757	NA	3.23	0.08379	NA
73	APOC2p853C4p4157/rs10425530	C4-3' UTR	6	AA/GA/GG	0.11003	0.24	0.43314	0.36562	-0.004	0.75183	0.63914	1.17	0.12757	0.00311
73	APOC2p1042C4p4346/rs12709885	C4-3'FR/C2-5'FR	5	AA/TA/TT	0.01781	1.1	0.13505	NA	-0.04	0.18665	NA	5.95	0.00071	NA
73	APOC2p1187C4p4491/rs111782345	C4-3'FR/C2-5'FR	5	AG/GG	0.01781	0.58	0.44007	NA	-0.01	0.63757	NA	3.23	0.08379	NA
73	APOC2p1229C4p4533/rs112698600	C4-3'FR/C2-5'FR	2b	CC/CT	0.01402	0.83	0.31821	NA	-0.01	0.81539	NA	3.2	0.12314	NA
74	APOC2p1042C4p4346/rs12709885	C4-3'FR/C2-5'FR	5	AA/TA/TT	0.01781	1.1	0.13505	0.26994	-0.04	0.18665	0.69332	5.95	0.00071	0.00273
74	APOC2p1187C4p4491/rs111782345	C4-3'FR/C2-5'FR	5	AG/GG	0.01781	0.58	0.44007	NA	-0.01	0.63757	NA	3.23	0.08379	NA
74	APOC2p1229C4p4533/rs112698600	C4-3'FR/C2-5'FR	2b	CC/CT	0.01402	0.83	0.31821	NA	-0.01	0.81539	NA	3.2	0.12314	NA
74	APOC2p1275C4p4579/rs111356234	C4-3'FR/C2-5'FR	4	GA/GG	0.03519	-0.18	0.7323	NA	0.01	0.74933	NA	0.35	0.79182	NA
75	APOC2p1187C4p4491/rs111782345	C4-3'FR/C2-5'FR	5	AG/GG	0.01781	0.58	0.44007	0.51163	-0.01	0.63757	0.71138	3.23	0.08379	0.1427
75	APOC2p1229C4p4533/rs112698600	C4-3'FR/C2-5'FR	2b	CC/CT	0.01402	0.83	0.31821	NA	-0.01	0.81539	NA	3.2	0.12314	NA
75	APOC2p1275C4p4579/rs111356234	C4-3'FR/C2-5'FR	4	GA/GG	0.03519	-0.18	0.7323	NA	0.01	0.74933	NA	0.35	0.79182	NA
75	APOC2p1357C4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	CC/GC/GG	0.25813	0.05	0.80869	NA	-0.01	0.36144	NA	0.8	0.13323	NA
76	APOC2p1229C4p4533/rs112698600	C4-3'FR/C2-5'FR	2b	CC/CT	0.01402	0.83	0.31821	0.79706	-0.01	0.81539	0.48636	3.2	0.12314	0.26557
76	APOC2p1275C4p4579/rs111356234	C4-3'FR/C2-5'FR	4	GA/GG	0.03519	-0.18	0.7323	NA	0.01	0.74933	NA	0.35	0.79182	NA
76	APOC2p1357C4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	CC/GC/GG	0.25813	0.05	0.80869	NA	-0.01	0.36144	NA	0.8	0.13323	NA
76	APOC2p1540C4p4844/rs75463753	C2-intron1	4	AA/GA/GG	0.1079	0.09	0.77127	NA	-0.01	0.50004	NA	0.48	0.5384	NA
77	APOC2p1275C4p4579/rs111356234	C4-3'FR/C2-5'FR	4	GA/GG	0.03519	-0.18	0.7323	0.97717	0.01	0.74933	0.52662	0.35	0.79182	0.3722
77	APOC2p1357C4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	CC/GC/GG	0.25813	0.05	0.80869	NA	-0.01	0.36144	NA	0.8	0.13323	NA
77	APOC2p1540C4p4844/rs75463753	C2-intron1	4	AA/GA/GG	0.1079	0.09	0.77127	NA	-0.01	0.50004	NA	0.48	0.5384	NA
77	APOC2p2486/rs9304645	intron1	4	AA/GA/GG	0.36554	0.09	0.65299	NA	0.01	0.14059	NA	0.75	0.13555	NA
78	APOC2p1357C4p4661/rs2288912	C4-3'FR/C2-5'FR	1a	CC/GC/GG	0.25813	0.05	0.80869	0.95561	-0.01	0.36144	0.10511	0.8	0.13323	0.35521
78	APOC2p1540C4p4844/rs75463753	C2-intron1	4	AA/GA/GG	0.1079	0.09	0.77127	NA	-0.01	0.50004	NA	0.48	0.5384	NA
78	APOC2p2486/rs9304645	intron1	4	AA/GA/GG	0.36554	0.09	0.65299	NA	0.01	0.14059	NA	0.75	0.13555	NA
78	APOC2p2935/rs11879392	intron1	2b	CC/GC	0.01351	0.57	0.49871	NA	-0.07	0.02851	NA	0.18	0.93035	NA
79	APOC2p1540C4p4844/rs75463753	C2-intron1	4	AA/GA/GG	0.1079	0.09	0.77127	0.62972	-0.01	0.50004	0.01057	0.48	0.5384	0.32093
79	APOC2p2486/rs9304645	intron1	4	AA/GA/GG	0.36554	0.09	0.65299	NA	0.01	0.14059	NA	0.75	0.13555	NA
79	APOC2p2935/rs11879392	intron1	2b	CC/GC	0.01351	0.57	0.49871	NA	-0.07	0.02851	NA	0.18	0.93035	NA
79	APOC2p3010/rs10419086	intron1	6	AA/AG/GG	0.12535	0.15	0.62186	NA	-0.02	0.12716	NA	-1.32	0.06568	NA

Cont. Table 40

80	APOC2p2486/rs9304645	intron1	4	AA/GA/GG	0.36554	0.09	0.65299	0.71956	0.01	0.14059	0.00893	0.75	0.13555	0.31915
80	APOC2p2935/rs11879392	intron1	2b	CC/GC	0.01351	0.57	0.49871	NA	-0.07	0.02851	NA	0.18	0.93035	NA
80	APOC2p3010/rs10419086	intron1	6	AA/AG/GG	0.12535	0.15	0.62186	NA	-0.02	0.12716	NA	-1.32	0.06568	NA
80	APOC2p3692/rs12721060	intron1	No Data	GT/TT	0.01719	0.76	0.3536	NA	-0.01	0.62291	NA	3.01	0.14108	NA
81	APOC2p2935/rs11879392	intron1	2b	CC/GC	0.01351	0.57	0.49871	0.8007	-0.07	0.02851	0.12282	0.18	0.93035	0.21883
81	APOC2p3010/rs10419086	intron1	6	AA/AG/GG	0.12535	0.15	0.62186	NA	-0.02	0.12716	NA	-1.32	0.06568	NA
81	APOC2p3692/rs12721060	intron1	No Data	GT/TT	0.01719	0.76	0.3536	NA	-0.01	0.62291	NA	3.01	0.14108	NA
81	APOC2p3778/rs5120	intron1	4	AA/AT/TT	0.18452	0.08	0.74123	NA	-7.31E-05	0.99372	NA	0.79	0.19964	NA
82	APOC2p3010/rs10419086	intron1	6	AA/AG/GG	0.12535	0.15	0.62186	0.8782	-0.02	0.12716	0.56244	-1.32	0.06568	0.16569
82	APOC2p3692/rs12721060	intron1	No Data	GT/TT	0.01719	0.76	0.3536	NA	-0.01	0.62291	NA	3.01	0.14108	NA
82	APOC2p3778/rs5120	intron1	4	AA/AT/TT	0.18452	0.08	0.74123	NA	-7.31E-05	0.99372	NA	0.79	0.19964	NA
82	APOC2p3805/rs7257095	intron1	2a	CC/CG/GG	0.16489	-0.16	0.53621	NA	-0.003	0.7465	NA	-0.55	0.40568	NA
83	APOC2p3692/rs12721060	intron1	No Data	GT/TT	0.01719	0.76	0.3536	0.64388	-0.01	0.62291	0.55285	3.01	0.14108	0.08769
83	APOC2p3778/rs5120	intron1	4	AA/AT/TT	0.18452	0.08	0.74123	NA	-7.31E-05	0.99372	NA	0.79	0.19964	NA
83	APOC2p3805/rs7257095	intron1	2a	CC/CG/GG	0.16489	-0.16	0.53621	NA	-0.003	0.7465	NA	-0.55	0.40568	NA
83	APOC2p3814/rs10422603	intron1	2b	GG/GT/TT	0.30081	0.25	0.23836	NA	0.01	0.14544	NA	0.97	0.06515	NA
84	APOC2p3778/rs5120	intron1	4	AA/AT/TT	0.18452	0.08	0.74123	0.78035	-7.31E-05	0.99372	0.67164	0.79	0.19964	0.13092
84	APOC2p3805/rs7257095	intron1	2a	CC/CG/GG	0.16489	-0.16	0.53621	NA	-0.003	0.7465	NA	-0.55	0.40568	NA
84	APOC2p3814/rs10422603	intron1	2b	GG/GT/TT	0.30081	0.25	0.23836	NA	0.01	0.14544	NA	0.97	0.06515	NA
84	APOC2p3892/rs5121	exon2	5	CC/TC/TT	0.03581	-0.03	0.95269	NA	0.004	0.8416	NA	0.2	0.87741	NA
85	APOC2p3805/rs7257095	intron1	2a	CC/CG/GG	0.16489	-0.16	0.53621	0.7583	-0.003	0.7465	0.65222	-0.55	0.40568	0.40381
85	APOC2p3814/rs10422603	intron1	2b	GG/GT/TT	0.30081	0.25	0.23836	NA	0.01	0.14544	NA	0.97	0.06515	NA
85	APOC2p3892/rs5121	exon2	5	CC/TC/TT	0.03581	-0.03	0.95269	NA	0.004	0.8416	NA	0.2	0.87741	NA
85	APOC2p4086/rs114780592	intron2	4	GA/GG	0.02778	0.49	0.40801	NA	-0.004	0.84856	NA	1.53	0.29745	NA
86	APOC2p3814/rs10422603	intron1	2b	GG/GT/TT	0.30081	0.25	0.23836	0.76741	0.01	0.14544	0.61933	0.97	0.06515	0.35166
86	APOC2p3892/rs5121	exon2	5	CC/TC/TT	0.03581	-0.03	0.95269	NA	0.004	0.8416	NA	0.2	0.87741	NA
86	APOC2p4086/rs114780592	intron2	4	GA/GG	0.02778	0.49	0.40801	NA	-0.004	0.84856	NA	1.53	0.29745	NA
86	APOC2p4319/rs5123	intron3	No Data	AA/GA/GG	0.05922	-0.14	0.71873	NA	-0.01	0.60254	NA	0.49	0.61561	NA
87	APOC2p3892/rs5121	exon2	5	CC/TC/TT	0.03581	-0.03	0.95269	0.79364	0.004	0.8416	0.9505	0.2	0.87741	0.33968

Cont. Table 40

87	APOC2p4086/rs114780592	intron2	4	GA/GG	0.02778	0.49	0.40801	NA	-0.004	0.84856	NA	1.53	0.29745	NA
87	APOC2p4319/rs5123	intron3	No Data	AA/GA/GG	0.05922	-0.14	0.71873	NA	-0.01	0.60254	NA	0.49	0.61561	NA
87	APOC2p4513/rs180809422	intron3	5	AA/AC/CC	0.01348	0.82	0.32552	NA	-0.02	0.50114	NA	3.47	0.09379	NA
88	APOC2p4086/rs114780592	intron2	4	GA/GG	0.02778	0.49	0.40801	0.1506	-0.004	0.84856	0.61636	1.53	0.29745	0.40068
88	APOC2p4319/rs5123	intron3	No Data	AA/GA/GG	0.05922	-0.14	0.71873	NA	-0.01	0.60254	NA	0.49	0.61561	NA
88	APOC2p4513/rs180809422	intron3	5	AA/AC/CC	0.01348	0.82	0.32552	NA	-0.02	0.50114	NA	3.47	0.09379	NA
88	APOC2p4587/rs5126	exon4	5	AA/CA/CC	0.04993	0.12	0.80049	NA	-0.01	0.51928	NA	0.68	0.54818	NA
89	APOC2p4319/rs5123	intron3	No Data	AA/GA/GG	0.05922	-0.14	0.71873	0.18546	-0.01	0.60254	0.81011	0.49	0.61561	0.12586
89	APOC2p4513/rs180809422	intron3	5	AA/AC/CC	0.01348	0.82	0.32552	NA	-0.02	0.50114	NA	3.47	0.09379	NA
89	APOC2p4587/rs5126	exon4	5	AA/CA/CC	0.04993	0.12	0.80049	NA	-0.01	0.51928	NA	0.68	0.54818	NA
89	APOC2p4754/rs7253690	exon4	5	AA/GA/GG	0.06057	-0.01	0.9801	NA	-0.004	0.78701	NA	1.17	0.22087	NA
90	APOC2p4513/rs180809422	intron3	5	AA/AC/CC	0.01348	0.82	0.32552	0.64317	-0.02	0.50114	0.86408	3.47	0.09379	0.17425
90	APOC2p4587/rs5126	exon4	5	AA/CA/CC	0.04993	0.12	0.80049	NA	-0.01	0.51928	NA	0.68	0.54818	NA
90	APOC2p4754/rs7253690	exon4	5	AA/GA/GG	0.06057	-0.01	0.9801	NA	-0.004	0.78701	NA	1.17	0.22087	NA
90	APOC2p4853/rs150448996	3'flamking	No Data	DD/WD/WW	0.27365	-0.18	0.40916	NA	0.001	0.90826	NA	-0.86	0.10718	NA
91	APOC2p4587/rs5126	exon4	5	AA/CA/CC	0.04993	0.12	0.80049	0.86082	-0.01	0.51928	0.95412	0.68	0.54818	0.42444
91	APOC2p4754/rs7253690	exon4	5	AA/GA/GG	0.06057	-0.01	0.9801	NA	-0.004	0.78701	NA	1.17	0.22087	NA
91	APOC2p4853/rs150448996	3'flamking	No Data	DD/WD/WW	0.27365	-0.18	0.40916	NA	0.001	0.90826	NA	-0.86	0.10718	NA
91	APOC2p4973/rs199828513	3'flamking	No Data	WI/WW	0.00816	-0.6	0.58323	NA	0.01	0.8053	NA	0.16	0.95293	NA
92	APOC2p4754/rs7253690	exon4	5	AA/GA/GG	0.06057	-0.01	0.9801	0.76271	-0.004	0.78701	0.65349	1.17	0.22087	0.37166
92	APOC2p4853/rs150448996	3'flamking	No Data	DD/WD/WW	0.27365	-0.18	0.40916	NA	0.001	0.90826	NA	-0.86	0.10718	NA
92	APOC2p4973/rs199828513	3'flamking	No Data	WI/WW	0.00816	-0.6	0.58323	NA	0.01	0.8053	NA	0.16	0.95293	NA
92	APOC2p5004/rs10421404	3'flanking	No Data	CC/CT/TT	0.2908	0.16	0.46461	NA	0.01	0.15992	NA	0.61	0.24821	NA
93	APOC2p4853/rs150448996	3'flamking	No Data	DD/WD/WW	0.27365	-0.18	0.40916	0.78688	0.001	0.90826	0.231	-0.86	0.10718	0.6192
93	APOC2p4973/rs199828513	3'flamking	No Data	WI/WW	0.00816	-0.6	0.58323	NA	0.01	0.8053	NA	0.16	0.95293	NA
93	APOC2p5004/rs10421404	3'flanking	No Data	CC/CT/TT	0.2908	0.16	0.46461	NA	0.01	0.15992	NA	0.61	0.24821	NA
93	APOC2p5018/rs78403558	3'flanking	5	DD/WD/WW	0.03521	0	0.9939	NA	-0.02	0.21115	NA	0.36	0.77793	NA
94	APOC2p4973/rs199828513	3'flamking	No Data	WI/WW	0.00816	-0.6	0.58323	0.73997	0.01	0.8053	0.19479	0.16	0.95293	0.86684
94	APOC2p5004/rs10421404	3'flanking	No Data	CC/CT/TT	0.2908	0.16	0.46461	NA	0.01	0.15992	NA	0.61	0.24821	NA

Cont. Table 40

94	APOC2p5018/rs78403558	3'flanking	5	DD/WD/WW	0.03521	0	0.9939	NA	-0.02	0.21115	NA	0.36	0.77793	NA
94	APOC2p5310/rs7258345	3'flanking	No Data	GG/GT/TT	0.30672	0.11	0.61363	NA	-0.01	0.21601	NA	-0.42	0.44209	NA
95	APOC2p5004/rs10421404	3'flanking	No Data	CC/CT/TT	0.2908	0.16	0.46461	0.85485	0.01	0.15992	0.12002	0.61	0.24821	0.83539
95	APOC2p5018/rs78403558	3'flanking	5	DD/WD/WW	0.03521	0	0.9939	NA	-0.02	0.21115	NA	0.36	0.77793	NA
95	APOC2p5310/rs7258345	3'flanking	No Data	GG/GT/TT	0.30672	0.11	0.61363	NA	-0.01	0.21601	NA	-0.42	0.44209	NA
95	APOC2p5398/rs12709889	3'flanking	6	AA/GA/GG	0.25869	-0.12	0.59063	NA	-0.001	0.92941	NA	-0.63	0.24337	NA
96	APOC2p5018/rs78403558	3'flanking	5	DD/WD/WW	0.03521	0	0.9939	0.94641	-0.02	0.21115	0.23866	0.36	0.77793	0.40777
96	APOC2p5310/rs7258345	3'flanking	No Data	GG/GT/TT	0.30672	0.11	0.61363	NA	-0-0.00101	0.21601	NA	-0.42	0.44209	NA
96	APOC2p5398/rs12709889	3'flanking	6	AA/GA/GG	0.25869	-0.12	0.59063	NA	0	0.92941	NA	-0.63	0.24337	NA
96	APOC2p5491	3'flanking	6	CC/TC	0.00066	6.53	0.0762	NA	-0.04	0.77499	NA	-5.71	0.53224	NA
97	APOC2p5310/rs7258345	3'flanking	No Data	GG/GT/TT	0.30672	0.11	0.61363	0.8772	-0.01	0.21601	0.14049	-0.42	0.44209	0.40161
97	APOC2p5398/rs12709889	3'flanking	6	AA/GA/GG	0.25869	-0.12	0.59063	NA	-0.001	0.92941	NA	-0.63	0.24337	NA
97	APOC2p5491	3'flanking	6	CC/TC	0.00066	6.53	0.0762	NA	-0.04	0.77499	NA	-5.71	0.53224	NA
97	APOC2p5512/rs12721064	3'flanking	6	CC/CT	0.00826	0.05	0.96332	NA	0.09	0.02969	NA	0.1	0.96886	NA
98	APOC2p5398/rs12709889	3'flanking	6	AA/GA/GG	0.25869	-0.12	0.59063	0.65752	-0.001	0.92941	0.23309	-0.63	0.24337	0.71321
98	APOC2p5491	3'flanking	6	CC/TC	0.00066	6.53	0.0762	NA	-0.04	0.77499	NA	-5.71	0.53224	NA
98	APOC2p5512/rs12721064	3'flanking	6	CC/CT	0.00826	0.05	0.96332	NA	0.09	0.02969	NA	0.1	0.96886	NA
98	APOC2p5562	3'flanking	No Data	CG/GG	0.01754	-0.67	0.37221	NA	-0.01	0.61087	NA	0.65	0.73492	NA
99	APOC2p5491	3'flanking	6	CC/TC	0.00066	6.53	0.0762	0.37011	-0.04	0.77499	0.19328	-5.71	0.53224	0.61336
99	APOC2p5512/rs12721064	3'flanking	6	CC/CT	0.00826	0.05	0.96332	NA	0.09	0.02969	NA	0.1	0.96886	NA
99	APOC2p5562	3'flanking	No Data	CG/GG	0.01754	-0.67	0.37221	NA	-0.01	0.61087	NA	0.65	0.73492	NA
99	APOC2p5586/rs73558127	3'flanking	No Data	GG/GT/TT	0.10014	0.47	0.13813	NA	-0.01	0.48499	NA	1	0.20571	NA
100	APOC2p5512/rs12721064	3'flanking	6	CC/CT	0.00826	0.05	0.96332	0.49943	0.09	0.02969	0.18213	0.1	0.96886	0.54365
100	APOC2p5562	3'flanking	No Data	CG/GG	0.01754	-0.67	0.37221	NA	-0.01	0.61087	NA	0.65	0.73492	NA
100	APOC2p5586/rs73558127	3'flanking	No Data	GG/GT/TT	0.10014	0.47	0.13813	NA	-0.01	0.48499	NA	1	0.20571	NA
100	APOC2p5771	3'flanking	6	WD/WW	0.0047	-0.58	0.67563	NA	0.03	0.55408	NA	-1.1	0.74972	NA
101	APOC2p5562	3'flanking	No Data	CG/GG	0.01754	-0.67	0.37221	0.62837	-0.01	0.61087	0.54062	0.65	0.73492	0.69283
101	APOC2p5586/rs73558127	3'flanking	No Data	GG/GT/TT	0.10014	0.47	0.13813	NA	-0.01	0.48499	NA	1	0.20571	NA
101	APOC2p5771	3'flanking	6	WD/WW	0.0047	-0.58	0.67563	NA	0.03	0.55408	NA	-1.1	0.74972	NA

Cont. Table 40

101	APOC2p5815/rs10423208	3'flanking	5	AA/GA/GG	0.31642	0.03	0.8759	NA	-0.01	0.20297	NA	-0.43	0.41044	NA
102	APOC2p5586/rs73558127	3'flanking	No Data	GG/GT/TT	0.10014	0.47	0.13813	0.64497	-0.01	0.48499	0.49479	1	0.20571	0.70402
102	APOC2p5771	3'flanking	6	WD/WW	0.0047	-0.58	0.67563	NA	0.03	0.55408	NA	-1.1	0.74972	NA
102	APOC2p5815/rs10423208	3'flanking	5	AA/GA/GG	0.31642	0.03	0.8759	NA	-0.01	0.20297	NA	-0.43	0.41044	NA
102	APOC2p5922/rs10422888	3'flanking	5	AA/AG/GG	0.07843	-0.01	0.98595	NA	0.02	0.25815	NA	0.05	0.95405	NA
103	APOC2p5771	3'flanking	6	WD/WW	0.0047	-0.58	0.67563	0.98058	0.03	0.55408	0.45755	-1.1	0.74972	0.80829
103	APOC2p5815/rs10423208	3'flanking	5	AA/GA/GG	0.31642	0.03	0.8759	NA	-0.01	0.20297	NA	-0.43	0.41044	NA
103	APOC2p5922/rs10422888	3'flanking	5	AA/AG/GG	0.07843	-0.01	0.98595	NA	0.02	0.25815	NA	0.05	0.95405	NA
103	APOC2p5965	3'flanking	5	GA/GG	0.00132	2.75	0.29064	NA	-0.01	0.95121	NA	-2.79	0.66578	NA
104	APOC2p5815/rs10423208	3'flanking	5	AA/GA/GG	0.31642	0.03	0.8759	0.77402	-0.01	0.20297	0.46584	-0.43	0.41044	0.57874
104	APOC2p5922/rs10422888	3'flanking	5	AA/AG/GG	0.07843	-0.01	0.98595	NA	0.02	0.25815	NA	0.05	0.95405	NA
104	APOC2p5965	3'flanking	5	GA/GG	0.00132	2.75	0.29064	NA	-0.01	0.95121	NA	-2.79	0.66578	NA
104	APOC2p6334	3'flanking	No Data	GA/GG	0.00959	0.6	0.52729	NA	0.01	0.68863	NA	-2.3	0.33277	NA

wind: 4-SNPs haplotype window; w.snps: SNPs that were included in each window; p-value: single-locus p-value; hap-P: haplotype global p-value; [a] Cox-Box transformed data.

Table 41. Haplotype-based association summary of significant windows with LDL-C in African Blacks

	LDL-C									
	Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
Geno.2	1	C	A	C	T	0.36494	0.53	0.20	2.65	0.00815
Geno.6	1	T	A	C	A	0.06140	-0.36	0.40	-0.91	0.36339
Geno.rare	1	*	*	*	*	0.00666	-0.25	1.29	-0.20	0.84412
haplo.base	1	C	A	C	A	0.56700	NA	NA	NA	NA
Geno.4	2	A	C	T	G	0.36464	0.59	0.19	3.01	0.00266
Geno.rare1	2	*	*	*	*	0.00731	-0.40	1.33	-0.30	0.76355
haplo.base1	2	A	C	A	G	0.62805	NA	NA	NA	NA
Geno.61	3	C	T	G	T	0.36310	0.54	0.20	2.79	0.00547
Geno.rare2	3	*	*	*	*	0.01303	-1.01	0.92	-1.10	0.27269
haplo.base2	3	C	A	G	T	0.62387	NA	NA	NA	NA
Geno.3	4	A	G	T	T	0.04221	0.50	0.50	1.01	0.31120
Geno.62	4	T	G	T	G	0.15663	0.43	0.28	1.54	0.12379
Geno.7	4	T	G	T	T	0.21424	0.67	0.23	2.88	0.00406
Geno.rare3	4	*	*	*	*	0.00716	-2.53	1.26	-2.01	0.04529
haplo.base3	4	A	G	T	G	0.57976	NA	NA	NA	NA
Geno.5	5	G	T	G	T	0.04142	0.24	0.46	0.53	0.59901
Geno.63	5	G	T	T	C	0.25707	0.58	0.21	2.76	0.00592
Geno.rare4	5	*	*	*	*	0.00715	-2.71	1.27	-2.13	0.03354
haplo.base4	5	G	T	G	C	0.69436	NA	NA	NA	NA
Geno.51	6	T	G	T	G	0.04209	0.19	0.46	0.41	0.67890
Geno.64	6	T	T	C	C	0.09836	0.65	0.32	2.00	0.04579
Geno.71	6	T	T	C	G	0.15818	0.53	0.26	2.01	0.04437
Geno.rare5	6	*	*	*	*	0.01387	-1.83	0.89	-2.05	0.04074
haplo.base5	6	T	G	C	G	0.68751	NA	NA	NA	NA
Geno.25	11	A	A	G	G	0.05634	-0.19	0.41	-0.47	0.64066
Geno.54	11	C	A	G	A	0.01593	-2.06	0.79	-2.59	0.00971
Geno.rare10	11	*	*	*	*	0.01631	-0.93	0.77	-1.21	0.22486
haplo.base10	11	C	A	G	G	0.91142	NA	NA	NA	NA
Geno.32	12	A	G	A	G	0.01681	-2.00	0.75	-2.69	0.00738
Geno.43	12	A	G	G	A	0.38633	0.09	0.20	0.42	0.67194
Geno.rare11	12	*	*	*	*	0.01549	-0.81	0.74	-1.09	0.27669
haplo.base11	12	A	G	G	G	0.58137	NA	NA	NA	NA
Geno.33	13	G	A	G	C	0.01681	-1.98	0.75	-2.66	0.00802
Geno.44	13	G	G	A	C	0.38655	0.10	0.20	0.49	0.62637
Geno.rare12	13	*	*	*	*	0.01405	-0.44	0.82	-0.54	0.59146
haplo.base12	13	G	G	G	C	0.58259	NA	NA	NA	NA
Geno.26	14	A	G	C	T	0.01682	-2.12	0.74	-2.84	0.00462
Geno.55	14	G	G	C	C	0.26690	0.23	0.23	0.98	0.32691
Geno.66	14	G	G	C	T	0.32732	-0.43	0.23	-1.85	0.06475
Geno.rare13	14	*	*	*	*	0.00712	-0.43	1.17	-0.37	0.71146
haplo.base13	14	G	A	C	T	0.38185	NA	NA	NA	NA
Geno.34	15	G	C	C	C	0.26692	0.22	0.23	0.94	0.34618
Geno.56	15	G	C	T	C	0.32485	-0.41	0.23	-1.78	0.07500
Geno.67	15	G	C	T	T	0.01952	-2.28	0.68	-3.37	0.00080
Geno.rare14	15	*	*	*	*	0.00712	-0.45	1.17	-0.38	0.70263

Cont. Table 41

haplo.base14	15	A	C	T	C	0.38160	NA	NA	NA	NA
Geno.11	16	C	C	C	G	0.26743	0.22	0.21	1.04	0.29819
Geno.35	16	C	T	C	A	0.05813	-2.05	0.40	-5.08	4.65E-07
Geno.57	16	C	T	T	G	0.01984	-2.47	0.67	-3.69	0.00024
Geno.rare1. 5	16	*	*	*	*	0.00601	-0.43	1.24	-0.35	0.72988
haplo.base15	16	C	T	C	G	0.64859	NA	NA	NA	NA
Geno.12	17	C	C	G	G	0.26686	0.19	0.21	0.92	0.35766
Geno.45	17	T	C	A	G	0.05813	-2.06	0.40	-5.11	4.14E-07
Geno.68	17	T	T	G	G	0.01983	-2.47	0.67	-3.69	0.00024
haplo.base16	17	T	C	G	G	0.65451	NA	NA	NA	NA
Geno.13	18	C	A	G	C	0.05810	-2.14	0.40	-5.39	9.62E-08
Geno.69	18	T	G	G	C	0.01979	-2.51	0.67	-3.78	0.00017
Geno.rare16	18	*	*	*	*	0.00589	-1.35	1.28	-1.06	0.28994
haplo.base17	18	C	G2	G	C	0.91623	NA	NA	NA	NA
Geno.27	19	A	G	C	T	0.05817	-2.04	0.40	-5.09	4.44E-07
Geno.36	19	G	G	C	G	0.02629	-0.16	0.56	-0.28	0.77761
Geno.rare17	19	*	*	*	*	0.00589	-1.25	1.37	-0.91	0.36338
haplo.base18	19	G	G	C	T	0.90966	NA	NA	NA	NA
Geno.16	24	A	I	C	C	0.13261	-0.32	0.30	-1.08	0.28098
Geno.38	24	A	W	C	C	0.16401	0.27	0.31	0.90	0.36953
Geno.59	24	G	I	C	C	0.13751	-0.61	0.32	-1.89	0.05977
Geno.82	24	G	W	C	T	0.02495	1.66	0.70	2.39	0.01713
Geno.rare22	24	*	*	*	*	0.00746	-2.54	1.33	-1.91	0.05649
haplo.base23	24	G	W	C	C	0.53345	NA	NA	NA	NA
Geno.17	25	I	C	C	G	0.27035	-0.49	0.22	-2.27	0.02351
Geno.39	25	W	C	C	A	0.06631	0.40	0.41	0.99	0.32384
Geno.611	25	W	C	T	G	0.02898	0.34	0.57	0.60	0.54773
Geno.rare23	25	*	*	*	*	0.00335	2.08	1.98	1.05	0.29342
haplo.base24	25	W	C	C	G	0.63100	NA	NA	NA	NA
Geno.113	35	G	D	A	G	0.21977	0.27	0.23	1.14	0.25378
Geno.315	35	G	W	A	A	0.06231	0.78	0.41	1.88	0.06102
Geno.514	35	G	W	G	A	0.03311	-1.36	0.60	-2.28	0.02300
Geno.615	35	G	W	G	G	0.02413	-0.23	0.68	-0.34	0.73547
Geno.78	35	T	W	G	A	0.08798	-0.44	0.34	-1.30	0.19301
haplo.base34	35	G	W	A	G	0.57271	NA	NA	NA	NA
Geno.215	36	D	A	G	G	0.21908	0.29	0.23	1.23	0.21764
Geno.414	36	W	A	A	C	0.06120	0.85	0.42	2.01	0.04461
Geno.616	36	W	A	G	G	0.05080	0.30	0.42	0.69	0.48774
Geno.79	36	W	G	A	C	0.12309	-0.69	0.31	-2.24	0.02534
Geno.9	36	W	G	G	C	0.02412	-0.13	0.71	-0.18	0.85506
haplo.base35	36	W	A	G	C	0.52097	NA	NA	NA	NA
Geno.114	37	A	A	C	G	0.06082	0.86	0.42	2.03	0.04284
Geno.515	37	A	G	G	G	0.26924	0.34	0.22	1.54	0.12471
Geno.710	37	G	A	C	G	0.12049	-0.69	0.31	-2.23	0.02617
Geno.91	37	G	G	C	G	0.02338	-0.03	0.71	-0.04	0.96558
Geno.rare31	37	*	*	*	*	0.00738	-0.48	1.17	-0.41	0.68376
haplo.base36	37	A	G	C	G	0.51869	NA	NA	NA	NA

Cont. Table 41

Geno.96	75	G	C	A	G	0.02667	-1.52	0.64	-2.35	0.01879
Geno.105	75	G	C	G	C	0.24608	0.40	0.23	1.79	0.07334
Geno.rare67	75	*	*	*	*	0.02585	0.31	0.67	0.45	0.64964
haplo.base74	75	G	C	G	G	0.70140	NA	NA	NA	NA
Geno.428	76	C	A	G	G	0.02498	-1.46	0.67	-2.18	0.02972
Geno.534	76	C	G	C	A	0.09245	0.67	0.35	1.93	0.05382
Geno.633	76	C	G	C	G	0.15584	0.22	0.28	0.80	0.42320
Geno.124	76	T	G	G	G	0.01110	-0.39	0.98	-0.40	0.69145
Geno.rare68	76	*	*	*	*	0.01745	0.98	0.87	1.13	0.25729
haplo.base75	76	C	G	G	G	0.69817	NA	NA	NA	NA
Geno.120	78	C	A	G	C	0.10388	0.56	0.34	1.67	0.09628
Geno.229	78	C	G	A	C	0.05838	-0.17	0.49	-0.35	0.72687
Geno.430	78	C	G	G	C	0.09877	0.30	0.41	0.75	0.45603
Geno.720	78	G	G	A	C	0.28994	-0.47	0.26	-1.84	0.06630
Geno.818	78	G	G	A	G	0.01323	0.91	0.85	1.07	0.28551
Geno.rare70	78	*	*	*	*	0.00422	1.74	1.62	1.07	0.28505
haplo.base77	78	G	G	G	C	0.43159	NA	NA	NA	NA
Geno.330	79	A	G	C	A	0.10305	0.57	0.35	1.64	0.10223
Geno.634	79	G	A	C	A	0.33439	-0.47	0.24	-1.99	0.04692
Geno.721	79	G	A	C	G	0.01326	-0.83	1.00	-0.83	0.40439
Geno.819	79	G	A	G	A	0.01314	0.85	0.85	1.00	0.31762
Geno.106	79	G	G	C	G	0.11232	0.01	0.35	0.04	0.96931
Geno.rare71	79	*	*	*	*	0.00495	0.83	1.78	0.47	0.64025
haplo.base78	79	G	G	C	A	0.41889	NA	NA	NA	NA
Geno.126	80	A	C	A	G	0.01486	0.26	0.86	0.31	0.75976
Geno.230	80	A	C	A	T	0.31966	-0.62	0.22	-2.76	0.00593
Geno.331	80	A	C	G	T	0.01588	-0.92	0.91	-1.01	0.31257
Geno.535	80	A	G	A	T	0.01202	1.12	0.90	1.24	0.21690
Geno.98	80	G	C	G	T	0.10905	0.02	0.34	0.07	0.94184
Geno.rare72	80	*	*	*	*	0.00261	-4.64	2.06	-2.25	0.02474
haplo.base79	80	G	C	A	T	0.52593	NA	NA	NA	NA
Geno.130	84	A	C	G	C	0.30079	-0.07	0.23	-0.28	0.78159
Geno.537	84	A	G	T	C	0.13216	0.52	0.31	1.69	0.09062
Geno.638	84	A	G	T	T	0.03586	-0.01	0.52	-0.02	0.98253
Geno.820	84	T	C	T	C	0.18380	0.65	0.27	2.41	0.01630
haplo.base83	84	A	C	T	C	0.34740	NA	NA	NA	NA
Geno.436	95	W	C	W	T	0.30785	0.31	0.24	1.27	0.20455
Geno.543	95	W	T	D	G	0.03499	0.77	0.52	1.48	0.13834
Geno.640	95	W	T	W	G	0.24705	-0.30	0.25	-1.18	0.23870
Geno.rare80	95	*	*	*	*	0.00896	-1.53	1.02	-1.50	0.13373
haplo.base94	95	W	C	W	G	0.40115	NA	NA	NA	NA
Geno.234	96	C	W	G	A	0.25779	-0.22	0.26	-0.86	0.39099
Geno.334	96	C	W	G	G	0.13634	-0.73	0.33	-2.24	0.02561
Geno.641	96	T	D	G	G	0.03499	0.38	0.53	0.72	0.47241
Geno.823	96	T	W	G	G	0.25475	-0.70	0.26	-2.69	0.00733
Geno.rare81	96	*	*	*	*	0.00332	-0.67	1.63	-0.41	0.68042
haplo.base95	96	C	W	T	G	0.31282	NA	NA	NA	NA

Cont. Table 41

Geno.139	97	D	G	G	C	0.03491	1.05	0.52	2.01	0.04463
Geno.335	97	W	G	A	C	0.25752	0.46	0.24	1.88	0.06011
Geno.824	97	W	T	G	C	0.30988	0.62	0.24	2.57	0.01042
haplo.base96	97	W	G	G	C	0.39702	NA	NA	NA	NA
Geno.143	102	C	T	A	A	0.01626	-0.21	0.78	-0.27	0.78644
Geno.338	102	G	G	A	A	0.10007	-0.30	0.33	-0.91	0.36180
Geno.545	102	G	T	A	G	0.07827	1.11	0.38	2.95	0.00323
Geno.643	102	G	T	G	A	0.31767	0.49	0.22	2.23	0.02630
haplo.base101	102	G	T	A	A	0.48750	NA	NA	NA	NA
Geno.144	103	G	A	A	G	0.10014	-0.27	0.33	-0.84	0.40117
Geno.728	103	T	A	G	G	0.07769	1.15	0.37	3.08	0.00218
Geno.826	103	T	G	A	G	0.31685	0.52	0.22	2.41	0.01626
Geno.rare86	103	*	*	*	*	0.00134	3.22	0.00	3.0E+16	<10E-06
haplo.base102	103	T	A	A	G	0.50398	NA	NA	NA	NA
Geno.644	104	A	G	G	G	0.07743	1.23	0.37	3.33	0.00090
Geno.827	104	G	A	G	G	0.31638	0.60	0.21	2.86	0.00430
Geno.rare87	104	*	*	*	*	0.01120	2.19	0.95	2.30	0.02184
haplo.base103	104	A	A	G	G	0.59500	NA	NA	NA	NA

hap.freq: haplotype frequency; coef: coefficient; se: standard errors; t.stat: test statistic; p-val: haplotyep p-value.

Table 42. Haplotype-based association summary of significant windows with TC in African Blacks

	TC									
	Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
Geno.4	2	A	C	T	G	0.3624	0.245	0.103	2.378	0.01764
Geno.rare1	2	*	*	*	*	0.0080	-0.262	0.588	-0.445	0.65610
haplo.base1	2	A	C	A	G	0.6295	NA	NA	NA	NA
Geno.41	3	C	T	G	T	0.3619	0.230	0.103	2.231	0.02597
Geno.rare2	3	*	*	*	*	0.0139	-0.423	0.447	-0.946	0.34462
haplo.base2	3	C	A	G	T	0.6242	NA	NA	NA	NA
Geno.3	4	A	G	T	T	0.0424	0.005	0.258	0.021	0.98317
Geno.61	4	T	G	T	G	0.1554	0.168	0.146	1.148	0.25134
Geno.7	4	T	G	T	T	0.2141	0.284	0.123	2.304	0.02149
Geno.rare3	4	*	*	*	*	0.0079	-1.334	0.614	-2.174	0.03002
haplo.base3	4	A	G	T	G	0.5802	NA	NA	NA	NA
Geno.5	5	G	T	G	T	0.0412	0.219	0.243	0.900	0.36837
Geno.62	5	G	T	T	C	0.2571	0.216	0.112	1.937	0.05312
Geno.rare4	5	*	*	*	*	0.0079	-1.387	0.618	-2.245	0.02508
haplo.base4	5	G	T	G	C	0.6938	NA	NA	NA	NA
Geno.34	15	G	C	C	C	0.2678	0.061	0.124	0.491	0.62327
Geno.46	15	G	C	T	C	0.3236	-0.190	0.122	-1.555	0.12041
Geno.55	15	G	C	T	T	0.0205	-0.907	0.351	-2.584	0.00995
Geno.rare13	15	*	*	*	*	0.0079	-0.096	0.589	-0.164	0.87005
haplo.base14	15	A	C	T	C	0.3802	NA	NA	NA	NA
Geno.11	16	C	C	C	G	0.2674	0.072	0.112	0.637	0.52426
Geno.35	16	C	T	C	A	0.0586	-0.825	0.212	-3.888	0.00011

Cont. Table 42

Geno.56	16	C	T	T	G	0.0207	-0.960	0.347	-2.771	0.00573
Geno.rare14	16	*	*	*	*	0.0068	-0.131	0.617	-0.212	0.83225
haplo.base15	16	C	T	C	G	0.6466	NA	NA	NA	NA
Geno.12	17	C	C	G	G	0.2677	0.059	0.112	0.525	0.59942
Geno.47	17	T	C	A	G	0.0588	-0.828	0.212	-3.908	0.00010
Geno.66	17	T	T	G	G	0.0207	-0.962	0.346	-2.777	0.00562
haplo.base16	17	T	C	G	G	0.6521	NA	NA	NA	NA
Geno.13	18	C	A	G	C	0.0588	-0.851	0.209	-4.080	0.00005
Geno.67	18	T	G	G	C	0.0206	-0.967	0.345	-2.806	0.00515
Geno.rare15	18	*	*	*	*	0.0060	-0.404	0.679	-0.594	0.55242
haplo.base17	18	C	G	G	C	0.9147	NA	NA	NA	NA
Geno.27	19	A	G	C	T	0.0588	-0.812	0.209	-3.880	0.00011
Geno.36	19	G	G	C	G	0.0252	-0.049	0.313	-0.157	0.87518
Geno.rare16	19	*	*	*	*	0.0060	-0.360	0.724	-0.498	0.61882
haplo.base18	19	G	G	C	T	0.9100	NA	NA	NA	NA
Geno.95	75	G	C	A	G	0.0258	-0.776	0.337	-2.303	0.02153
Geno.105	75	G	C	G	C	0.2451	0.231	0.119	1.935	0.05331
Geno.rare65	75	*	*	*	*	0.0251	0.251	0.360	0.697	0.48596
haplo.base74	75	G	C	G	G	0.7040	NA	NA	NA	NA
Geno.431	76	C	A	G	G	0.0241	-0.725	0.350	-2.070	0.03884
Geno.534	76	C	G	C	A	0.0938	0.365	0.182	2.007	0.04514
Geno.629	76	C	G	C	G	0.1538	0.136	0.147	0.921	0.35750
Geno.125	76	T	G	G	G	0.0101	-0.048	0.561	-0.086	0.93140
Geno.rare66	76	*	*	*	*	0.0177	0.500	0.468	1.068	0.28583
haplo.base75	76	C	G	G	G	0.7005	NA	NA	NA	NA
Geno.145	102	C	T	A	A	0.0180	-0.118	0.390	-0.303	0.76200
Geno.337	102	G	G	A	A	0.1005	-0.099	0.174	-0.572	0.56761
Geno.545	102	G	T	A	G	0.0805	0.540	0.196	2.751	0.00608
Geno.639	102	G	T	G	A	0.3143	0.218	0.117	1.872	0.06166
haplo.base101	102	G	T	A	A	0.4867	NA	NA	NA	NA
Geno.146	103	G	A	A	G	0.1005	-0.080	0.173	-0.466	0.64169
Geno.731	103	T	A	G	G	0.0797	0.571	0.197	2.902	0.00382
Geno.825	103	T	G	A	G	0.3135	0.240	0.115	2.080	0.03791
Geno.rare85	103	*	*	*	*	0.0014	1.801	NA	NA	NA
haplo.base102	103	T	A	A	G	0.5050	NA	NA	NA	NA
Geno.640	104	A	G	G	G	0.0793	0.596	0.192	3.103	0.00199
Geno.826	104	G	A	G	G	0.3130	0.266	0.111	2.410	0.01617
Geno.rare86	104	*	*	*	*	0.0113	1.160	0.502	2.310	0.02114
haplo.base103	104	A	A	G	G	0.5963	NA	NA	NA	NA

hap.freq: haplotype frequency; coef: coefficient; se: standard errors; t.stat: test statistic; p-val: haplotyep p-value.

Table 43. Haplotype-based association summary of significant windows with ApoB in African Blacks

ApoB										
	Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
Geno.12	17	C	C	G	G	0.2652	-0.30	0.60	-0.50	0.61601
Geno.47	17	T	C	A	G	0.0593	-2.59	1.13	-2.29	0.02206
Geno.67	17	T	T	G	G	0.0198	-3.83	1.90	-2.01	0.04480
haplo.base16	17	T	C	G	G	0.6551	NA	NA	NA	NA
Geno.13	18	C	A	G	C	0.0592	-2.51	1.11	-2.25	0.02478
Geno.56	18	T	G	G	C	0.0198	-3.80	1.91	-1.99	0.04669
Geno.rare16	18	*	*	*	*	0.0052	-0.89	3.90	-0.23	0.81963
haplo.base17	18	C	G	G	C	0.9158	NA	NA	NA	NA

hap.freq: haplotype frequency; coef: coefficient; se: standard errors; t.stat: test statistic; p-val: haplotyep p-value.

Table 44. Haplotype-based association summary of significant windows with TG in African Blacks

TG										
	Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
Geno.2	1	C	A	C	T	0.36137	0.003	0.008	0.424	0.67171
Geno.6	1	T	A	C	A	0.06186	0.039	0.015	2.641	0.00843
Geno.rare	1	*	*	*	*	0.00668	0.060	0.045	1.313	0.18941
haplo.base	1	C	A	C	A	0.57009	NA	NA	NA	NA
Geno.419	46	C	T	G	T	0.03746	0.061	0.018	3.375	0.00078
Geno.516	46	C	T	T	G	0.04651	-0.009	0.017	-0.556	0.57807
Geno.rare40	46	*	*	*	*	0.00470	0.060	0.056	1.084	0.27891
haplo.base45	46	C	T	G	G	0.91133	NA	NA	NA	NA
Geno.517	47	T	G	T	T	0.03746	0.061	0.018	3.388	0.00074
Geno.622	47	T	T	G	T	0.04651	-0.009	0.017	-0.537	0.59118
Geno.rare41	47	*	*	*	*	0.00337	0.131	0.068	1.933	0.05362
haplo.base46	47	T	G	G	T	0.91266	NA	NA	NA	NA
Geno.420	48	G	T	T	T	0.03808	0.063	0.018	3.506	0.00048
Geno.518	48	T	G	T	T	0.04650	-0.009	0.017	-0.543	0.58745
Geno.rare42	48	*	*	*	*	0.00205	0.159	0.096	1.653	0.09882
haplo.base47	48	G	G	T	T	0.91336	NA	NA	NA	NA
Geno.317	49	G	T	T	A	0.01264	-0.003	0.032	-0.104	0.91684
Geno.519	49	T	T	T	G	0.03809	0.063	0.018	3.527	0.00044
Geno.rare43	49	*	*	*	*	0.00205	0.160	0.096	1.662	0.09696
haplo.base48	49	G	T	T	G	0.94723	NA	NA	NA	NA
Geno.332	79	A	G	C	A	0.10358	-0.009	0.013	-0.683	0.49486
Geno.632	79	G	A	C	A	0.33332	0.006	0.009	0.621	0.53458
Geno.721	79	G	A	C	G	0.01407	0.079	0.037	2.124	0.03400
Geno.818	79	G	A	G	A	0.01382	-0.071	0.031	-2.310	0.02116
Geno.106	79	G	G	C	G	0.11102	-0.034	0.013	-2.540	0.01129
Geno.rare69	79	*	*	*	*	0.00482	0.031	0.077	0.404	0.68667
haplo.base78	79	G	G	C	A	0.41936	NA	NA	NA	NA
Geno.125	80	A	C	A	G	0.01492	-0.004	0.032	-0.140	0.88873

Cont. Table 44

Geno.228	80	A	C	A	T	0.31847	0.007	0.009	0.804	0.42170
Geno.333	80	A	C	G	T	0.01670	0.078	0.035	2.234	0.02579
Geno.535	80	A	G	A	T	0.01293	-0.073	0.032	-2.308	0.02126
Geno.98	80	G	C	G	T	0.10829	-0.033	0.013	-2.493	0.01287
Geno.rare70	80	*	*	*	*	0.00188	-0.082	0.127	-0.647	0.51751
haplo.base79	80	G	C	A	T	0.52681	NA	NA	NA	NA

hap.freq: haplotype frequency; coef: coefficient; se: standard errors; t.stat: test statistic; p-val: haplotyep p-value.

Table 45. Haplotype-based association summary of significant windows with HDL-C in African Blacks

	HDL-C									
	Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
Geno.87	40	G	A	G	C	0.2123	0.770	0.328	2.349	0.0191
Geno.94	40	G	A	G	G	0.1305	0.258	0.383	0.674	0.5005
Geno.114	40	G	G	C	G	0.2259	0.592	0.326	1.815	0.0699
Geno.121	40	G	G	G	C	0.0751	0.330	0.522	0.633	0.5269
Geno.131	40	G	G	G	G	0.0602	0.414	0.581	0.712	0.4770
Geno.rare33	40	*	*	*	*	0.0188	0.176	0.801	0.220	0.8263
haplo.base39	40	G	A	C	G	0.2772	NA	NA	NA	NA
Geno.419	41	A	C	G	G	0.0261	1.084	0.801	1.353	0.1766
Geno.514	41	A	G	C	C	0.1872	1.067	0.318	3.350	0.0008
Geno.616	41	A	G	C	G	0.0245	-1.566	0.849	-1.844	0.0655
Geno.714	41	A	G	G	C	0.0937	-0.049	0.401	-0.123	0.9023
Geno.88	41	A	G	G	G	0.0374	2.071	0.594	3.488	0.0005
Geno.102	41	G	C	G	C	0.1867	0.501	0.343	1.461	0.1444
Geno.115	41	G	C	G	G	0.0382	1.672	0.682	2.450	0.0145
Geno.122	41	G	G	C	C	0.0565	0.759	0.552	1.374	0.1699
Geno.132	41	G	G	C	G	0.0184	0.842	1.129	0.746	0.4562
Geno.141	41	G	G	G	C	0.0506	0.645	0.527	1.223	0.2215
Geno.151	41	G	G	G	G	0.0103	-3.702	1.653	-2.239	0.0254
Geno.rare34	41	*	*	*	*	0.0118	-1.657	0.978	-1.694	0.0906
haplo.base40	41	A	C	G	C	0.2583	NA	NA	NA	NA
Geno.116	42	C	C	C	G	0.0109	-2.013	1.026	-1.963	0.0501
Geno.315	42	C	G	C	A	0.0197	-1.155	0.813	-1.421	0.1557
Geno.617	42	C	G	G	G	0.0576	1.377	0.525	2.622	0.0089
Geno.715	42	G	C	C	A	0.0111	1.192	1.246	0.957	0.3390
Geno.89	42	G	C	C	G	0.2355	0.764	0.246	3.109	0.0020
Geno.103	42	G	C	G	G	0.0411	-1.408	0.571	-2.467	0.0139
Geno.123	42	G	G	C	G	0.1371	-0.131	0.319	-0.412	0.6802
Geno.142	42	G	G	G	G	0.0460	1.089	0.591	1.843	0.0658
Geno.rare35	42	*	*	*	*	0.0164	-0.707	1.091	-0.648	0.5170
haplo.base41	42	C	G	C	G	0.4248	NA	NA	NA	NA
Geno.117	43	C	C	A	C	0.0123	1.011	1.122	0.901	0.3677
Geno.218	43	C	C	G	C	0.2435	0.671	0.225	2.978	0.0030
Geno.515	43	C	G	G	C	0.0404	-1.407	0.573	-2.455	0.0143
Geno.618	43	G	C	A	C	0.0250	-1.129	0.642	-1.759	0.0789
Geno.104	43	G	G	G	C	0.1041	1.252	0.340	3.678	0.0003

Cont. Table 45

Geno.rare36	43	*	*	*	*	0.0126	-0.046	1.002	-0.046	0.9637
haplo.base42	43	G	C	G	C	0.5620	NA	NA	NA	NA

hap.freq: haplotype frequency; coef: coefficient; se: standard errors; t.stat: test statistic; p-val: haplotyep p-value.

Table 46. Haplotype-based association summary of significant windows with ApoA1 in African Blacks

	ApoA1									
	Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
Geno.11	16	C	C	C	G	0.2641	-0.69	0.53	-1.30	0.19546
Geno.35	16	C	T	C	A	0.0601	3.63	0.98	3.69	0.00024
Geno.56	16	C	T	T	G	0.0205	-0.56	1.65	-0.34	0.73524
Geno.rare15	16	*	*	*	*	0.0067	3.80	2.88	1.32	0.18695
haplo.base15	16	C	T	C	G	0.6486	NA	NA	NA	NA
Geno.12	17	C	C	G	G	0.2645	-0.75	0.53	-1.41	0.16024
Geno.47	17	T	C	A	G	0.0600	3.60	0.98	3.66	0.00027
Geno.66	17	T	T	G	G	0.0205	-0.63	1.65	-0.38	0.70465
haplo.base16	17	T	C	G	G	0.6543	NA	NA	NA	NA
Geno.13	18	C	A	G	C	0.0600	3.87	0.97	3.98	0.00008
Geno.57	18	T	G	G	C	0.0205	-0.29	1.65	-0.18	0.85797
Geno.rare16	18	*	*	*	*	0.0052	3.55	3.42	1.04	0.29928
haplo.base17	18	C	G	G	C	0.9143	NA	NA	NA	NA
Geno.27	19	A	G	C	T	0.0600	3.89	0.97	4.01	0.00007
Geno.36	19	G	G	C	G	0.0270	0.20	1.39	0.14	0.88674
Geno.rare17	19	*	*	*	*	0.0052	3.57	3.64	0.98	0.32651
haplo.base18	19	G	G	C	T	0.9078	NA	NA	NA	NA
Geno.418	41	A	C	G	G	0.0289	3.56	2.18	1.64	0.10196
Geno.516	41	A	G	C	C	0.1977	2.48	0.78	3.17	0.00160
Geno.616	41	A	G	C	G	0.0226	-1.02	2.11	-0.48	0.62939
Geno.712	41	A	G	G	C	0.0964	-0.07	1.08	-0.06	0.94838
Geno.89	41	A	G	G	G	0.0351	2.90	1.70	1.71	0.08848
Geno.102	41	G	C	G	C	0.1882	0.34	0.92	0.37	0.71262
Geno.116	41	G	C	G	G	0.0350	1.79	1.85	0.97	0.33243
Geno.122	41	G	G	C	C	0.0562	-1.20	1.32	-0.91	0.36309
Geno.132	41	G	G	C	G	0.0203	1.27	2.58	0.49	0.62174
Geno.141	41	G	G	G	C	0.0483	2.02	1.46	1.38	0.16697
Geno.151	41	G	G	G	G	0.0105	-4.83	4.01	-1.20	0.22894
Geno.rare35	41	*	*	*	*	0.0111	-3.08	2.43	-1.27	0.20511
haplo.base40	41	A	C	G	C	0.2496	NA	NA	NA	NA
Geno.118	43	C	C	A	C	0.0119	5.27	2.82	1.87	0.06164
Geno.217	43	C	C	G	C	0.2512	1.08	0.56	1.92	0.05535
Geno.517	43	C	G	G	C	0.0410	-0.97	1.42	-0.68	0.49511
Geno.618	43	G	C	A	C	0.0244	-3.38	1.61	-2.10	0.03593
Geno.104	43	G	G	G	C	0.1001	1.85	0.89	2.08	0.03812
Geno.rare37	43	*	*	*	*	0.0131	2.12	2.64	0.80	0.42278
haplo.base42	43	G	C	G	C	0.5583	NA	NA	NA	NA
Geno.119	54	I	G	G	C	0.0337	2.50	1.36	1.84	0.06673

Cont. Table 46

Geno.319	54	W	G	A	C	0.0138	-2.46	2.00	-1.23	0.21953
Geno.526	54	W	G	G	T	0.0964	-1.33	0.80	-1.66	0.09749
Geno.623	54	W	T	G	C	0.0138	2.85	2.01	1.42	0.15609
haplo.base53	54	W	G	G	C	0.8423	NA	NA	NA	NA
Geno.321	63	G	A	C	G	0.1338	-1.15	0.71	-1.62	0.10520
Geno.717	63	G	G	T	G	0.2364	0.73	0.57	1.28	0.20162
Geno.rare53	63	*	*	*	*	0.0075	4.40	3.12	1.41	0.15918
haplo.base62	63	G	G	C	G	0.6223	NA	NA	NA	NA
Geno.225	71	A	G	A	A	0.0916	0.18	0.83	0.22	0.82698
Geno.326	71	A	G	A	T	0.0174	5.81	1.74	3.34	0.00088
Geno.rare61	71	*	*	*	*	0.0095	-2.37	2.69	-0.88	0.37862
haplo.base70	71	A	G	G	A	0.8815	NA	NA	NA	NA
Geno.226	72	G	A	A	A	0.0142	2.53	2.03	1.25	0.21301
Geno.327	72	G	A	A	G	0.0777	-0.21	0.88	-0.24	0.81144
Geno.430	72	G	A	T	G	0.0174	5.91	1.74	3.40	0.00071
Geno.rare62	72	*	*	*	*	0.0037	3.97	4.41	0.90	0.36868
haplo.base71	72	G	G	A	G	0.8869	NA	NA	NA	NA
Geno.227	73	A	A	A	T	0.0133	3.16	2.05	1.54	0.12390
Geno.328	73	A	A	G	C	0.0775	-0.33	0.88	-0.38	0.70749
Geno.533	73	A	T	G	C	0.0174	5.93	1.74	3.41	0.00068
Geno.rare63	73	*	*	*	*	0.0042	5.37	4.50	1.19	0.23390
haplo.base72	73	G	A	G	C	0.8876	NA	NA	NA	NA
Geno.431	74	A	A	T	G	0.0130	2.87	2.11	1.36	0.17354
Geno.534	74	A	G	C	A	0.0337	0.18	1.34	0.14	0.89176
Geno.816	74	T	G	C	G	0.0175	5.98	1.73	3.45	0.00060
Geno.rare64	74	*	*	*	*	0.0047	6.17	4.42	1.39	0.16367
haplo.base73	74	A	G	C	G	0.9312	NA	NA	NA	NA

hap.freq: haplotype frequency; coef: coefficient; se: standard errors; t.stat: test statistic; p-val: haplotyep p-value.

3.6.4 Rare variants association analysis

3.6.4.1 NHWs

Rare variants association analyses showed significant associations with total cholesterol in NHWs and the association signal is more likely derived from rare variants with MAF<1% (**Table 47**).

Table 47. Rare variants association results with lipid traits in NHWs

LDL-C						
	MAF ≤0.01		MAF ≤0.02		MAF <0.05	
Test	**N.RV**	**P**	**N.RV**	**P**	**N.RV**	**P**
SKATO	31	0.1508	32	0.2309	41	0.1461
HDL-C						
	MAF ≤0.01		MAF ≤0.02		MAF <0.05	
Test	**N.RV**	**P**	**N.RV**	**P**	**N.RV**	**P**
SKATO	31	0.1222	32	0.1792	41	0.1206
TC						
	MAF ≤0.01		MAF ≤0.02		MAF <0.05	
Test	**N.RV**	**P**	**N.RV**	**P**	**N.RV**	**P**
SKATO	31	0.0088	32	0.0165	41	0.0498
TG						
	MAF ≤0.01		MAF ≤0.02		MAF <0.05	
Test	**N.RV**	**P**	**N.RV**	**P**	**N.RV**	**P**
SKATO	31	0.2975	32	0.3971	41	0.2951
ApoB						
	MAF ≤0.01		MAF ≤0.02		MAF <0.05	
Test	**N.RV**	**P**	**N.RV**	**P**	**N.RV**	**P**
SKATO	31	0.4424	32	0.5605	41	0.0574
ApoA1						
	MAF ≤0.01		MAF ≤0.02		MAF ≤0.05	
Test	**N.RV**	**P**	**N.RV**	**P**	**N.RV**	**P**
SKATO	31	0.1951	32	0.2628	41	0.3951

SKAT-O (optimal sequencing Kernel association test), N.RV (number of rare variants), P (p-value).

3.6.4.2 African Blacks

Rare variants with MAF<1% were associated with TG while less common variants with MAF (1-5%) were associated with apoA1 in Blacks (**Table 48**).

Table 48. Rare variants association results with lipid traits in Blacks

LDL-C						
	MAF (0.01)		MAF (0.02)		MAF (0.05)	
Test	**N.RV**	**P**	**N.RV**	**P**	**N.RV**	**P**
SKATO	29	0.2981	45	0.0826	61	0.2337
HDL-C						
	MAF (0.01)		MAF (0.02)		MAF (0.05)	
Test	**N.RV**	**P**	**N.RV**	**P**	**N.RV**	**P**
SKATO	29	0.6361	45	0.4110	61	0.3466
TC						
	MAF (0.01)		MAF (0.02)		MAF (0.05)	
Test	**N.RV**	**P**	**N.RV**	**P**	**N.RV**	**P**
SKATO	29	0.5931	45	0.3806	61	0.7164
TG						
	MAF (0.01)		MAF (0.02)		MAF (0.05)	
Test	**N.RV**	**P**	**N.RV**	**P**	**N.RV**	**P**
SKATO	29	0.0302	45	0.6291	61	0.2645
ApoB						
	MAF (0.01)		MAF (0.02)		MAF (0.05)	
Test	**N.RV**	**P**	**N.RV**	**P**	**N.RV**	**P**
SKATO	29	0.4289	45	0.5518	61	0.2123
ApoA1						
	MAF (0.01)		MAF (0.02)		MAF (0.05)	
Test	**N.RV**	**P**	**N.RV**	**P**	**N.RV**	**P**
SKATO	29	0.0756	45	0.0248	61	0.0213

SKAT-O (optimal sequencing Kernel association test), N.RV (number of rare variants), P (p-value).

4.0 DISCUSSION

Dyslipidemia is a major risk factor for CVD, which is the leading cause of death worldwide and apolipoproteins are considered major determinants of plasma lipoprotein–lipid variation. Therefore, genetic variation in genes coding for apolipoproteins could have significant impact on lipid metabolism and consequently may affect the CVD risk. The opposite effects of HDL-C and LDL-C on CVD risk have been well established where higher levels of HDL-C are considered antiatherogenic and higher levels of LDL-C are proatherogenic. Since a substantial portion of plasma lipid levels is under genetic control (Beekman et al., 2003; Lusis et al., 2004) and genetic variation in apolipoprotein genes impacts variation in plasma lipids, it is important to comprehensively examine the role of this genetic variation in relation to plasma lipid levels in the general population.

The *APOE-C1-C4-C2* gene cluster, encompassing 45 kb, is located on chromosome 19q13.32. The members of this gene cluster have arisen from the same ancestral gene family sharing high sequencing similarities and functional properties (Allan et al., 1995; Lauer et al., 1988; Li et al., 1988) and they play an important role in lipid metabolism. Multiple genome-wide association studies (GWAS) have confirmed the contribution of this gene cluster to plasma lipid variation and CVD risk. Although the established contribution of the *APOE* gene cluster is on LDL-related traits, recent GWAS meta-analysis reported multiple SNPs in this gene cluster to be associated with TG and HDL-C (Teslovich et al., 2010). However, all identified common

variants together explain small portion of lipid traits heritability, implying that there could be additional rare variants with larger effect sizes that contribute to the remaining unexplained heritability (Teslovich et al., 2010; Kathiresan et al., 2009; Weisglass-Volkov and Pajukanta, 2010). Therefore, sequencing candidate genes in selected subjects with extreme lipid traits increases the possibility of discovering potential functional rare variants. In this study, we have examined the role of both common and rare variants in relation to plasma lipoprotein-lipid levels.

We resequenced the *APOE-C1-C4-C2* gene cluster along with its hepatic control regions (*HCR-1* and *HCR-2*) in selected subjects with extreme HDL-C/TG distribution in order to examine the role of common and rare variants with plasma lipid levels in two epidemiologically well-characterized samples of U.S non-Hispanic Whites (NHWs) and African Blacks. In the un-sequenced intergenic regions, we used HapMap tagSNPs to cover the entire cluster. Since recent GWAS data indicate that this gene cluster affect both LDL and non-LDL traits, we examined the association of SNPs in this gene cluster with both LDL-related (LDL-C, TC and apoB) and non-LDL (HDL-C, TG and apoA1) traits for genotype-phenotype association analysis.

4.1 COMPARISON OF OUR SEQUENCING RESULTS WITH PUBLICLY AVAILABLE DATABASES

We compared our sequencing data to publicly available databases (SeattleSNPs and NCBI db SNPs databases). SeattleSNPs database sequenced these four genes (*APOE* = 5,491 bp, *APOC1* = 4,941 bp, *APOC4* = 4,510 bp, and *APOC2* = 6,438 bp) in 48 African Americans and 48 individuals with European descent. By comparison, we sequenced these four genes (*APOE* =

5,491 bp, *APOC1* = 6,687 bp, *APOC4* = 5,086 bp, and *APOC2* = 6,438 bp) along with their two hepatic control regions (*HCR-1 = 820 bp,* and *HCR-2 = 849 bp*) in 190 subjects with extreme HDL-C/TG levels in NHWs and African blacks.

Sequencing the four genes and their two hepatic control regions in 190 subjects with extreme lipid traits revealed a total of 230 variants (215 substitutions, 15 indels), of which 63 variants were common in both racial groups, 52 were NHW-specific and 115 were Black-specific. While 70% (160/230) of the identified variants in the sequencing subsets have been reported previously in public databases (NCBI build 138), the remaining 30% (70/230) are novel.

We observed all SeattleSNPs reported variants of *APOE* in our study, except two variants at nucleotides 545/rs1081103 (MAF=0.02) and 1522/rs769447 (MAF=0.04). In *APOC1,* we observed all the reported variants in SeattleSNPs database, except two common variants (4180/rs3925681 [MAF=0.28] and 4824/rs12721056 [MAF=0.27]) and 3 rare variants (1249/rs127210471 [MAF=0.02], 4298/rs12721044 [MAF=0.02] and 5338/rs12721050 [MAF=0.02]). In *APOC4*, we observed all the reported variants in SeattleSNPs database, except two variants (2753/rs12721106 [MAF=0.02] and 2886/rs12709883 [MAF=0.02]). In *APOC2*, we observed all the reported variants in SeattleSNPs database, except three variants (3289/rs12721058 [MAF=0.014), 3459/rs12721062 [MAF=0.02] and 3820/rs12709888 [MAF=0.28]).

We also compared our sequencing data to Chip bioinformatics database (hg19, build 131) and NCBI db SNPs (build 138). We observed all the reported variants in YRI (Yoruba in Ibadan, Nigeria) and CEU (Utah residents with Northern and Western European ancestry from the CEPH collection) populations, except *APOC2*-4852/rs5127 [MAF=0.3 in CEU and 0.17 in YRI] in

APOC2, which might be overlooked due to the nearby common deletion *APOC2*p4853/rs199828513.

We observed more variation in our study as compared to the publicly available databases (SeattleSNPs, Chip Bioinformatics, and NCBI db SNPs), which are more likely due to: 1) our sequencing sample size was larger, 2) we selected individuals based on their extreme low or high HDL-C/TG levels, and 3) we sequenced larger genomic regions of *APOC1* and *APOC4* as well as we sequenced the two hepatic control regions. Furthermore, we used African sample compared to African Americans used in SeattleSNPs that have considerable white admixture and could explain why we did not observe rare variants in our sample that were reported in African Americans. The lack of observation of some reported variants in our sample could also be due to the use of different software tools and algorithms applied in variant analyses and/or difficulties in annotation of particular sequencing regions.

4.2 ASSOCIATION WITH LIPID TRAITS

Association of Common Variants: To our knowledge, this is the first study that has considered both common and rare variants for genotype-phenotype association analysis in this gene cluster. A total of 70 variants (65 sequencing-identified, 5 HapMap intergenic tagSNPs) in NHWs and 108 variants (103 sequencing-identified, and 5 HapMap intergenic tagSNPs) in Blacks were successfully genotyped in the entire datasets of 623 NHWs and 788 African Blacks and were considered for the association analysis. The established association of *APOE*2* (rs7412) and *APOE*4* (rs426538) with lipid traits (Medina-Urrutia et al., 2004; Sanna et al., 2011; Lucatelli et al., 2011) was confirmed in our study in which *APOE*2* (rs7412) allele was associated with

lower LDL-C, TC, and apoB in NHWs (P=1.84E-07, P=9.50E-06, and P=9.70E-13, respectively) and Blacks (P=5.35E-07, P=0.0001, and P=0.035, respectively). On the other hand, *APOE*4* (rs426538) allele was associated with higher LDL-C, TC, and apoB in NHWs (P=0.0103, P=0.038, and P=0.0005, respectively) and with higher LDL-C in Blacks (P=0.0317). Although *APOE*4* did not show significant association with TC and apoB in Blacks, we observed similar trend of association as seen in NHWs.

Gene-based association analysis of all 63 variants in NHWs and 106 variants in Blacks with complete phenotype data revealed significant association with LDL-C in both racial groups (P=0.0004 in NHWs, P=0.0011 in Blacks) and TC (P=0.0002 in NHWs, P=0.036 in Blacks). On the other hand, gene-based analysis showed race-specific association for apoB (P=3.6E-05 in NHWs, P=0.23 in Blacks) and apoA1 (P=0.607 in NHWs, P=0.028 in Blacks).

Single-locus association analysis of 39 common/less common variants (MAF>1%) in NHWs and 79 common/less common variants (MAF>1%) in African Blacks revealed nominal significant association ($P < 0.05$) with at least one lipid trait for 20 variants in NHWs and 24 variants in Blacks. We observed 21 variants that showed association with LDL-related traits (LDL-C, TC, and apoB) independent of the effects of *APOE*2/E*4* alleles, and two of them (*APOE*560/rs449647 and *APOE*832/rs405509) were present in both racial groups. The first variant exerts opposite effect on LDL-C and TC in the two racial groups where it was associated with lowering effect in NHWs and elevating effect in Blacks. The second variant was observed to be associated with higher apoB in NHWs and higher LDL-C in Blacks. Six significant LDL-related traits variants showed association in NHWs only (*APOE*2440/rs769450, *APOC1*p5641/rs1064725, *APOC4*p2683/rs12721109, rs4803770, rs5112, and rs7259004) and 13 variants showed association in Blacks only (*APOE*1163/rs440446, *APOC1*p720/rs72654451,

*APOC4*p2623/rs5157, *APOC4*p4661/rs2288912, *APOC2*p2486/rs9304645, *APOC2*p3778/rs5120, *APOC2*p5815/rs10423208, *APOC2*p5922/rs10422888, *APOE*2269/rs6135770, *APOE*4036/rs769455, *APOC1*p5667/rs12721054, *APOC4*p4346/rs12709885, and *APOC2*p1540/rs75463753). Of the above-mentioned 21 LDL-traits associated variants, only 9 variants have been examined before in relation to lipid traits, including *APOE*560/rs449647, *APOE*832/rs405509, *APOE*1163/rs440446, rs4803770, rs7259004, *APOC1*p720/rs71962921, *APOC4*p2683/rs12721109, *APOC1*p5667/rs12721054 and *APOE*4036/rs769455. Previously *APOE*560/rs449647 was found to be associated with lowering effect on LDL-C in US-whites but increasing effect on LDL-C in African Americans (Ozturk et al., 2010). Interestingly, we have observed the identical opposite trend in our study on LDL-C and TC in the two racial groups. This variant is located in the promoter region and it could be functional by itself although it is unlikely to exert opposite effect in Whites and Blacks. Alternatively, this SNP could be in LD with a yet to be characterized functional SNP that has different LD pattern in Whites and Blacks.

*APOE*832/rs405509 was previously found to be associated with LDL-related traits (LDL-C, TC, and apoB) (Klos et al., 2006; Ken-Dror et al., 2010; Chasman et al., 2009), and in agreement, we observed this variant to be associated with apoB in NHWs and LDL-C in Blacks. *APOE*1163/rs440446 was earlier reported to be associated with CHD risk (Silander et al., 2008) and our current finding of its association with apoB indirectly supports the reported association as elevated apoB level is a risk indicator for CHD. Recently, Ken-Dror et al. (2010) have reported the association of rs4803770 with LDL-C and apoB. Likewise, we found this variant to be associated with LDL-C and TC in NHWs. Although its association with apoB did not achieve the significance level, we observed similar trend of association in NHWs (β=0.56; P=0.219). One

additional intergenic variant, rs7259004**,** was previously found to be associated with LDL-C, and apoB in US-whites (Ken-Dror et al., 2010). In our study, this variant also showed similar association with LDL-C and TC and a trend of association with apoB in NHWs. Previous studies have shown the association of *APOC1*p720/rs71962921 with elevating *APOC1* gene expression, dysbetalipoproteinemia, and higher risk of CVD and Alzheimer's disease (Gao et al., 2002; Shi et al., 2004; Retz et al., 2001). Moreover, this variant was found to be associated with lower TG and apoB and higher HDL-C among *APOE*3* carriers (Xu et al., 1999). In our study, *APOC1*p720/rs71962921 was associated with lower LDL-C and higher apoA1 in Blacks and with a similar trend of associations in NHWs. Although we did not observe significant association with apoB and HDL-C, we observed association with their corresponding lipoprotein and apolipoprotein, respectively. We have confirmed the previously reported association of a NHW-specific variant, *APOC4*p2683/rs12721109**,** with LDL-C (Jeemon et al., 2011), and apoB (Talmud et al., 2009) of observing significant association with LDL-C and apoB.

In our study, a Black-specific non-synonymous variant [*APOE*4036/rs769455 (Arg163Cys)] was associated with higher TG and lower LDL-C and TC. Previously the same variant was found to be associated with type III hyperlipoproteinemia in five Latin-American family members (Havel et al., 1983; Rall et al., 1989). Although *APOC1*p5667/rs12721054 was previously found to be associated with TG (Coram et al., 2013)**,** we found its association with TG as well as with LDL-related traits.

The remaining 12 LDL-traits associated variants found in this study (*APOE*2440/rs769450, *APOC2*p1357C4p4661/rs2288912, rs5112, *APOC2*p3778/rs5120, *APOC4*p2623/rs5157, *APOE*2269/rs6135770, *APOC1*p5641/rs1064725, *APOC2*p1042C4p4346/rs12709885, *APOC2*p1540C4p4844/rs75463753,

*APOC2*p2486/rs9304645, *APOC2*p5815/rs10423208, and *APOC2*p5922/rs10422888) have not been examined before in relation to lipid traits and thus our observations should be considered provisional until replicated in independent samples. *APOE*2440/rs769450 was observed to be associated with TG and LDL-C only in NHWs without significant effect on any other lipid traits in Blacks, which is more likely due to its correlation with other functional variants in this racial group. Its RegulomeDB score of 5 is only suggestive of affecting regulatory function. Similarly, *APOC2*p1357C4p4661/rs2288912 was found to be associated with LDL-C, TC, and apoB in Blacks without any effect on lipid traits in NHWs. This variant seems to be functional because of its location in the flanking region between *APOC4* and *APOC2* genes and its RegulomeDB score of 1a, indicating its involvement in gene regulation and gene expression. However, this seems counterintuitive that apparently a functional variant shows significant effect on lipid trait in one racial group but not in the other. Alternatively, this variant may directly be associated with CHD, although we do not have this data to confirm our hypothesis. Although this intergenic variant, rs5112**,** was observed in both population groups, it was associated with TC in NHWs only, which could be due to its different LD with a functional variant(s) in the two populations. However, this variant was not in LD with any variants in this gene cluster that showed association with TC.

Similarly, *APOC2*p3778/rs5120 and *APOC4*p2623/rs5157 variants were present in both population groups and they showed significant association with LDL-related traits in Blacks only but not in the other racial group. While both of these variants were in moderate LD (r^2=0.30) in Blacks where they showed significant associations, they were in strong LD (r^2=0.93) in NHWs implying that the strong correlation between them lessens their significant effect in NHWs suggesting that their effect on LDL-related traits in Blacks is independent of each other. Another variant, *APOE*2269/rs6135770, is in complete LD with a functional variant,

*APOE*4036/rs769455, and thus its association with LDL-C and TC is not independent. *APOC1*p5641/rs1064725 located in the 3' flanking region of *APOC1* and it is not in LD with any other variant in this gene cluster and thus it could be functional by itself. Alternatively, its significant association with LDL-C, and TC in NHWs could be mediated by tagging another functional variant present outside of the examined genomic region in this racial group, although we do not have direct evidence to support this hypothesis.

For the remaining five Black-specific variants, *APOC2*p1042C4p4346/rs12709885 was observed to be associated with apoB, *APOC2*p1540C4p4844/rs75463753 with LDL-C and TC, and *APOC2*p2486/rs9304645, *APOC2*p5815/rs10423208, and *APOC2*p5922/rs10422888 with LDL-C. Their genomic locations in introns or flanking regions along with their RegulomeDB scores of 4-5 suggest their potential involvement in gene regulation process. Since they were not in LD with each other, their association with LDL-related traits could be independent of each other.

Although the major contribution of SNPs in the *APOE* gene cluster was with LDL-related traits, we also observed multiple associations with non-LDL traits (HDL-C, apoA1, and TG). Two variants in NHWs (*APOE*1575/rs769448, and *HCR2*p188/rs35136575), and two variants in Blacks (rs439401, and *APOC1*p3573/rs10424339) showed significant association with HDL-C. Moreover, four variants showed significant association with apoA1, including two in NHWs (*HCR2*p188/rs35136575, and rs7259004), and two in Blacks (*APOC1*p720/rs71962921, and *APOC4*p4346/rs12709885). Six variants showed significant association with TG in NHWs (*APOE*832/rs405509, *APOE*1163/rs440446, *APOE*2440/rs769450, *APOC1*p2041/rs3826688, *APOC4*p2683/rs12721109, and rs439401). While the first three TG-associated variants (*APOE*832/rs405509, *APOE*1163/rs440446, and

*APOE*2440/rs769450) were in modest LD with each other ($0.60 < r^2 < 0.61$), these two variants (*APOC1*p2041/rs3826688 and rs439401) were in strong LD (r^2=0.94). In Blacks, seven variants showed significant association with TG (*APOE*73/rs1081101, *APOE*4036/rs769455, *APOC1*p5667/rs12721054, *APOC1*p5926/rs56131196, *APOC4*p757/rs12721105, *APOC4*p2640/rs5158, and *APOC2*p2935/rs11879392). While two of them (*APOC1*p5667/rs12721054 and *APOC1*p5926/rs56131196) were in modest LD (r^2=0.47), *APOC4*p2640/rs5158, and *APOC2*p2935/rs11879392 were in strong LD (r^2=0.84). The RegulomeDB score of the strongly correlated variants is 2b, which is highly suggestive of their regulatory function. Eight of the 13 TG-associated variants have been previously reported to be associated with TG, including *APOE*832/rs405509 (Chasman et al., 2009), *APOE*1163/rs440446 (Silander et al., 2008), *APOE*4036/rs769455 (Havel et al., 1983; Rall et al., 1989), rs439401 (Jeemon et al., 2011; Chasman et al., 2009), *APOC1*p5667/rs12721054 (Coram et al., 2013), *APOC4*p2683/rs12721109 (Jeemon et al., 2011), rs7259004 (Ken-Dror et al., 2010), and *APOC1*p720/rs71962921 (Xu et al., 1999). One of these variants (rs439401) has shown genome-wide significant association with TG (Chasman et al., 2009; Teslovich et al., 2010; Jeemon et al., 2011), which we replicated in NHWs; the same variant also showed association with HDL-C in Blacks. We found significant association of *HCR2*p188/rs35136575 with HDL-C, and apoA1 in NHWs, which is consistent with its reported association with these traits in Whites (Klos et al., 2008). In concordance with previous findings showing association of rs7259004 with apoA1 (Ken-Dror et al., 2010), and association of *APOC1*p720/rs71962921 with HDL-C (Xu et al., 1999), we observed the same associations in NHWs. The associations of remaining ten variants with non-LDL related traits should be considered provisional until they are validated in independent studies

Association of Rare Variants: Our observations confirm the significant contribution of rare variants to plasma lipid traits variation as it has been shown previously for some lipid genes, including *ABCA1*, *LIPG*, *PCSK9*, *ANGPTL3*, *ANGPTL4*, *APOA5*, *GCKR*, *LPL*, and *APOB* where rare variants were associated with dyslipidemia and were accumulated in patients with extreme lipid traits (Evans et al., 2011; Johansen et al., 2010; Johansen and Hegele, 2012; Cohen et al., 2004; Cohen et al., 2005; Kotowski et al., 2006; Romeo et al., 2007; Pollin et al., 2008). In addition to the significant association of common variants with lipid traits, rare and uncommon variants showed significant association with TC in NHWs (P=0.008) and with TG (P=0.030) and apoA1 (P=0.021) in Blacks in SKAT-O analysis of rare variants. The significant signal with TC in NHWs is more likely derived from 4 rare variants with MAF<1% that showed nominal association with TC in the single-locus association analysis: *APOC1*p3494 located in intron 3 (P=0.00044), *APOC4*p1150/rs148247675 located in intron 1 (P=0.00043, RegulomeDB score = 5), *APOE*4310/rs199768005 [Val254Glu] (P=0.01279, Regulome DB score = 5), and *APOC2*p2870 located in intron 1 (P=0.00179, Regulome DB score = 4). As expected, all these four rare variants that showed significant single-locus association with TC also were associated with LDL-C in NHWs. Of the 3 intronic variants mentioned above, two are predicted to affect gene regulation process based on their Regulome DB scores of 4 and 5. The non-synonymous variant has been reported previously to be associated with type III hyperlipoproteinemia (van den Maagdenberg et al., 1993). In Blacks, the association signal with TG is more likely derived either from a synonymous variant, *APOC2*p708C4p4012 [APOC4-exon 3, Lys124Lys] (P=0.038, Regulome DB score = 6), or *APOC2*p5512/rs12721064 located in 3'flanking region (P=0.0297, Regulome DB score = 6) with MAF<1% that were significant in single-locus analysis. The association signal with apoA1 is seemed to be derived from either

*HCR1*p424/rs117664574 (P=0.048, Regulome DB score=4) located in the first hepatic control region, or *APOC2*p1042C4p4346/rs12709885, located in the flanking region between *APOC4* and *APOC2* genes (P=0.00071, Regulome DB score=5) with MAF<2%. Since their Regulome DB score is only suggestive of their involvement in the gene regulatory process, further studies are warranted to elucidate their role in affecting plasma TG and apoA1 levels.

Haplotype Association: Haplotype-based association analysis is more powerful than the single-locus analysis to detect the cumulative effect for set of markers (Liu et al., 2008) because the power of single-marker analysis in detection the significance signal depends primarily on the LD structure between the tested marker and the disease-causing marker. In this study, haplotype-based association analysis confirmed the single-locus association results and was more powerful in detecting functionally relevant regions that did not have significant single-locus effect. For example, window 52 that mapped to *APOC4* variation showed significant global p-value with apoA1 in NHWs (P=0.042), but none of the variants included in this window had significant effect in single-locus analysis. The significant haplotype association in NHWs with apoA1 in window 52 seems to be mediated by a non-synonymous variant rs5167/Leu96Arg in *APOC4* (P=0.672 in single-locus analysis), a previously reported variant to be associated with HDL-C and apoA1 (Ken-Dror et al., 2010). This non-synonymous variant is mapped to *APOC4*-exon3 that results in amino acid change and could affect the protein function. Single-locus analysis could not detect its weak effect on apoA1 but haplotype-based association analysis was more powerful in detecting its joint effect on apoA1. Similarly, we observed three windows to be associated with HDL-C (window 41, 42, and 43) and apoA1 (window 41, and 43) in Blacks where none of the variants included in these windows showed significant association in single-locus analysis. However, two of the variants mapped to this region (rs7259004, and

*HCR2*p188/rs35136575) showed significant association with HDL-C/apoA1 in the single-locus association analysis. The first variant: rs7259004 was associated with apoA1 (P=0.046) and the second one: *HCR2*p188/rs35136575 was associated with HDL-C (P=0.033) and apoA1 (P=0.049) in NHWs and they could contribute to the significant signal in haplotype association analysis that was found in Blacks.

4.3 CONCLUSIONS AND FURTHER DIRECTIONS

Coronary heart disease continues to be a leading cause of premature mortality and co-morbidity in western countries and dyslipidemia with elevated level of LDL-C and decreased level of HDL-C is a major risk factor for CHD. As compared to *APOE* polymorphisms, little attention has been paid to the role of *APOE-C1-C4-C2* genetic variants in relations to plasma lipid levels. To our knowledge, this is the first comprehensive association study targeting the four genes in the *APOE* gene cluster on chromosome 19q13.32 to characterize both common and rare variants and to evaluate their associations with major lipid traits in two distinct racial groups.

In addition to the established association of *APOE* variation with LDL-C and apoB, we observed multiple variants to be associated with the other lipid traits, including TG, HDL-C, and apoA1. Moreover, in addition to the significant contribution of common variants, we observed rare and less common variants to be associated with lipid traits, confirming the significant contribution of rare variation in modulating complex lipid phenotype. Our findings confirm the complicated genetic architecture of complex lipid traits and future evaluation of the complex

interaction with other genetic and environmental factors would provide better insight of the genetic basis of complex traits.

Strengths of our study include the use of two extreme lipid groups for resequencing from two racial groups and then genotyping the entire sample sets for genotype-phenotype association analyses. Limitations of our study include the use of relatively small sample sizes in two extreme lipid groups and not adjusting p-values for multiple comparisons. Many of our significant findings with rare variants should be considered provisional until replicated in independent and larger data sets.

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